

SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 70%.

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 28, 2004, 08:30:53 ; Search time 12 Seconds
(without alignments)
3.585 Million cell updates/sec

Title: US-10-798-923A-4
Perfect score: 3405
Sequence: 1 cgcccaaccgaattcaag.....acacactcaaaaaaaaaa 3405

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 304 seqs, 6318 residues

Total number of hits satisfying chosen parameters: 608

Minimum DB seq length: 8
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 304 summaries

Database : rge4.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	28	0.8	29	AR038876	ACCESSION:AR038876
C 2	27	0.8	27	AR135179	ACCESSION:AR135179
C 3	27	0.8	27	BD274686	ACCESSION:BD274686
C 4	27	0.8	27	AR382343	ACCESSION:AR382343
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C 6	27	0.8	27	AX419081	ACCESSION:AX419081
C 7	26	0.8	26	BD274751	ACCESSION:BD274751
C 8	26	0.8	26	BD274754	ACCESSION:BD274754
C 9	26	0.8	26	AX419075	ACCESSION:AX419075
C 10	26	0.8	26	AX419077	ACCESSION:AX419077
C 11	26	0.8	26	AX419084	ACCESSION:AX419084
C 12	25.4	0.7	27	AX419082	ACCESSION:AX419082
C 13	25.4	0.7	32	E43996	ACCESSION:E43996
C 14	25.2	0.7	32	E43995	ACCESSION:E43995
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C 18	25	0.7	25	BD274736	ACCESSION:BD274736
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C 26	25	0.7	25	AX419060	ACCESSION:AX419060
C 27	25	0.7	25	AX419061	ACCESSION:AX419061
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C 77	17.4	0.5	21	1	AX096971	ACCESSION:AX096971
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C 79	17.2	0.5	24	1	AX445931	ACCESSION:AX445931
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C 104	15.8	0.5	21	1	AX286309	ACCESSION:AX286309
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C 106	15.8	0.5	22	1	BOVDIK31	ACCESSION:D44532

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C 113	15.4	0.5	22	1	AX217230	ACCESSION: AX217230	186	14.8	0.4	19	1	BD173560	ACCESSION: BD173560
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C 123	15.4	0.5	20	1	BD138319	ACCESSION: BD138319	C 196	14.8	0.4	20	1	AR136443	ACCESSION: AR136443
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C 126	15.4	0.5	21	1	AX097058	ACCESSION: AX097058	C 199	14.8	0.4	20	1	AR158980	ACCESSION: AR158980
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RESULT 1	
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LOCUS	29 bp DNA linear PAT 29-SEP-1999
DEFINITION	Sequence 33 from patent US 5807703.
ACCESSION	AR038876
VERSION	AR038876.1 GI:5958239
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 29) Jacobs,K., McCoy,J.M., LaVallie,E.R., Racie,L.A., Merberg,D., Treacy,M., Evans,C., Spaulding,V. and Bowman,M. Secreted proteins and polynucleotides encoding them Patent: US 5807703-A 33 15-SEP-1998; Location/Qualifiers
TITLE	
JOURNAL	
FEATURES	

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Query Match
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Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 27 GAGATAGTTGGGTGGTGGAACTGTG 1

RESULT 4
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Sequence 13 from patent US 6610497.
ACCESSION
AR382343
VERSION
AR382343.1 GI:40090760
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 27)
AUTHORS
Acton, S.L., Robison, K.E. and Hsieh, F.Y.
TITLE
Angiotensin converting enzyme homolog and therapeutic and
diagnostic uses therefor
JOURNAL
Patent: US 6610497-A 13 26-AUG-2003;
LOCATION/Qualifiers
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Query Match
Best Local Similarity 0.8%; Score 27; DB 1; Length 27;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 27 GAGATAGTTGGGTGGTGGAACTGTG 1

RESULT 5
AX418994/c
LOCUS
DEFINITION
Sequence 13 from Patent WO0212471.
ACCESSION
AX418994
VERSION
AX418994.1 GI:21523784
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Acton, S., Robison, K.E. and Hsieh, F.Y.
TITLE
Angiotensin converting enzyme homolog and uses therefor
JOURNAL
Patent: WO 0212471-A 13 14-FEB-2002;
MILLENNIUM Pharmaceuticals, Inc. (US)
LOCATION/Qualifiers
1. .27
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/db_xref="taxon:32630"
/note="motifs"

Query Match
Best Local Similarity 0.8%; Score 27; DB 1; Length 27;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1550 GAGATAGTTGGGTGGTGGAACTGTG 1576
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Db 27 GAGATAGTTGGGTGGTGGAACTGTG 1

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="motifs"

Query Match
Best Local Similarity 100.0%; Pred. No. 10;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3242 GTTCTCTAACTGGAGTGAATGAAA 3268
    |||||
Db 1 GTTCTCTAACTGGAGTGAATGAAA 27

Query Match
Best Local Similarity 100.0%; Pred. No. 10;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3242 GTTCTCTAACTGGAGTGAATGAAA 3268
    |||||
Db 1 GTTCTCTAACTGGAGTGAATGAAA 27

RESULT 6
AX419081
LOCUS
DEFINITION
Sequence 100 from Patent WO0212471.
ACCESSION
AX419081
VERSION
AX419081.1 GI:21523855
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Acton, S., Robison, K.E. and Hsieh, F.Y.
TITLE
Angiotensin converting enzyme homolog and uses therefor
JOURNAL
Patent: WO 0212471-A 100 14-FEB-2002;
MILLENNIUM Pharmaceuticals, Inc. (US)
LOCATION/Qualifiers
1. .27
source
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="motifs"

Query Match
Best Local Similarity 100.0%; Pred. No. 10;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3242 GTTCTCTAACTGGAGTGAATGAAA 3268
    |||||
Db 1 GTTCTCTAACTGGAGTGAATGAAA 27

RESULT 7
BD274751
LOCUS
DEFINITION
Angiotensin converting enzyme homolog and its use.
ACCESSION
BD274751
VERSION
BD274751.1 GI:33084519
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 26)
AUTHORS
Acton, L.S., Robison, K.E. and Hsieh, F.Y.
TITLE
Angiotensin converting enzyme homolog and its use
JOURNAL
Patent: JP 2002525108-A 68 13-AUG-2002;
MILLENNIUM PHARMACEUTICALS INC
COMMENT
OS Homo sapiens (human)
PN JP 2002525108-A/68
PD 13-AUG-2002
PR 29-SEP-1999 JP 2000572346
PI LAURENE SUSAN ACTON, KEITH EARL, ROBISON, FRANK Y HSIEH PC
C12N15/09, A61K45/00, A61P9/04, A61P9/10, A61P9/12, A61P13/PC
12,
PC A61P43/00, A61P43/00, C12N9/50, C12Q1/37, G01N33/15, G01N33/50//PC
(C12N9/50, C12R1:91), C12N15/00
CC Angiotensin converting enzyme homolog and its use FH Key
LOCATION/Qualifiers
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/db_xref="taxon:9606"

Query Match
Best Local Similarity 100.0%; Pred. No. 13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2844 AGTTGAAACAGGATATATCATTTGG 2869
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Db      1 AGTTGAAAACAGGATATATCATTCGG 26
RESULT 8
LOCUS   BD274754 26 bp DNA linear PAT 17-JUL-2003
DEFINITION Angiotensin converting enzyme homolog and its use.
ACCESSION BD274754
VERSION   BD274754.1 GI:33084522
KEYWORDS  JP 2002525108-A/71.
SOURCE   synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS  Acton,L.S., Robison,K.E. and Hsieh,F.Y.
TITLE     Angiotensin converting enzyme homolog and its use
JOURNAL   Patent: JP 2002525108-A 71 13-AUG-2002;
MILLENNIUM PHARMACEUTICALS INC
COMMENT   OS Artificial Sequence
PN JP 2002525108-A/71
PD 13-AUG-2002
PF 29-SEP-1999 JP 2000572346
PR 30-SEP-1998 US 09/163648
PI LAURENE SUSAN ACTON,KEITH EARL ROBISON,FRANK Y HSIEH PC
C12N15/09,A61K45/00,A61P9/04,A61P9/10,A61P9/12,A61P13/ PC
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PC A61P43/00,A61P43/00,C12N9/50,C12Q1/37,G01N33/15,G01N33/50// PC
CC (C12N9/50,C12R1:91),C12N15/00
FH Key Location/Qualifiers
FT source 1..26
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source
1..26
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.8%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred.No.13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3045 GCCTACAGTGATGTTTGGATCGATC 3070
Db 26 GCCTACAGTGATGTTTGGATCGATC 1

RESULT 9
LOCUS   AX419075 26 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 94 from Patent WO0212471.
ACCESSION AX419075
VERSION   AX419075.1 GI:21523849
KEYWORDS  synthetic construct
SOURCE   synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS  Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE     Angiotensin converting enzyme homolog and uses therefor
JOURNAL   Patent: WO 0212471-A 94 14-FEB-2002;
MILLENNIUM PHARMACEUTICALS, INC. (US)
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/db_xref="taxon:32630"
/note="motifs"

Query Match 0.8%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred.No.13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
LOCUS   AX419075 26 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 94 from Patent WO0212471.
ACCESSION AX419075
VERSION   AX419075.1 GI:21523849
KEYWORDS  synthetic construct
SOURCE   synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS  Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE     Angiotensin converting enzyme homolog and uses therefor
JOURNAL   Patent: WO 0212471-A 103 14-FEB-2002;
MILLENNIUM PHARMACEUTICALS, INC. (US)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="motifs"

Query Match 0.8%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred.No.13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3045 GCCTACAGTGATGTTTGGATCGATC 3070
Db 26 GCCTACAGTGATGTTTGGATCGATC 1

RESULT 10
LOCUS   AX419077 26 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 96 from Patent WO0212471.
ACCESSION AX419077
VERSION   AX419077.1 GI:21523851
KEYWORDS  synthetic construct
SOURCE   synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS  Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE     Angiotensin converting enzyme homolog and uses therefor
JOURNAL   Patent: WO 0212471-A 96 14-FEB-2002;
MILLENNIUM PHARMACEUTICALS, INC. (US)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="motifs"

Query Match 0.8%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred.No.13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 58 CTAGGGAAGTCATTCAGTGGATGTC 83
Db 1 CTAGGGAAGTCATTCAGTGGATGTC 26

RESULT 11
LOCUS   AX419084 26 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 103 from Patent WO0212471.
ACCESSION AX419084
VERSION   AX419084.1 GI:21523858
KEYWORDS  synthetic construct
SOURCE   synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS  Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE     Angiotensin converting enzyme homolog and uses therefor
JOURNAL   Patent: WO 0212471-A 103 14-FEB-2002;
MILLENNIUM PHARMACEUTICALS, INC. (US)
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source
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="motifs"

Query Match 0.8%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred.No.13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3045 GCCTACAGTGATGTTTGGATCGATC 3070
Db 26 GCCTACAGTGATGTTTGGATCGATC 1

RESULT 12
LOCUS   AX419082 27 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 101 from Patent WO0212471.
ACCESSION AX419082
VERSION   AX419082.1 GI:21523856

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KEYWORDS
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE
1
AUTHORS     Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE       Angiotensin converting enzyme homolog and uses therefor
JOURNAL     Patent: WO 0212471-A 101 14-FEB-2002;
            Millennium Pharmaceuticals, Inc. (US)
FEATURES
source
1. .27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="motifs"

Query Match      0.7%; Score 25.4; DB 1; Length 27;
Best Local Similarity 96.3%; Pred. No. 17;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3242 GTTCTCTAACTGGAGTGAATGAAA 3268
Db      1 GTTCTCTAACTGAGAGTGAATGAAA 27

RESULT 13
LOCUS      E43996
DEFINITION ACE-analogous gene.
ACCESSION E43996
VERSION   E43996.1 GI:18629199
KEYWORDS  JP 2001046072-A/10.
SOURCE    unidentified
ORGANISM  unclassified.
REFERENCE 1 (bases 1 to 32)
AUTHORS   Sugano,S. and Komatsu,T.
TITLE     ACE-analogous gene
JOURNAL   Patent: JP 2001046072-A 10 20-FEB-2001;
            OTSUKA PHARMACEUT CO LTD
COMMENT   OS Unidentified
          PN JP 2001046072-A/9
          PD 20-FEB-2001
          PF 06-AUG-1999 JP 1999223892
          PR
          PI SUMIO SUGANO,TAKAMI KOMATSU
          PC C12N15/09,A61K31/00,A61K31/7088,A61K38/00,A61K38/55,A61K39/395, PC
          A61K39/395,
          PC A61K39/395,A61K48/00,A61P9/12,C07K14/47,C07K16/08,C12N1/15, PC
          C12N1/19,
          PC C12N1/21,C12N5/10,C12Q1/68,G01N33/53,C12N15/00,A61K37/02, PC
          A61K37/64,
          PC C12N5/00
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          FH Key Location/Qualifiers
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source
1. .32
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match      0.7%; Score 25.2; DB 1; Length 32;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      98 GGGACGATGTCAGCTCTTCCTGGCTCCTT 127
Db      3 GGTCCATGTCAGCTCTTCCTGGCTCCTT 32

RESULT 14
LOCUS      E43995
DEFINITION ACE-analogous gene.
ACCESSION E43995
VERSION   E43995.1 GI:18629198
KEYWORDS  JP 2001046072-A/9.
SOURCE    unidentified
ORGANISM  unclassified.
REFERENCE 1 (bases 1 to 32)
AUTHORS   Sugano,S. and Komatsu,T.
TITLE     ACE-analogous gene
JOURNAL   Patent: JP 2001046072-A 9 20-FEB-2001;
            OTSUKA PHARMACEUT CO LTD
COMMENT   OS Unidentified
          PN JP 2001046072-A/9
          PD 20-FEB-2001
          PF 06-AUG-1999 JP 1999223892
          PR
          PI SUMIO SUGANO,TAKAMI KOMATSU
          PC C12N15/09,A61K31/00,A61K31/7088,A61K38/00,A61K38/55,A61K39/395, PC
          A61K39/395,
          PC A61K39/395,A61K48/00,A61P9/12,C07K14/47,C07K16/08,C12N1/15, PC
          C12N1/19,
          PC C12N1/21,C12N5/10,C12Q1/68,G01N33/53,C12N15/00,A61K37/02, PC
          A61K37/64,
          PC C12N5/00
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          FH Key Location/Qualifiers
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match      0.7%; Score 25.2; DB 1; Length 32;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      98 GGGACGATGTCAGCTCTTCCTGGCTCCTT 127
Db      3 GGTCCATGTCAGCTCTTCCTGGCTCCTT 32

RESULT 15
LOCUS      BD274704
DEFINITION Angiotensin converting enzyme homolog and its use.
ACCESSION BD274704
VERSION   BD274704.1 GI:33084472
KEYWORDS  JP 2002525108-A/21.
SOURCE    synthetic construct
ORGANISM  synthetic construct
          artificial sequences.
REFERENCE 1 (bases 1 to 25)
AUTHORS   Acton,L.S., Robison,K.E. and Hsieh,F.Y.
TITLE     Angiotensin converting enzyme homolog and its use
JOURNAL   Patent: JP 2002525108-A 21 13-AUG-2002;
            MILLENNIUM PHARMACEUTICALS INC
COMMENT   OS Artificial Sequence
          PN JP 2002525108-A/21
          PD 13-AUG-2002
          PF 29-SEP-1999 JP 2000572346
          PR 30-SEP-1998 US 09/163648
          PI LAURENE SUSAN ACTON,KEITH EARL ROBISON,FRANK Y HSIEH PC
          C12N15/09,A61K45/00,A61P9/04,A61P9/10,A61P9/12,A61P13/ PC
          12, A61P43/00,A61P43/00,C12N9/50,C12Q1/37,G01N33/15,G01N33/50// PC
          PC C12N9/50,C12R1/91,C12N15/00

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    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
Query Match
  Best Local Similarity 0.7%; Score 25; DB 1; Length 25;
  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 905 GGTGATATGTGGGTAGATTGGA 929
Db 1 GGTGATATGTGGGTAGATTGGA 25
RESULT 16
BD274708 25 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Angiotensin converting enzyme homolog and its use.
ACCESSION BD274708
VERSION BD274708.1 GI:33084476
KEYWORDS JP 2002525108-A/25.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
  1 (bases 1 to 25)
  Acton,L.S., Robison,K.E. and Hsieh,F.Y.
  Angiotensin converting enzyme homolog and its use
  Patent: JP 2002525108-A 25 13-AUG-2002;
  MILLENNIUM PHARMACEUTICALS INC
COMMENT
  OS Artificial Sequence
  PN JP 2002525108-A/25
  PD 13-AUG-2002
  PF 30-SEP-1999 JP 2000572346
  PR 30-SEP-1998 US 09/163648
  PI LAURENE SUSAN ACTON,KEITH EARL ROBISON,FRANK Y HSIEH PC
  C12N15/09,A61K45/00,A61P9/04,A61P9/10,A61P9/12,A61P13/ PC
  12,
  PC A61P43/00,A61P43/00,C12N9/50,C12Q1/37,G01N33/15,G01N33/50// PC
  (C12N9/50,C12R1:91),C12N15/00
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  FH Key Location/Qualifiers
  FT source
    1..25
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
Query Match
  Best Local Similarity 100.0%; Pred.No.15;
  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1294 TGAAGGATTCCATGAAGCTGTTGGG 1318
Db 25 TGAAGGATTCCATGAAGCTGTTGGG 1
RESULT 18
BD274736 25 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Angiotensin converting enzyme homolog and its use.
ACCESSION BD274736
VERSION BD274736.1 GI:33084504
KEYWORDS JP 2002525108-A/53.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
  1 (bases 1 to 25)
  Acton,L.S., Robison,K.E. and Hsieh,F.Y.
  Angiotensin converting enzyme homolog and its use
  Patent: JP 2002525108-A 53 13-AUG-2002;
  MILLENNIUM PHARMACEUTICALS INC
COMMENT
  OS Artificial Sequence
  PN JP 2002525108-A/53
  PD 13-AUG-2002
  PF 29-SEP-1999 JP 2000572346
  PR 30-SEP-1998 US 09/163648
  PI LAURENE SUSAN ACTON,KEITH EARL ROBISON,FRANK Y HSIEH PC
  C12N15/09,A61K45/00,A61P9/04,A61P9/10,A61P9/12,A61P13/ PC
  12,
  PC A61P43/00,A61P43/00,C12N9/50,C12Q1/37,G01N33/15,G01N33/50// PC
  (C12N9/50,C12R1:91),C12N15/00
  CC Description of Artificial Sequence: primer
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    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
Query Match
  Best Local Similarity 100.0%; Pred.No.15;
  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1088 GAAATTCATGCTAACGACCCAG 1112
Db 1 GAAATTCATGCTAACGACCCAG 25
RESULT 17
BD274713/c 25 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Angiotensin converting enzyme homolog and its use.
ACCESSION BD274713
VERSION BD274713.1 GI:33084481
KEYWORDS JP 2002525108-A/30.
SOURCE synthetic construct
ORGANISM artificial sequences.

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QY 2990 GTCAAGGATGACATGCTTTCTTCAC 3014
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 Db 1 GTCAAGGATGACATGCTTTCTTCAC 25

RESULT 19
 BD274737/c
 LOCUS BD274737 25 bp DNA linear PAT 17-JUL-2003
 DEFINITION Angiotensin converting enzyme homolog and its use.
 ACCESSION BD274737
 VERSION BD274737.1 GI:33084505
 KEYWORDS JP 2002525108-A/54.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 25)
 ACTON, L.S., ROBISON, K.E. and HSIEH, F.Y.
 TITLES Angiotensin converting enzyme homolog and its use
 JOURNAL Patent: JP 2002525108-A 54 13-AUG-2002;
 COMMENT MILLENNIUM PHARMACEUTICALS INC

OS Artificial Sequence
 PN JP 2002525108-A/54
 PD 13-AUG-2002
 PF 29-SEP-1999 JP 2000572346
 PR 30-SEP-1998 US 09/163648
 PI LAURENE SUSAN ACTON, KEITH EARL ROBISON, FRANK Y HSIEH PC
 C12N15/09, A61K45/00, A61P9/04, A61P9/10, A61P9/12, A61P13/ PC
 12, A61P43/00, A61P43/00, C12N9/50, C12Q1/37, G01N33/15, G01N33/50// PC
 (C12N9/50, C12R1:91), C12N15/00
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Query Match 0.7%; Score 25; DB 1; Length 25;
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 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3049 ACAGTGTGTTTGGATCGATCATG 3073
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 Db 25 ACAGTGTGTTTGGATCGATCATG 1

RESULT 20
 BD274738
 LOCUS BD274738 25 bp DNA linear PAT 17-JUL-2003
 DEFINITION Angiotensin converting enzyme homolog and its use.
 ACCESSION BD274738
 VERSION BD274738.1 GI:33084506
 KEYWORDS JP 2002525108-A/55.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 25)
 ACTON, L.S., ROBISON, K.E. and HSIEH, F.Y.
 TITLES Angiotensin converting enzyme homolog and its use
 JOURNAL Patent: JP 2002525108-A 55 13-AUG-2002;
 COMMENT MILLENNIUM PHARMACEUTICALS INC

OS Artificial Sequence
 PN JP 2002525108-A/55
 PD 13-AUG-2002
 PF 29-SEP-1999 JP 2000572346
 PR 30-SEP-1998 US 09/163648
 PI LAURENE SUSAN ACTON, KEITH EARL ROBISON, FRANK Y HSIEH PC
 C12N15/09, A61K45/00, A61P9/04, A61P9/10, A61P9/12, A61P13/ PC
 12, A61P43/00, A61P43/00, C12N9/50, C12Q1/37, G01N33/15, G01N33/50// PC

(C12N9/50, C12R1:91), C12N15/00
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
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Query Match 0.7%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2712 CTGCTCTCGATTGACTTCTGTTTC 2736
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 Db 1 CTGCTCTCGATTGACTTCTGTTTC 25

RESULT 21
 BD274739/c
 LOCUS BD274739 25 bp DNA linear PAT 17-JUL-2003
 DEFINITION Angiotensin converting enzyme homolog and its use.
 ACCESSION BD274739
 VERSION BD274739.1 GI:33084507
 KEYWORDS JP 2002525108-A/56.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 25)
 ACTON, L.S., ROBISON, K.E. and HSIEH, F.Y.
 TITLES Angiotensin converting enzyme homolog and its use
 JOURNAL Patent: JP 2002525108-A 56 13-AUG-2002;
 COMMENT MILLENNIUM PHARMACEUTICALS INC

OS Artificial Sequence
 PN JP 2002525108-A/56
 PD 13-AUG-2002
 PF 29-SEP-1999 JP 2000572346
 PR 30-SEP-1998 US 09/163648
 PI LAURENE SUSAN ACTON, KEITH EARL ROBISON, FRANK Y HSIEH PC
 C12N15/09, A61K45/00, A61P9/10, A61P9/12, A61P13/ PC
 12, A61P43/00, A61P43/00, C12N9/50, C12Q1/37, G01N33/15, G01N33/50// PC
 (C12N9/50, C12R1:91), C12N15/00
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 FH Key Location/Qualifiers
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 FT /organism='Artificial Sequence'.
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 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

Query Match 0.7%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2776 AAAGTGTGTTTGGTCTCAGGC 2800
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 Db 25 AAAGTGTGTTTGGTCTCAGGC 1

RESULT 22
 BD274740
 LOCUS BD274740 25 bp DNA linear PAT 17-JUL-2003
 DEFINITION Angiotensin converting enzyme homolog and its use.
 ACCESSION BD274740
 VERSION BD274740.1 GI:33084508
 KEYWORDS JP 2002525108-A/57.
 SOURCE synthetic construct
 ORGANISM synthetic construct

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artificial sequences.
1 (bases 1 to 25)
Acton,S., Robison,K.E. and Hsieh,F.Y.
Angiotensin converting enzyme homolog and its use
Patent: JP 2002525108-A 57 13-AUG-2002;
MILLENNIUM PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002525108-A/57
PD 13-AUG-2002
PF 29-SEP-1999 JP 2000572346
PR 30-SEP-1998 US 09/163648
PI LAURENE SUSAN ACTON,KEITH EARL ROBISON,FRANK Y HSIEH PC
C12N15/09,A61K45/00,A61P9/04,A61P9/10,A61P9/12,A61P13/ PC
12,A61P43/00,A61P43/00,C12N9/50,C12Q1/37,G01N33/15,G01N33/50// PC
(C12N9/50,C12R1:91),C12N15/00
CC Description of Artificial Sequence: primer
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FT Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2494 CACTGATGATGTTGAGACCTCTCTT 2518
Db 1 CACTGATGATGTTGAGACCTCTCTT 25

RESULT 23
AX419028 25 bp DNA linear PAT 18-JUN-2002
LOCUS
DEFINITION Sequence 47 from Patent WO0212471.
ACCESSION AX419028
VERSION AX419028.1 GI:21523802
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1
REFERENCE
AUTHORS Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE Angiotensin converting enzyme homolog and uses therefor
JOURNAL Patent: WO 0212471-A 47 14-FEB-2002;
MILLENNIUM PHARMACEUTICALS, Inc. (US)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="motifs"

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 905 GGTGATATGCGGTAGATTGGA 929
Db 1 GGTGATATGCGGTAGATTGGA 25

RESULT 24
AX419032 25 bp DNA linear PAT 18-JUN-2002
LOCUS
DEFINITION Sequence 51 from Patent WO0212471.
ACCESSION AX419032
VERSION AX419032.1 GI:21523806
KEYWORDS

artificial sequences.
1 (bases 1 to 25)
Acton,S., Robison,K.E. and Hsieh,F.Y.
Angiotensin converting enzyme homolog and its use
Patent: JP 2002525108-A 57 13-AUG-2002;
MILLENNIUM PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002525108-A/57
PD 13-AUG-2002
PF 29-SEP-1999 JP 2000572346
PR 30-SEP-1998 US 09/163648
PI LAURENE SUSAN ACTON,KEITH EARL ROBISON,FRANK Y HSIEH PC
C12N15/09,A61K45/00,A61P9/04,A61P9/10,A61P9/12,A61P13/ PC
12,A61P43/00,A61P43/00,C12N9/50,C12Q1/37,G01N33/15,G01N33/50// PC
(C12N9/50,C12R1:91),C12N15/00
CC Description of Artificial Sequence: primer
FH Key Location/Qualifiers
FT source 1..25
FT Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="motifs"

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1088 GAAAATTCCTGCTAAGCGACCCAG 1112
Db 1 GAAAATTCCTGCTAAGCGACCCAG 25

RESULT 25
AX419037/c 25 bp DNA linear PAT 18-JUN-2002
LOCUS
DEFINITION Sequence 56 from Patent WO0212471.
ACCESSION AX419037
VERSION AX419037.1 GI:21523811
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1
REFERENCE
AUTHORS Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE Angiotensin converting enzyme homolog and uses therefor
JOURNAL Patent: WO 0212471-A 56 14-FEB-2002;
MILLENNIUM PHARMACEUTICALS, Inc. (US)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="motifs"

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1294 TGAAGGATTCCTGAGCTGTGGG 1318
Db 25 TGAAGGATTCCTGAGCTGTGGG 1

RESULT 26
AX419060 25 bp DNA linear PAT 18-JUN-2002
LOCUS
DEFINITION Sequence 79 from Patent WO0212471.
ACCESSION AX419060
VERSION AX419060.1 GI:21523834
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1
REFERENCE
AUTHORS Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE Angiotensin converting enzyme homolog and uses therefor
JOURNAL Patent: WO 0212471-A 79 14-FEB-2002;
MILLENNIUM PHARMACEUTICALS, Inc. (US)
FEATURES
source
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/organism="synthetic construct"

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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="motifs"

Query Match
Best Local Similarity 0.7%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2990 GTCAAGGATGACATGCTTTCTTCAC 3014
Db 1 GTCAGATGACATGCTTTCTTCAC 25

RESULT 27
AX419061/c
LOCUS
DEFINITION
Sequence 80 from Patent WO0212471.
ACCESSION
AX419061
VERSION
AX419061.1 GI:21523835
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1
AUTHORS
Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE
Angiotensin converting enzyme homolog and uses therefor
JOURNAL
Patent: WO 0212471-A 80 14-FEB-2002;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
Location/Qualifiers
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="motifs"

Query Match
Best Local Similarity 0.7%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3049 ACAGTCATGTTTGGATCGATCATG 3073
Db 25 ACAGTCATGTTTGGATCGATCATG 1

RESULT 28
AX419062
LOCUS
DEFINITION
Sequence 81 from Patent WO0212471.
ACCESSION
AX419062
VERSION
AX419062.1 GI:21523836
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1
AUTHORS
Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE
Angiotensin converting enzyme homolog and uses therefor
JOURNAL
Patent: WO 0212471-A 81 14-FEB-2002;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
Location/Qualifiers
source
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="motifs"

Query Match
Best Local Similarity 0.7%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2712 CTGCTCTGGATTGACTTCTGTTTC 2736
Db 1 CTGCTCTGGATTGACTTCTGTTTC 25

RESULT 29
AX419063/c
LOCUS
DEFINITION
Sequence 82 from Patent WO0212471.
ACCESSION
AX419063
VERSION
AX419063.1 GI:21523837
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1
AUTHORS
Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE
Angiotensin converting enzyme homolog and uses therefor
JOURNAL
Patent: WO 0212471-A 82 14-FEB-2002;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
Location/Qualifiers
source
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="motifs"

Query Match
Best Local Similarity 0.7%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2776 AAAGTGTGATTGGTCTCACAGGC 2800
Db 25 AAAGTGTGATTGGTCTCACAGGC 1

RESULT 30
AX419064
LOCUS
DEFINITION
Sequence 83 from Patent WO0212471.
ACCESSION
AX419064
VERSION
AX419064.1 GI:21523838
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1
AUTHORS
Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE
Angiotensin converting enzyme homolog and uses therefor
JOURNAL
Patent: WO 0212471-A 83 14-FEB-2002;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
Location/Qualifiers
source
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="motifs"

Query Match
Best Local Similarity 0.7%; Score 25; DB 1; Length 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2494 CACTGATGATGTTTCAGACCTCTTT 2518
Db 1 CACTGATGATGTTTCAGACCTCTTT 25

RESULT 31
BD274752
LOCUS
DEFINITION
Angiotensin converting enzyme homolog and its use.
ACCESSION
BD274752
VERSION
BD274752.1 GI:33084520
KEYWORDS
JP 2002525108-A/69.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 26)
REFERENCE
AUTHORS Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE Angiotensin converting enzyme homolog and its use
JOURNAL PATENT: JP 2002525108-A 69 13-AUG-2002;
COMMENT MILLENNIUM PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002525108-A/69
PD 13-AUG-2002
PF 29-SEP-1999 JP 2000572346
PI 30-SEP-1998 US 09/163648
PR LAURENE SUSAN ACTON,KEITH EARL ROBISON,FRANK Y HSIEH PC
C12N15/09,A61K45/00,A61P9/04,A61P9/10,A61P9/12,A61P13/ PC
12, A61P43/00,A61P43/00,C12N9/50,C12Q1/37,G01N33/15,G01N33/50// PC
(C12N9/50,C12RI:91),C12N15/00
CC Angiotensin converting enzyme homolog and its use FH Key
Location/Qualifiers
FT source 1..26
FT Location/Qualifiers
/organism='Homo sapiens (human)'.
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 21;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2844 AGTTGAAACAAAGGATATATCATTTGG 2869
Db 1 AGTTGAAACAAAGGATATATCATTTGG 26

RESULT 32
AX419076 26 bp DNA linear PAT 18-JUN-2002
LOCUS
DEFINITION Sequence 95 from Patent WO0212471.
ACCESSION AX419076
VERSION AX419076.1 GI:215233850
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE Angiotensin converting enzyme homolog and uses therefor
JOURNAL PATENT: WO 0212471-A 95 14-FEB-2002;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="motifs"

Query Match 0.7%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 21;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2844 AGTTGAAACAAAGGATATATCATTTGG 2869
Db 1 AGTTGAAACAAAGGATATATCATTTGG 26

RESULT 33
AX419078 26 bp DNA linear PAT 18-JUN-2002
LOCUS
DEFINITION Sequence 97 from Patent WO0212471.
ACCESSION AX419078
VERSION AX419078.1 GI:215233852

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KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE Angiotensin converting enzyme homolog and uses therefor
JOURNAL PATENT: WO 0212471-A 97 14-FEB-2002;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="motifs"

Query Match 0.7%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 21;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 58 CTAGGGAAGTCATTTCAGTGGATGTG 83
Db 1 CTAGGGAAGTCATTTCAGTGGATGTG 26

RESULT 34
BD274692 24 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Angiotensin converting enzyme homolog and its use.
ACCESSION BD274692
VERSION BD274692.1 GI:33084460
KEYWORDS JP 2002525108-A/9.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Acton,L.S., Robison,K.E. and Hsieh,F.Y.
TITLE Angiotensin converting enzyme homolog and its use
JOURNAL PATENT: JP 2002525108-A 9 13-AUG-2002;
MILLENNIUM PHARMACEUTICALS INC
COMMENT
OS Artificial Sequence
PN JP 2002525108-A/9
PD 13-AUG-2002
PF 29-SEP-1999 JP 2000572346
PI 30-SEP-1998 US 09/163648
PR LAURENE SUSAN ACTON,KEITH EARL ROBISON,FRANK Y HSIEH PC
C12N15/09,A61K45/00,A61P9/04,A61P9/10,A61P9/12,A61P13/ PC
12, A61P43/00,A61P43/00,C12N9/50,C12Q1/37,G01N33/15,G01N33/50// PC
(C12N9/50,C12RI:91),C12N15/00
CC Description of Artificial Sequence: primer
FH Key Location/Qualifiers
FT source 1..24
FT Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 ATCTCACAGTCAAGTTCAGTGC 395
Db 1 ATCTCACAGTCAAGTTCAGTGC 24

RESULT 35
BD274693 24 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Angiotensin converting enzyme homolog and its use.

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ACCESSION      BD274693
KEYWORDS       BD274693.1 GI:33084461
SOURCE         JP 2002525108-A/10
ORGANISM       synthetic construct
               artificial sequences
REFERENCE       1 (bases 1 to 24)
AUTHORS        Acton,L.S., Robison,K.E. and Hsieh,F.Y.
TITLE          Angiotensin converting enzyme homolog and its use
JOURNAL        Patent: JP 2002525108-A 10 13-AUG-2002;
               MILLENNIUM PHARMACEUTICALS INC
COMMENT        OS Artificial Sequence
               PN JP 2002525108-A/10
               PD 13-AUG-2002
               PF 29-SEP-1999 JP 2000572346
               PR 30-SEP-1998 US 09/163648
               PI LAURENE SUSAN ACTON,KEITH EARL ROBISON,FRANK Y HSIEH PC
               C12N15/09,A61K45/00,A61P9/10,A61P9/12,A61P13/ PC
               12,
               PC A61P43/00,A61P43/00,C12N9/50,C12Q1/37,G01N33/15,G01N33/50// PC
               (C12N9/50,C12R1.91),C12N15/00
               CC Description of Artificial Sequence: primer
               FH Key Location/Qualifiers
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               /organism='Artificial Sequence'
               /location/Qualifiers
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               /organism='synthetic construct'
               /mol_type='genomic DNA'
               /db_xref='taxon:32630'

Query Match    0.7%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No.18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 CAGTGTCTCAGAACAGACGCA 443
      |||||
      24 CAGTGTCTCAGAACAGACGCA 1

RESULT 36
BD274705/c
LOCUS          BD274705          24 bp DNA linear PAT 17-JUL-2003
DEFINITION    Angiotensin converting enzyme homolog and its use.
ACCESSION     BD274705
VERSION       BD274705.1 GI:33084473
KEYWORDS      JP 2002525108-A/22.
SOURCE        synthetic construct
ORGANISM      artificial sequences
REFERENCE      1 (bases 1 to 24)
AUTHORS        Acton,L.S., Robison,K.E. and Hsieh,F.Y.
TITLE          Angiotensin converting enzyme homolog and its use
JOURNAL        Patent: JP 2002525108-A 22 13-AUG-2002;
               MILLENNIUM PHARMACEUTICALS INC
COMMENT        OS Artificial Sequence
               PN JP 2002525108-A/22
               PD 13-AUG-2002
               PF 29-SEP-1999 JP 2000572346
               PR 30-SEP-1998 US 09/163648
               PI LAURENE SUSAN ACTON,KEITH EARL ROBISON,FRANK Y HSIEH PC
               C12N15/09,A61K45/00,A61P9/10,A61P9/12,A61P13/ PC
               12,
               PC A61P43/00,A61P43/00,C12N9/50,C12Q1/37,G01N33/15,G01N33/50// PC
               (C12N9/50,C12R1.91),C12N15/00
               CC Description of Artificial Sequence: primer
               FH Key Location/Qualifiers
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/db_xref='taxon:32630'

Query Match    0.7%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No.18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 978 ATGTTACTGATGCAATGGTGGACC 1001
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      24 ATGTTACTGATGCAATGGTGGACC 1

RESULT 37
BD274709/c
LOCUS          BD274709          24 bp DNA linear PAT 17-JUL-2003
DEFINITION    Angiotensin converting enzyme homolog and its use.
ACCESSION     BD274709
VERSION       BD274709.1 GI:33084477
KEYWORDS      JP 2002525108-A/26.
SOURCE        synthetic construct
ORGANISM      artificial sequences
REFERENCE      1 (bases 1 to 24)
AUTHORS        Acton,L.S., Robison,K.E. and Hsieh,F.Y.
TITLE          Angiotensin converting enzyme homolog and its use
JOURNAL        Patent: JP 2002525108-A 26 13-AUG-2002;
               MILLENNIUM PHARMACEUTICALS INC
COMMENT        OS Artificial Sequence
               PN JP 2002525108-A/26
               PD 13-AUG-2002
               PF 29-SEP-1999 JP 2000572346
               PR 30-SEP-1998 US 09/163648
               PI LAURENE SUSAN ACTON,KEITH EARL ROBISON,FRANK Y HSIEH PC
               C12N15/09,A61K45/00,A61P9/10,A61P9/12,A61P13/ PC
               12,
               PC A61P43/00,A61P43/00,C12N9/50,C12Q1/37,G01N33/15,G01N33/50// PC
               (C12N9/50,C12R1.91),C12N15/00
               CC Description of Artificial Sequence: primer
               FH Key Location/Qualifiers
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               /organism='Artificial Sequence'
               /location/Qualifiers
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               /organism='synthetic construct'
               /mol_type='genomic DNA'
               /db_xref='taxon:32630'

Query Match    0.7%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No.18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1119 TTCAGAAAGCAGTCTGCCATCCCA 1142
      |||||
      24 TTCAGAAAGCAGTCTGCCATCCCA 1

RESULT 38
BD274734/c
LOCUS          BD274734          24 bp DNA linear PAT 17-JUL-2003
DEFINITION    Angiotensin converting enzyme homolog and its use.
ACCESSION     BD274734
VERSION       BD274734.1 GI:33084502
KEYWORDS      JP 2002525108-A/51.
SOURCE        synthetic construct
ORGANISM      artificial sequences
REFERENCE      1 (bases 1 to 24)
AUTHORS        Acton,L.S., Robison,K.E. and Hsieh,F.Y.
TITLE          Angiotensin converting enzyme homolog and its use
JOURNAL        Patent: JP 2002525108-A 51 13-AUG-2002;
               MILLENNIUM PHARMACEUTICALS INC
COMMENT        OS Artificial Sequence
               PN JP 2002525108-A/51
               PD 13-AUG-2002

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PF 29-SEP-1999 JP 2000572346
PR 30-SEP-1998 US 09/163648
PI LAURENE SUSAN ACTON,KEITH EARL ROBISON,FRANK Y HSIEH PC
C12N15/09,A61K45/00,A61P9/04,A61P9/10,A61P9/12,A61P13/ PC
12,
PC A61P43/00,A61P43/00,C12N9/50,C12Q1/37,G01N33/15,G01N33/50// PC
(C12N9/50,C12R1:91),C12N15/00
CC Description of Artificial Sequence: primer
FH Key Location/Qualifiers
FT source 1..24
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            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
    Query Match          0.7%; Score 24; DB 1; Length 24;
    Best Local Similarity 100.0%; Pred. No. 18;
    Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3210 CAGAGCATGCTGATAGAACTCA 3233
    |||||
Db 1 CAGAGCATGCTGATAGAACTCA 24

RESULT 39
BD274741/c
LOCUS BD274741 24 bp DNA linear PAT 17-JUL-2003
DEFINITION Angiotensin converting enzyme homolog and its use.
ACCESSION BD274741
VERSION BD274741.1 GI:33084509
KEYWORDS JP 2002525108-A/58.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
    1 (bases 1 to 24)
AUTHORS Acton,L.S., Robison,K.E. and Hsieh,F.Y.
TITLE Angiotensin converting enzyme homolog and its use
JOURNAL Patent: JP 2002525108-A 58 13-AUG-2002;
MILLENNIUM PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2002525108-A/58
PD 13-AUG-2002
PF 29-SEP-1999 JP 2000572346
PR 30-SEP-1998 US 09/163648
PI LAURENE SUSAN ACTON,KEITH EARL ROBISON,FRANK Y HSIEH PC
C12N15/09,A61K45/00,A61P9/04,A61P9/10,A61P9/12,A61P13/ PC
12,
PC A61P43/00,A61P43/00,C12N9/50,C12Q1/37,G01N33/15,G01N33/50// PC
(C12N9/50,C12R1:91),C12N15/00
CC Description of Artificial Sequence: primer
FH Key Location/Qualifiers
FT source 1..24
    /organism='Artificial Sequence'
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    source
        1..24
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
    Query Match          0.7%; Score 24; DB 1; Length 24;
    Best Local Similarity 100.0%; Pred. No. 18;
    Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2648 TTGTCCAAAGACACATGGCCAG 2671
    |||||
Db 24 TTGTCCAAAGACACATGGCCAG 1

RESULT 40
BD274749
LOCUS BD274749 24 bp DNA linear PAT 17-JUL-2003

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DEFINITION Angiotensin converting enzyme homolog and its use.
ACCESSION BD274749
VERSION BD274749.1 GI:33084517
KEYWORDS JP 2002525108-A/66.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
    Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1 (bases 1 to 24)
AUTHORS Acton,L.S., Robison,K.E. and Hsieh,F.Y.
TITLE Angiotensin converting enzyme homolog and its use
JOURNAL Patent: JP 2002525108-A 66 13-AUG-2002;
MILLENNIUM PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002525108-A/66
PD 13-AUG-2002
PF 29-SEP-1999 JP 2000572346
PR 30-SEP-1998 US 09/163648
PI LAURENE SUSAN ACTON,KEITH EARL ROBISON,FRANK Y HSIEH PC
C12N15/09,A61K45/00,A61P9/04,A61P9/10,A61P9/12,A61P13/ PC
12,
PC A61P43/00,A61P43/00,C12N9/50,C12Q1/37,G01N33/15,G01N33/50// PC
(C12N9/50,C12R1:91),C12N15/00
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Qy 2249 GCTCTGAATGACACAGCCTAGAG 2272
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Db 1 GCTCTGAATGACACAGCCTAGAG 24

RESULT 41
AX419016
LOCUS AX419016 24 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 35 from Patent WO0212471.
ACCESSION AX419016
VERSION AX419016.1 GI:21523790
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
    1
AUTHORS Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE Angiotensin converting enzyme homolog and uses therefor
JOURNAL Patent: WO 0212471-A 35 14-FEB-2002;
MILLENNIUM Pharmaceuticals, Inc. (US)
FEATURES
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            /note="motifs"
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    Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 372 ATCTCACAGTCAAGCTTCAGCTGC 395
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Db 1 ATCTCACAGTCAAGCTTCAGCTGC 24

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RESULT 42
AX419017/c
LOCUS      24 bp      DNA      linear      PAT 18-JUN-2002
DEFINITION Sequence 36 from Patent WO0212471.
ACCESSION  AX419017
VERSION     AX419017.1 GI:21523791
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE      Angiotensin converting enzyme homolog and uses therefor
JOURNAL    Patent: WO 0212471-A 36 14-FEB-2002;
           Millennium Pharmaceuticals, Inc. (US)
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               /db_xref="taxon:32630"
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Best Local Similarity 100.0%; Pred. No. 18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 420 CAGTGCTCTCAGAGACAGAGCA 443
Db 24 CAGTGCTCTCAGAGACAGAGCA 1
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RESULT 43
AX419029/c
LOCUS      24 bp      DNA      linear      PAT 18-JUN-2002
DEFINITION Sequence 48 from Patent WO0212471.
ACCESSION  AX419029
VERSION     AX419029.1 GI:21523803
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE      Angiotensin converting enzyme homolog and uses therefor
JOURNAL    Patent: WO 0212471-A 48 14-FEB-2002;
           Millennium Pharmaceuticals, Inc. (US)
FEATURES   Location/Qualifiers
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               /db_xref="taxon:32630"
               /note="motifs"
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Best Local Similarity 100.0%; Pred. No. 18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 978 ATGTTACTGATGCAATGGTGACC 1001
Db 24 ATGTTACTGATGCAATGGTGACC 1
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RESULT 44
AX419033/c
LOCUS      24 bp      DNA      linear      PAT 18-JUN-2002
DEFINITION Sequence 52 from Patent WO0212471.
ACCESSION  AX419033
VERSION     AX419033.1 GI:21523807
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE      Angiotensin converting enzyme homolog and uses therefor
JOURNAL    Patent: WO 0212471-A 84 14-FEB-2002;
           Millennium Pharmaceuticals, Inc. (US)
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               /db_xref="taxon:32630"
               /note="motifs"
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Best Local Similarity 100.0%; Pred. No. 18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3210 CAGAGCATGCTGATAGAACTCA 3233
Db 1 CAGAGCATGCTGATAGAACTCA 24
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RESULT 45
AX419058/c
LOCUS      24 bp      DNA      linear      PAT 18-JUN-2002
DEFINITION Sequence 77 from Patent WO0212471.
ACCESSION  AX419058
VERSION     AX419058.1 GI:21523832
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE      Angiotensin converting enzyme homolog and uses therefor
JOURNAL    Patent: WO 0212471-A 77 14-FEB-2002;
           Millennium Pharmaceuticals, Inc. (US)
FEATURES   Location/Qualifiers
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               /db_xref="taxon:32630"
               /note="motifs"
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Best Local Similarity 100.0%; Pred. No. 18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1119 TTCAGAAAGCAGTCTGCCATCCCA 1142
Db 24 TTCAGAAAGCAGTCTGCCATCCCA 1
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RESULT 46
AX419065/c
LOCUS      24 bp      DNA      linear      PAT 18-JUN-2002
DEFINITION Sequence 84 from Patent WO0212471.
ACCESSION  AX419065
VERSION     AX419065.1 GI:21523839
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE      Angiotensin converting enzyme homolog and uses therefor
JOURNAL    Patent: WO 0212471-A 84 14-FEB-2002;
           Millennium Pharmaceuticals, Inc. (US)
FEATURES   Location/Qualifiers
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               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="motifs"
Query Match      0.7%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3210 CAGAGCATGCTGATAGAACTCA 3233
Db 1 CAGAGCATGCTGATAGAACTCA 24
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Query Match      0.7%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2648 TTGTCCAAAGACACATGGCCAAAG 2671
DB 24 TTGTCCAAAGACACATGGCCAAAG 1

RESULT 47
BD274689/c
LOCUS BD274689 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Angiotensin converting enzyme homolog and its use.
ACCESSION BD274689
VERSION BD274689.1 GI:33084457
KEYWORDS JP 2002525108-A/6.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Acton,L.S., Robison,K.E. and Hsieh,F.Y.
TITLE Angiotensin converting enzyme homolog and its use
JOURNAL Patent: JP 2002525108-A 6 13-AUG-2002;
MILLENNIUM PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2002525108-A/6
PD 13-AUG-2002
PF 29-SEP-1999 JP 2000572346
PR 30-SEP-1998 US 09/163648
PI LAURENE SUSAN ACTON,KEITH EARL ROBISON,FRANK Y HSIEH PC
C12N15/09,A61K45/00,A61P9/10,A61P9/12,A61P13/ PC
12, A61P43/00,A61P43/00,C12N9/50,C12Q1/37,G01N33/15,G01N33/50// PC
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FH Key Location/Qualifiers
FT source 1..23 /organism='Artificial Sequence'

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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1252 GGCATATGCTGCACAACTTTTC 1274
DB 1 GGCATATGCTGCACAACTTTTC 23

RESULT 49
BD274730
LOCUS BD274730 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Angiotensin converting enzyme homolog and its use.
ACCESSION BD274730
VERSION BD274730.1 GI:33084498
KEYWORDS JP 2002525108-A/47.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Acton,L.S., Robison,K.E. and Hsieh,F.Y.
TITLE Angiotensin converting enzyme homolog and its use
JOURNAL Patent: JP 2002525108-A 47 13-AUG-2002;
MILLENNIUM PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2002525108-A/47
PD 13-AUG-2002
PF 29-SEP-1999 JP 2000572346
PR 30-SEP-1998 US 09/163648
PI LAURENE SUSAN ACTON,KEITH EARL ROBISON,FRANK Y HSIEH PC
C12N15/09,A61K45/00,A61P9/10,A61P9/12,A61P13/ PC
12, A61P43/00,A61P43/00,C12N9/50,C12Q1/37,G01N33/15,G01N33/50// PC
(C12N9/50,C12R1:91),C12N15/00
CC Description of Artificial Sequence: primer
FH Key Location/Qualifiers
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/db_xref="taxon:32630"

Query Match      0.7%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1252 GGCATATGCTGCACAACTTTTC 1274
DB 1 GGCATATGCTGCACAACTTTTC 23

RESULT 49
BD274730
LOCUS BD274730 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Angiotensin converting enzyme homolog and its use.
ACCESSION BD274730
VERSION BD274730.1 GI:33084498
KEYWORDS JP 2002525108-A/47.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Acton,L.S., Robison,K.E. and Hsieh,F.Y.
TITLE Angiotensin converting enzyme homolog and its use
JOURNAL Patent: JP 2002525108-A 47 13-AUG-2002;
MILLENNIUM PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2002525108-A/47
PD 13-AUG-2002
PF 29-SEP-1999 JP 2000572346
PR 30-SEP-1998 US 09/163648
PI LAURENE SUSAN ACTON,KEITH EARL ROBISON,FRANK Y HSIEH PC
C12N15/09,A61K45/00,A61P9/10,A61P9/12,A61P13/ PC
12, A61P43/00,A61P43/00,C12N9/50,C12Q1/37,G01N33/15,G01N33/50// PC
(C12N9/50,C12R1:91),C12N15/00
CC Description of Artificial Sequence: primer
FH Key Location/Qualifiers
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Query Match      0.7%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2286 AGCCAACTTGGACCTCTTAC 2308
DB 1 AGCCAACTTGGACCTCTTAC 23

RESULT 50
BD274731/c
LOCUS BD274731
DEFINITION Angiotensin converting enzyme homolog and its use.
ACCESSION BD274731

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VERSION BD274731.1 GI:33084499
 KEYWORDS JP 2002525108-A/48.
 SOURCE synthetic construct
 ORGANISM artificial construct
 artificial sequences.
 1 (bases 1 to 23)
 Acton,L.S., Robison,K.E. and Hsieh,F.Y.
 Angiotensin converting enzyme homolog and its use
 Patent: JP 2002525108-A 48 13-AUG-2002;
 JOURNAL MILLENNIUM PHARMACEUTICALS INC

COMMENT OS Artificial Sequence
 PN JP 2002525108-A/48
 PD 13-AUG-2002
 PF 29-SEP-1999 JP 2000572346
 PR 30-SEP-1998 US 09/163648
 PI LAURENE SUSAN ACTON,KEITH EARL,ROBISON,FRANK Y HSIEH PC
 C12N15/09,A61K45/00,A61P9/10,A61P9/10,A61P9/12,A61P13/ PC
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Query Match 0.7%; Score 23; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2369 GGCATTGTCATCTGATCTTCAC 2391
 Db 23 GGCATTGTCATCTGATCTTCAC 1

RESULT 51
 BD274735/c
 LOCUS BD274735 23 bp DNA linear PAT 17-JUL-2003
 DEFINITION Angiotensin converting enzyme homolog and its use.
 ACCESSION BD274735
 VERSION BD274735.1 GI:33084503
 KEYWORDS JP 2002525108-A/52.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 1 (bases 1 to 23)
 Acton,L.S., Robison,K.E. and Hsieh,F.Y.
 Angiotensin converting enzyme homolog and its use
 Patent: JP 2002525108-A 52 13-AUG-2002;
 JOURNAL MILLENNIUM PHARMACEUTICALS INC

COMMENT OS Artificial Sequence
 PN JP 2002525108-A/52
 PD 13-AUG-2002
 PF 29-SEP-1999 JP 2000572346
 PR 30-SEP-1998 US 09/163648
 PI LAURENE SUSAN ACTON,KEITH EARL,ROBISON,FRANK Y HSIEH PC
 C12N15/09,A61K45/00,A61P9/10,A61P9/10,A61P9/12,A61P13/ PC
 12, A61P43/00,A61P43/00,C12N9/50,C12Q1/37,G01N33/15,G01N33/50// PC
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 CC Description of Artificial Sequence: primer
 FH Key Location/Qualifiers
 FT source 1..23
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 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3279 ATGTTACCCCTCTGAAGTGGTA 3301
 Db 23 ATGTTACCCCTCTGAAGTGGTA 1

RESULT 52
 BD274753
 LOCUS BD274753 23 bp DNA linear PAT 17-JUL-2003
 DEFINITION Angiotensin converting enzyme homolog and its use.
 ACCESSION BD274753
 VERSION BD274753.1 GI:33084521
 KEYWORDS JP 2002525108-A/70.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 1 (bases 1 to 23)
 Acton,L.S., Robison,K.E. and Hsieh,F.Y.
 Angiotensin converting enzyme homolog and its use
 Patent: JP 2002525108-A 70 13-AUG-2002;
 JOURNAL MILLENNIUM PHARMACEUTICALS INC

COMMENT OS Artificial Sequence
 PN JP 2002525108-A/70
 PD 13-AUG-2002
 PF 29-SEP-1999 JP 2000572346
 PR 30-SEP-1998 US 09/163648
 PI LAURENE SUSAN ACTON,KEITH EARL,ROBISON,FRANK Y HSIEH PC
 C12N15/09,A61K45/00,A61P9/10,A61P9/10,A61P9/12,A61P13/ PC
 12, A61P43/00,A61P43/00,C12N9/50,C12Q1/37,G01N33/15,G01N33/50// PC
 (C12N9/50,C12R1:91),C12N15/00
 CC Description of Artificial Sequence: primer
 FH Key Location/Qualifiers
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 FT /organism='Artificial Sequence'.

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 /db_xref="taxon:32630"

Query Match 0.7%; Score 23; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2902 GGATCATTGTAAGGACAGTGCC 2924
 Db 1 GGATCATTGTAAGGACAGTGCC 23

RESULT 53
 AX419013/c
 LOCUS AX419013 23 bp DNA linear PAT 18-JUN-2002
 DEFINITION Sequence 32 from Patent WO0212471.
 ACCESSION AX419013
 VERSION AX419013.1 GI:21523787
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 1
 Acton,S., Robison,K.E. and Hsieh,F.Y.
 Angiotensin converting enzyme homolog and uses therefor
 Patent: WO 0212471-A 32 14-FEB-2002;
 JOURNAL Millennium Pharmaceuticals, Inc. (US)

FEATURES
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 /mol_type="unassigned DNA"

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/db_xref="taxon:32630"
/note="motifs"

Query Match      0.7%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 CACCATTTAGGACAGGCGCAAGA 182
Db 23 CACCATTTAGGACAGGCGCAAGA 1

RESULT 54
AX419036
LOCUS AX419036 23 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 55 from Patent WO0212471.
ACCESSION AX419036
VERSION AX419036.1 GI:21523810
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Acton,S., Robison,K.E. and Hsieh,F.Y.
AUTHORS Angiotensin converting enzyme homolog and uses therefor
TITLE Patent: WO 0212471-A 55 14-FEB-2002;
JOURNAL Millennium Pharmaceuticals, Inc. (US)
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="motifs"

Query Match      0.7%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1252 GGCATATGCTGCACACCTTTTC 1274
Db 1 GGCATATGCTGCACACCTTTTC 23

RESULT 55
AX419054
LOCUS AX419054 23 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 73 from Patent WO0212471.
ACCESSION AX419054
VERSION AX419054.1 GI:21523828
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Acton,S., Robison,K.E. and Hsieh,F.Y.
AUTHORS Angiotensin converting enzyme homolog and uses therefor
TITLE Patent: WO 0212471-A 73 14-FEB-2002;
JOURNAL Millennium Pharmaceuticals, Inc. (US)
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="motifs"

Query Match      0.7%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2286 AGCCAACACTTGGACCTCTTAAC 2308
Db 1 AGCCAACACTTGGACCTCTTAAC 23

RESULT 56
AX419055/c
LOCUS AX419055 23 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 74 from Patent WO0212471.
ACCESSION AX419055
VERSION AX419055.1 GI:21523829
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Acton,S., Robison,K.E. and Hsieh,F.Y.
AUTHORS Angiotensin converting enzyme homolog and uses therefor
TITLE Patent: WO 0212471-A 74 14-FEB-2002;
JOURNAL Millennium Pharmaceuticals, Inc. (US)
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="motifs"

Query Match      0.7%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2369 GGCATTGTCATCCTGATCTTCAC 2391
Db 23 GGCATTGTCATCCTGATCTTCAC 1

RESULT 57
AX419059/c
LOCUS AX419059 23 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 78 from Patent WO0212471.
ACCESSION AX419059
VERSION AX419059.1 GI:21523833
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Acton,S., Robison,K.E. and Hsieh,F.Y.
AUTHORS Angiotensin converting enzyme homolog and uses therefor
TITLE Patent: WO 0212471-A 78 14-FEB-2002;
JOURNAL Millennium Pharmaceuticals, Inc. (US)
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="motifs"

Query Match      0.7%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3279 ATGTTACCCCTCTGAAGTGGGTA 3301
Db 23 ATGTTACCCCTCTGAAGTGGGTA 1

RESULT 58
AX419073
LOCUS AX419073 23 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 92 from Patent WO0212471.
ACCESSION AX419073
VERSION AX419073.1 GI:21523847
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
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REFERENCE
1  Acton,S., Robison,K.E. and Hsieh,F.Y.
   TITLE
   Angiotensin converting enzyme homolog and uses therefor
   JOURNAL
   Millennium Pharmaceuticals, Inc. (US)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="motifs"

Query Match      0.7%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2249 CGTCTGAATGACACAGCCTAGAG 2271
      |||||
      1 CGTCTGAATGACACAGCCTAGAG 23
      |||||

RESULT 59
AX419083
LOCUS
AX419083
DEFINITION
Sequence 102 from Patent WO0212471.
ACCESSION
AX419083
VERSION
AX419083.1 GI:21523857
KEYWORDS
synthetic construct
synthetic construct
artificial sequences.
ORGANISM
Acton,S., Robison,K.E. and Hsieh,F.Y.
AUTHORS
Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE
Angiotensin converting enzyme homolog and uses therefor
JOURNAL
Patent: WO 0212471-A 102 14-FEB-2002;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="motifs"

Query Match      0.7%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2902 GGATCACTTGTAGGACAGTGCC 2924
      |||||
      1 GGATCACTTGTAGGACAGTGCC 23
      |||||

RESULT 60
BD274750
LOCUS
BD274750
DEFINITION
Angiotensin converting enzyme homolog and its use.
ACCESSION
BD274750
VERSION
BD274750.1 GI:33084518
KEYWORDS
JP 2002525108-A/67.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 24)
AUTHORS
Acton,L.S., Robison,K.E. and Hsieh,F.Y.
TITLE
Angiotensin converting enzyme homolog and its use
JOURNAL
Patent: JP 2002525108-A 67 13-AUG-2002;
MILLENNIUM PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002525108-A/67
PD 13-AUG-2002
PF 29-SEP-1999 JP 2000572346
PR 30-SEP-1998 US 09/163648

PI  LAURENE SUSAN ACTON,KEITH EARL ROBISON,FRANK Y HSIEH PC
   C12N15/09,A61K45/00,A61P9/04,A61P9/10,A61P9/12,A61P13/ PC
   12,A61P43/00,A61P43/00,C12N9/50,C12Q1/37,G01N33/15,G01N33/50// PC
   (C12N9/50,C12Q1/37,G01N33/15,G01N33/50)
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      /organism="Homo sapiens (human)".
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Query Match      0.7%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 30;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2249 CGTCTGAATGACACAGCCTAGAG 2272
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      1 CGTCTGAATGACACAGCCTAGAG 24
      |||||

RESULT 61
AX419074
LOCUS
AX419074
DEFINITION
Sequence 93 from Patent WO0212471.
ACCESSION
AX419074
VERSION
AX419074.1 GI:21523848
KEYWORDS
synthetic construct
synthetic construct
artificial sequences.
ORGANISM
Acton,S., Robison,K.E. and Hsieh,F.Y.
AUTHORS
Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE
Angiotensin converting enzyme homolog and uses therefor
JOURNAL
Patent: WO 0212471-A 93 14-FEB-2002;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source
1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="motifs"

Query Match      0.7%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 30;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2249 CGTCTGAATGACACAGCCTAGAG 2272
      |||||
      1 CGTCTGAATGACACAGCCTAGAG 24
      |||||

RESULT 62
BD274688
LOCUS
BD274688
DEFINITION
Angiotensin converting enzyme homolog and its use.
ACCESSION
BD274688
VERSION
BD274688.1 GI:33084456
KEYWORDS
JP 2002525108-A/5.
SOURCE
synthetic construct
synthetic construct
artificial sequences.
ORGANISM
Acton,L.S., Robison,K.E. and Hsieh,F.Y.
AUTHORS
Acton,L.S., Robison,K.E. and Hsieh,F.Y.
TITLE
Angiotensin converting enzyme homolog and its use
JOURNAL
Patent: JP 2002525108-A 5 13-AUG-2002;
MILLENNIUM PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002525108-A/5
PD 13-AUG-2002

```


PN	JP	2001046072-A/7
PD	20-FEB-2001	
PF	06-AUG-1999	JP 1999223892
PI	SUMIO SUGANO,TAKAMI KOMATSU	
PC	C12N15/09,A61K31/00,A61K31/7088,A61K38/00,A61K38/55,A61K39/395, PC A61K39/395,	
PC	A61K39/395,A61K48/00,A61P9/12,C07K14/47,C07K16/08,C12N1/15, PC C12N1/19,	
PC	C12N1/21,C12N5/10,C12Q1/68,G01N33/53,C12N15/00,A61K37/02, PC A61K37/64,	
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Dbb		
	1 GGCTTGGAAAATCAGAACCC 20	
RESULT 65		
E43994/C		
LOCUS	E43994	20 bp DNA linear PAT 31-JAN-2002
DEFINITION	ACE-analogous gene.	
ACCESSION	E43994	
VERSION	E43994.1 GI:18629197	
KEYWORDS	JP 2001046072-A/8.	
SOURCE	unidentified	
ORGANISM	unclassified.	
REFERENCE	1 (bases 1 to 20)	
AUTHORS	Sugano,S. and Komatsu,T.	
TITLE	ACE-analogous gene	
JOURNAL	Patent: JP 2001046072-A 8 20-FEB-2001;	
COMMENT	OTSUKA PHARMACEUT CO LTD	
	OS Unidentified	
	PN JP 2001046072-A/8	
	PD 20-FEB-2001	
	PF 06-AUG-1999 JP 1999223892	
	PR SUMIO SUGANO,TAKAMI KOMATSU	
PC	C12N15/09,A61K31/00,A61K31/7088,A61K38/00,A61K38/55,A61K39/395, PC A61K39/395,	
PC	A61K39/395,A61K48/00,A61P9/12,C07K14/47,C07K16/08,C12N1/15, PC C12N1/19,	
PC	C12N1/21,C12N5/10,C12Q1/68,G01N33/53,C12N15/00,A61K37/02, PC A61K37/64,	
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		/db_xref="taxon:32644"
Query Match	0.6%; Score 20; DB 1; Length 20;	
Best Local Similarity	100.0%; Pred. No. 36;	

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2352 TGGGAGTGATAGGTTGGC 2371
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Db 20 TGGGAGTGATAGGTTGGC 1

RESULT 66
BD274690
LOCUS BD274690 22 bp DNA linear PAT 17-JUL-2003
DEFINITION Angiotensin converting enzyme homolog and its use.
ACCESSION BD274690
VERSION BD274690.1 GI:33084458
KEYWORDS JP 2002525108-A/7.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 22)
AUTHORS Acton,L.S., Robison,K.E. and Hsieh,F.Y.
TITLE Angiotensin converting enzyme homolog and its use
JOURNAL Patent: JP 2002525108-A 7 13-AUG-2002;
COMMENT MILLENNIUM PHARMACEUTICALS INC
OS Artificial Sequence
FN JP 2002525108-A/7
PD 13-AUG-2002
PF 29-SEP-1999 JP 2000572346
PR 30-SEP-1998 US 09/163648
PI LAURENE SUSAN ACTON KEITH EARL ROBISON FRANK Y HSIEH PC
C12N15/09,A61K45/00,A61P9/04,A61P9/10,A61P9/12,A61P13/ PC
12, A61P43/00,A61P43/00,C12N9/50,C12Q1/37,G01N33/15,G01N33/50// PC
(C12N9/50,C12R1.91),C12N15/00
CC Description of Artificial Sequence: primer
FH Key Location/Qualifiers
FT source 1..22
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source Location/Qualifiers
1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 20; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCCAACCCAGTTCAAAG 20
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Db 3 CGCCCAACCCAGTTCAAAG 22

RESULT 67
AX419014
LOCUS AX419014 22 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 33 from Patent WO0212471.
ACCESSION AX419014
VERSION AX419014.1 GI:21523788
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Acton,S., Robison,K.E. and Hsieh,F.Y.
TITLE Angiotensin converting enzyme homolog and uses therefor
JOURNAL Patent: WO 0212471-A 33 14-FEB-2002;
MILLENNIUM PHARMACEUTICALS, INC. (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="motifs"

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Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCCAACCCAGTTCAAAG 20
|||||
Db 3 CGCCCAACCCAGTTCAAAG 22

RESULT 68
S63429
LOCUS S63429 23 bp DNA linear PRI 07-MAY-1993
DEFINITION beta-globin [human, Genomic Mutant, 23 nt].
ACCESSION S63429
VERSION S63429.1 GI:238239
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 23)
AUTHORS Cai,S.P., Eng,B., Kan,Y.W. and Chui,D.H.
TITLE A rapid and simple electrophoretic method for the detection of
mutations involving small insertion or deletion: application to
beta-thalassemia
JOURNAL Hum. Genet. 87 (6), 728-730 (1991)
MEDLINE 92039638
PUBMED 1937477
REMARK Genbank staff at the National Library of Medicine created this
entry [NCBI gibbsq 63429] from the original journal article.
This sequence comes from Fig.4.
four bp deletion between nucleotides 201 and 207 in IVS-II.
FEATURES
source Location/Qualifiers
1..23
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/gene="beta-globin"

Query Match 0.6%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 56;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2407 GAAGAGAAAATAAAGCAAGAA 2429
|||||
Db 23 GGAGAGAAAATAAAGCAAGAA 1

RESULT 69
AX043623/c
LOCUS AX043623 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 1189 from Patent WO005088.
ACCESSION AX043623
VERSION AX043623.1 GI:11342231
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 005088-A 1189 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
FEATURES
source Location/Qualifiers
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="HLA-C Heterozygote Primer Sequence"

Query Match 0.5%; Score 18.4; DB 1; Length 25;
Best Local Similarity 95.0%; Pred. No. 1e+02;

ACCESSION	AR369297
VERSION	AR369297.1 GI:34605413
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 24)
TITLE	Misael,A., Loffert,D., Kang,J. and Korfhage,C. Generation and amplification of nucleic acids from ribonucleic acids
JOURNAL	Patent: US 6300069-A 1 09-OCT-2001;
FEATURES	Location/Qualifiers
source	1..24 /organism="unknown" /mol_type="genomic DNA"
Query Match	0.5%; Score 17.6; DB 1; Length 24;
Best Local Similarity	83.3%; Pred.No.1.2e+02;
Matches	20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy	1466 ATGTTAGAGAAGTGGAGGTGCATG 1489
Dd	 1 ATGTTAGTGAAGAAGAGGAGCATG 24
RESULT 73	
AX291257/c	
LOCUS	AX291257 24 bp DNA linear PAT 21-NOV-2001
DEFINITION	Sequence 3019 from Patent WO0179548.
ACCESSION	AX291257
VERSION	AX291257.1 GI:17052940
KEYWORDS	.
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1
AUTHORS	Barany,P., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE	Method of designing addressable array for detection of nucleic acid sequence differences using ligase detection reaction
JOURNAL	Patent: WO 0179548-A 3019 25-OCT-2001; CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES	Location/Qualifiers
source	1..24 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Hypothetical Probe Sequence"
Query Match	0.5%; Score 17.6; DB 1; Length 24;
Best Local Similarity	83.3%; Pred.No.1.2e+02;
Matches	20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy	2939 GTCGCAAGGATTGAGATGCCATG 2962
Dd	 24 GTCGCAAGGATTGAGATCCGGTG 1
RESULT 74	
BD000636	
LOCUS	BD000636 24 bp DNA linear PAT 31-JAN-2002
DEFINITION	Formation and amplification of nucleic acids from ribonucleic acids.
ACCESSION	BD000636
VERSION	BD000636.1 GI:18623749
KEYWORDS	JP 2000342287-A/1.
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1 (bases 1 to 24)
AUTHORS	Michel,A., Refart,D., Can,J. and Cowheig,C.
TITLE	Formation and amplification of nucleic acids from ribonucleic acids
JOURNAL	Patent: JP 2000342287-A 1 12-DEC-2000; KIAGEN GMBH

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COMMENT      OS      Artificial Sequence
PN      JP 2000342287-A/1
PD      12-DEC-2000
PF      02-MAY-2000 JP 2000133664
PR      03-MAY-1999 US 09/304452
PI      ANDREAS MICHEL,DIRK REFPART,JE CAN,CHRISTIAN COMHEIG PC
CC      C12N15/09,C12Q1/68,C12N15/00
FH      Key      Location/Qualifiers
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             Location/Qualifiers
             1..24
             /organism="synthetic construct"
             /mol_type="genomic DNA"
             /db_xref="taxon:32630"

Query Match      0.5%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1466 ATGTTAGAGAGTGAGGTGGATG 1489
Db      1 AUGTTAGTAGAGAGAGGAGGATG 24

RESULT 75
LOCUS      AX042684/c      25 bp      DNA      linear      PAT 23-NOV-2000
DEFINITION      Sequence 250 from Patent WO0065088.
ACCESSION      AX042684
VERSION      AX042684.1 GI:11341292
KEYWORDS      synthetic construct
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1
AUTHORS      Ulfendahl,P.J. and Wong,K.C.
TITLE      Primers for identifying typing or classifying nucleic acids
JOURNAL      Patent: WO 0065088-A 250 02-NOV-2000;
              Amer sham Pharmacia Biotech AB (SE)
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source      1..25
             /organism="synthetic construct"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"
             /note="HLA-A Homozygote Primer Sequence"

Query Match      0.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      3382 ATTTACACACTCAAAAAA 3405
Db      25 ACTCACGACTGAAAAA 2

RESULT 76
LOCUS      AX043487/c      25 bp      DNA      linear      PAT 23-NOV-2000
DEFINITION      Sequence 1053 from Patent WO0065088.
ACCESSION      AX043487
VERSION      AX043487.1 GI:11342095
KEYWORDS      synthetic construct
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1
AUTHORS      Ulfendahl,P.J. and Wong,K.C.
TITLE      Primers for identifying typing or classifying nucleic acids
JOURNAL      Patent: WO 0065088-A 1053 02-NOV-2000;
              Amer sham Pharmacia Biotech AB (SE)
FEATURES
source      1..25
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             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"
             /note="HLA-A Homozygote Primer Sequence"

Query Match      0.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      3382 ATTTACACACTCAAAAAA 3405
Db      25 ACTCACGACTGAAAAA 2

RESULT 77
LOCUS      AX096971      21 bp      DNA      linear      PAT 30-MAR-2001
DEFINITION      Sequence 2149 from Patent WO0118250.
ACCESSION      AX096971
VERSION      AX096971.1 GI:13513239
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
REFERENCE      1
AUTHORS      Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
              McCarthy,J.J.
TITLE      Single nucleotide polymorphisms in genes
JOURNAL      Patent: WO 0118250-A 2149 15-MAR-2001;
              WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
              Pharmaceuticals, Inc. (US)
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source      1..21
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             1..21
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             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 87;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1714 CCTCTGCACAAATGTGCAT 1734
Db      1 CCCACTGCACAAAGTGTGCAT 21

RESULT 78
LOCUS      AR261750      23 bp      DNA      linear      PAT 29-JAN-2003
DEFINITION      Sequence 1 from patent US 6322985.
ACCESSION      AR261750
VERSION      AR261750.1 GI:28072884
KEYWORDS      Unknown.
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 23)
AUTHORS      Kashi,Y., Gur-Arie,R., Cohen,C., Eitan,Y., Shelef,L. and
              Hallerman,B.
TITLE      Abundant, well distributed and hyperpolymorphic simple sequence
              repeats in prokaryote genomes and use of same for prokaryote
              classification and typing
JOURNAL      Patent: US 6322985-A 1 27-NOV-2001;
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             /mol_type="genomic DNA"

Query Match      0.5%; Score 17.2; DB 1; Length 23;
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Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 2751 GATTTCGATAGAGTATATTA 2772
Db 1 GATTTCGATAGAGTATATTA 22

RESULT 79
AX445931/c
LOCUS AX445931 24 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 2386 from Patent WO0216649.
ACCESSION AX445931
VERSION AX445931.1 GI:21694830
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Gunderson,K.
TITLE Probes and decoder oligonucleotides
JOURNAL Patent: WO 0216649-A 2386 28-FEB-2002;
Illumina, Inc. (US)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."
Query Match 0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1100 CTAACGACCCAGGAATGTTTC 1121
Db 23 CTGAGGACCCAGGAGATGTTTC 2

RESULT 80
AX494150/c
LOCUS AX494150 24 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 1124 from Patent WO02059355.
ACCESSION AX494150
VERSION AX494150.1 GI:23339782
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Fieldhouse,D. and Kobler,D.
TITLE Polynucleotides for use as tags and tag complements, manufacture
and use thereof
JOURNAL Patent: WO 02059355-A 1124 01-AUG-2002;
TM BIOSCIENCE CORP (CA)
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/db_xref="taxon:32630"
/note="Artificially Synthesized DNA Sequence"
Query Match 0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3233 ATTTCTACTGTTCTCTAACTGT 3254
Db 23 ATTTCTACTGTTCTCTAACTTT 2

RESULT 81
BD089635
LOCUS BD089635 20 bp DNA linear PAT 27-AUG-2002
DEFINITION A method of arraying genome clone.

ACCESSION BD089635
VERSION BD089635.1 GI:22635245
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 1879 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECHS
COMMENT OS Artificial Sequence
PN JP 2001321190-A/1879
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/00,
CC Description of Artificial Sequence:Synthetic DNA FH Key
FT source
1..20
Location/Qualifiers
FT Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Best Local Similarity 90.0%; Pred. No. 91;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1533 GGTGGAGATGACGAGAG 1552
Db 1 GGTGGAGATGACGAGAG 20

RESULT 82
AR183664/c
LOCUS AR183664 22 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 14 from patent US 6342351.
ACCESSION AR183664
VERSION AR183664.1 GI:20227633
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Chen,H. and Freimer,N.B.
TITLE Methods and compositions for diagnosing and treating chromosome-18p
related disorders
JOURNAL Patent: US 6342351-A 14 29-JAN-2002;
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source
1..22
Location/Qualifiers
/organism="unknown"
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Query Match 0.5%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3356 CAAAGCAGACACTCAATAAA 3375
Db 22 CACAGCAGACACACAATAAA 3

RESULT 83
AR212423/c
LOCUS AR212423 22 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 14 from patent US 6399762.
ACCESSION AR212423

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VERSION AR212423.1 GI:21515994
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Chen,H. and Freimer,N.B.
TITLE Methods and compositions for diagnosing and treating chromosome
-18p related disorders
JOURNAL Patent: US 6399762-A 14 04-JUN-2002;
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source
Location/Qualifiers
1..22
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3356 CAAAGCAGACACTCAATAAA 3375
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Db 22 CACAGCAGACACACATAAA 3

RESULT 84
AX397588/c 22 bp DNA linear PAT 18-MAY-2002
LOCUS
DEFINITION Sequence 14 from Patent WO0210366.
ACCESSION AX397588
VERSION AX397588.1 GI:21068334
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Chen,H., Freimer,N.B. and Novak,T.
TITLE Methods and compositions for diagnosing and treating chromosome-18p
related disorders
JOURNAL Patent: WO 0210366-A 14 07-FEB-2002;
Millennium Pharmaceuticals, Inc. (US) ; The Regents of The
University of California (US)
FEATURES
source
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 0.5%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3356 CAAAGCAGACACTCAATAAA 3375
||| ||||| ||||| |||||
Db 22 CACAGCAGACACACATAAA 3

RESULT 85
BD137386/c 22 bp DNA linear PAT 18-SEP-2002
LOCUS
DEFINITION Method and composition for diagnosing and treating 18p
chromosome-associated disorder.
ACCESSION BD137386
VERSION BD137386.1 GI:23232331
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Chen,H. and Freimer,N.B.
TITLE Method and composition for diagnosing and treating 18p
chromosome-associated disorder
JOURNAL Patent: JP 2002506875-A 12 05-MAR-2002;

```

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MILLENNIUM PHARMACEUTICALS INC, REGENTS OF THE UNIVERSITY OF
CALIFORNIA
OS Artificial Sequence
PN JP 2002506875-A/12
PD 05-MAR-2002
PF 16-MAR-1999 JP 2000536728
PR 16-MAR-1998 US 60/078044,05-JUN-1998 US 60/088312 PR
28-OCT-1998 US 60/106056,22-JAN-1999 US 09/236134 PI HONG
CHEN,NELSON B FREIMER
PC C07K14/435,A61K45/00,A61P25/00,C07K16/18,C12N1/15,C12N1/19, PC
C12N1/21,
PC C12N5/10,C12N15/01,C12N15/09,C12P21/06,C12Q1/68,C12N5/00, PC
C12N15/00,
PC C12N15/00
CC Primer
FH Key 1..22 Location/Qualifiers
FT source /organism='Artificial Sequence'.
FEATURES
source
Location/Qualifiers
1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.5%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3356 CAAAGCAGACACTCAATAAA 3375
||| ||||| ||||| |||||
Db 22 CACAGCAGACACACATAAA 3

RESULT 86
AX292229
LOCUS
DEFINITION Sequence 3991 from Patent WO0179548.
ACCESSION AX292229
VERSION AX292229.1 GI:17053912
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Barany,P., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid
sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 3991 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
source
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

Query Match 0.5%; Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1788 AATCGAACCCTGGACCCCTA 1807
||| ||||| ||||| |||||
Db 5 AATCGAACCCTGGACCCCTA 24

RESULT 87
AX750656/c 23 bp DNA linear PAT 20-JUN-2003
LOCUS
DEFINITION Sequence 6 from Patent WO03032713.
ACCESSION AX750656
VERSION AX750656.1 GI:32133032
KEYWORDS
SOURCE synthetic construct

```

```

ORGANISM
REFERENCE
  1
  Marracchini,P.R., Deshayes,A. and Rogers,J.
  TITLE
  Coffee plant with reduced g(a)-d-galactosidase activity
  JOURNAL
  Patent: WO 03032713-A 6 24-APR-2003;
  Societe des Produits Nestle S.A.(CH)
  FEATURES
    source
      1..23
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Primer BETA101"
  Query Match
    0.5%; Score 16.6; DB 1; Length 23;
  Best Local Similarity
    82.6%; Pred. No. 1.4e+02;
  Matches
    19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 792 TTGAAGAGATTAAACATTATAT 814
Db 23 TTGAAGAGATTAAAGTCAATAAAT 1

RESULT 88
AR036155/c
LOCUS
  AR036155
  DEFINITION
  Sequence 13 from patent US 5871992.
  ACCESSION
  AR036155
  VERSION
  AR036155.1 GI:5952823
  KEYWORDS
  Unknown.
  SOURCE
  Unknown.
  ORGANISM
  Unclassified.
  REFERENCE
  1 (bases 1 to 21)
  AUTHORS
  Teebor,G.W. and Hilbert,T.P.
  TITLE
  Mammalian endonuclease III, and diagnostic and therapeutic uses
  JOURNAL
  Patent: US 5871992-A 13 16-FEB-1999;
  FEATURES
    source
      1..21
      /organism="unknown"
      /mol_type="unassigned DNA"
  Query Match
    0.5%; Score 16.4; DB 1; Length 21;
  Best Local Similarity
    94.4%; Pred. No. 1.2e+02;
  Matches
    17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 385 GCTTCAGCTGCGGCTCT 402
Db 21 GCTTCGCTGCGAGGCTCT 4

RESULT 89
AX096571/c
LOCUS
  AX096571
  DEFINITION
  Sequence 1749 from Patent WO0118250.
  ACCESSION
  AX096571
  VERSION
  AX096571.1 GI:13512825
  KEYWORDS
  Homo sapiens (human)
  SOURCE
  Homo sapiens
  ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
  1
  Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.G. and
  McCarthy,J.J.
  TITLE
  Single nucleotide polymorphisms in genes
  JOURNAL
  Patent: WO 0118250-A 1749 15-MAR-2001;
  WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
  Pharmaceuticals, Inc. (US)
  FEATURES
    Location/Qualifiers
      1..21
      /organism="Homo sapiens"

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/mol_type="unassigned DNA"

Query Match      0.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2407 GAAGAAGAAAATAAAGCAAG 2427
Db 21 GGAGAGAGAAAATAAAGAAAG 1

RESULT 92
I43369
LOCUS      21 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION Sequence 3 from patent US 5631162.
ACCESSION  I43369
VERSION     I43369.1 GI:2468613
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 21)
AUTHORS   LeBoulch,P., London,I.M. and Tuan,D.
TITLE     Retroviral vectors for transducing .beta.-globin gene and
          .beta.-locus control region derivatives
JOURNAL   Patent: US 5631162-A 3 20-MAY-1997;
FEATURES   Location/Qualifiers
            source
              1..21
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      0.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2407 GAAGAAGAAAATAAAGCAAG 2427
Db 1 GGAGAGAGAAAATAAAGAAAG 21

RESULT 93
AX804400/c
LOCUS      21 bp      DNA      linear      PAT 25-NOV-2003
DEFINITION Sequence 568 from Patent WO03060160.
ACCESSION  AX804400
VERSION     AX804400.1 GI:38521541
KEYWORDS   .
SOURCE     Oreochromis niloticus (Nile tilapia)
ORGANISM   Oreochromis niloticus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
          Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
          Labroidae; Cichlidae; Oreochromis.
REFERENCE  1
AUTHORS   Lie,Y., Slettan,A., Hoeyum,M. and Lingaas,F.
TITLE     Verification of food origin based on nucleic acid pattern
          recognition
JOURNAL   Patent: WO 03060160-A 568 24-JUL-2003;
          Genomar ASA (NO)
FEATURES   Location/Qualifiers
            source
              1..21
              /organism="Oreochromis niloticus"
              /mol_type="unassigned DNA"
              /db_xref="taxon:8128"

Query Match      0.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 850 GAATGCCTATCCTTCCCTATAT 870
Db 21 GAATGCCTCCTTCCCTGAT 1

/mol_type="unassigned DNA"

RESULT 94
AX420193/c
LOCUS      22 bp      DNA      linear      PAT 18-JUN-2002
DEFINITION Sequence 82 from Patent WO0208289.
ACCESSION  AX420193
VERSION     AX420193.1 GI:21524444
KEYWORDS   .
SOURCE     synthetic construct
          synthetic construct
          artificial sequences.
ORGANISM   .
REFERENCE  1
AUTHORS   Padigar,M., Mezes,P., Mishra,V., Burgess,C., Casman,S. and
          Smithson,G.
TITLE     G-protein coupled receptors and nucleic acids encoding same
JOURNAL   Patent: WO 0208289-A 82 31-JAN-2002;
          Curagen Corporation (US)
FEATURES   Location/Qualifiers
            source
              1..22
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Agl269 PCR Primer Sequences"

Query Match      0.5%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2637 CAGAAAAAAATTTGTCCAAG 2657
Db 22 CAGAAAGAAATTTGTCACAG 2

RESULT 95
AR293108/c
LOCUS      19 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 4843 from patent US 6537751.
ACCESSION  AR293108
VERSION     AR293108.1 GI:31680392
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 19)
AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE     Biallelic markers for use in constructing a high density
          disequilibrium map of the human genome
JOURNAL   Patent: US 6537751-A 4843 25-MAR-2003;
          Location/Qualifiers
            source
              1..19
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      0.5%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 TTTCCTCTCTCGATT 2724
Db 17 TTTCCTCTCTCGATT 2

RESULT 96
AX674963/c
LOCUS      20 bp      DNA      linear      PAT 27-MAR-2003
DEFINITION Sequence 90 from Patent WO03005034.
ACCESSION  AX674963
VERSION     AX674963.1 GI:29333296
KEYWORDS   .
SOURCE     Homo sapiens (human)
          Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE 1
AUTHORS Macdonald,M.L., Zeisler,J.M., Samuels,M., Goldberg,Y.P.,
        Robatillie,J.M. and Hayden,M.R.
TITLE Processes for identifying therapeutic agents useful in treating
        diseases involving fzd4 gene
JOURNAL Patent: WO 03005034-A 90 16-JAN-2003;
        Xenon Genetics, Inc. (CA) ; The University of British Columbia (CA)
FEATURES
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        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
Best Local Similarity 100.0%; Score 16; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 547 GAATGAATATGCA 562
    |||||
Db 19 GAATGAATATGCA 4

RESULT 97
A58751
LOCUS Sequence 5 from Patent WO9641868.
DEFINITION
ACCESSION A58751
VERSION A58751.1 GI:3714289
KEYWORDS
SOURCE
ORGANISM
unclassified.

REFERENCE 1
AUTHORS Fischer,B., Schlokot,U., Mitterer,A., Falkner, Falko-Guenter and
        Eibl,J.
TITLE PROTHROMBIN DERIVATIVES
JOURNAL Patent: WO 9641868-A 5 27-DEC-1996;
        IMMUNO AG (AT)
COMMENT Other publication AU 5887196 970109.
FEATURES
    source
        1. .20
        /organism="unidentified"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32644"

Query Match
Best Local Similarity 0.5%; Score 15.8; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1967 ATAAGCCTAAATCAGCTC 1985
    |||||
Db 2 ATAAGCCTGAATCAACTC 20

RESULT 98
A102459
LOCUS Sequence 5 from patent US 6086871.
DEFINITION
ACCESSION A102459
VERSION A102459.1 GI:12814047
KEYWORDS
SOURCE
ORGANISM
Unknown.
unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Fischer,B., Schlokot,U., Mitterer,A., Falkner,F.-G. and Eibl,J.
TITLE Prothrombin derivatives
JOURNAL Patent: US 6086871-A 5 11-JUL-2000;
        Xenon Genetics, Inc. (CA) ; The University of British Columbia (CA)
FEATURES
    source
        1. .20
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        /mol_type="unassigned DNA"

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Query Match
Best Local Similarity 0.5%; Score 15.8; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1967 ATAAGCCTAAATCAGCTC 1985
    |||||
Db 2 ATAAGCCTGAATCAACTC 20

RESULT 99
E23761
LOCUS Immortalized human papilla pili cell and method for evaluating hair
        growth stimulants with the use of the same.
DEFINITION
ACCESSION E23761
VERSION E23761.1 GI:13024509
KEYWORDS
SOURCE
ORGANISM
unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Jun,S., Eriko,T., Chika,H., Akihiro,I., Masahiro,T. and Hiroshi,H.
TITLE Immortalized human papilla pili cell and method for evaluating hair
        growth stimulants with the use of the same
JOURNAL Patent: JP 1999089565-A 50 06-APR-1999;
        SHISEIDO CO LTD
COMMENT
OS Unidentified
PN JP 1999089565-A/50
PD 06-APR-1999
PF 19-SEP-1997 JP 1997271927
PR
PI JUN SUZUKI, ERIKO TAKEOKA, CHIKA HAMADA, AKIHIRO ISHINO, PI
        MASAHIRO TAJIMA,
        PI HIROSHI HANDA
PC C12N5/10,A61K7/06,C12N15/09,C12P21/02,C12Q1/02//(C12N5/10, PC
        C12R1:91),
        PC (C12P21/02,C12R1:91),C12N5/00,C12N15/00,(C12N5/00,C12R1:91) CC
        Strandedness: Single;
CC Topology: Linear;
FH Key
FT source
        1. .20
        /organism="unidentified"
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        /db_xref="taxon:32644"

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        Location/Qualifiers
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Best Local Similarity 0.5%; Score 15.8; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1038 AGAAGTCTCTTTGTATCTGT 1056
    |||||
Db 1 AGAAGTCTGGGTATCTGT 19

RESULT 100
AR221001
LOCUS Sequence 54 from patent US 6426188.
DEFINITION
ACCESSION AR221001
VERSION AR221001.1 GI:23327886
KEYWORDS
SOURCE
ORGANISM
Unknown.
unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Wyatt,J.
TITLE Antisense modulation of phosphorylase kinase alpha 1 expression
JOURNAL Patent: US 6426188-A 54 30-JUL-2002;
        Xenon Genetics, Inc. (CA) ; The University of British Columbia (CA)
FEATURES
    source
        1. .20
        Location/Qualifiers

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Best Local Similarity		89.5%; Pred. No. 1.2e+02;		1..21	
Matches		17; Conservative		0; Mismatches 2; Indels 0; Gaps 0;	
Qy	3249	AACTGTGGAGTGAAATGAA	3267		
Db	2	AACTGTGGAGTGAAGTAA	20		
RESULT 101					
AX047768/c					
LOCUS					
Sequence 11 from Patent WO0070032.					
AX047768					
ACCESSION					
VERSION					
AX047768.1 GI:11876774					
KEYWORDS					
synthetic construct					
synthetic construct					
artificial sequences.					
SOURCE					
ORGANISM					
1					
REFERENCE					
Fiddington,C.S., Petrie,C.R., Shoemaker,K.E. and Bishop,P.D.					
AUTHORS					
Zace2: a human metalloenzyme					
TITLE					
Patent: WO 0070032-A 11 23-NOV-2000;					
JOURNAL					
ZymoGenetics, Inc. (US)					
FEATURES					
Location/Qualifiers					
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/organism="synthetic construct"					
/mol_type="unassigned DNA"					
/db_xref="taxon:32630"					
/note="PCR primer."					
Query Match					
0.5%; Score 15.8; DB 1; Length 20;					
Best Local Similarity					
89.5%; Pred. No. 1.2e+02;					
Matches					
17; Conservative					
0; Mismatches 2; Indels 0; Gaps 0;					
Qy	876	CAATTGGATGCTCCCTGC	894		
Db	20	CCACTGGATGCTCCCTGC	2		
RESULT 102					
E01836/c					
LOCUS					
silencer gene of murine F9 cell.					
E01836					
ACCESSION					
VERSION					
E01836.1 GI:2170088					
KEYWORDS					
JP 1989039991-A/1.					
SOURCE					
Mus musculus (house mouse)					
ORGANISM					
Mus musculus					
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
1 (bases 1 to 21)					
REFERENCE					
Takahashi,H., Yamazaki,N. and Yamamoto,M.					
AUTHORS					
SILENCER BASE SEQUENCE					
TITLE					
Patent: JP 1989039991-A 1 10-FEB-1989;					
JOURNAL					
TAIYO KAGAKU CO LTD					
COMMENT					
OS (mouse)					
PN JP 1989039991-A/1					
PD 10-FEB-1989					
PF 07-AUG-1987 JP 1987197464					
PI TAKAHASHI HIDEHISA, YAMAZAKI NAGATAKA, YAMAMOTO MITSUYOSHI PC					
C12N15/00,C07H21/04;					
CC strandedness: Double;					
CC topology: Linear;					
CC hypothetical: No;					
CC anti-sense: No;					
CC *source: cell_line=F9 cell;					
FH Key					
Location/Qualifiers					
1..21					
misc feature					
FT					

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QY 1072 GACTCAAGGATTCGGGA 1090
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Db 20 GACTCAAGACTTCGGGA 2

RESULT 105
AB087734/c
LOCUS AB087734 21 bp DNA linear PRI 08-JAN-2003
DEFINITION Homo sapiens gene for beta-globin, intron, partial sequence, CTTT
deletion at IVS 2.
ACCESSION AB087734
VERSION AB087734.1 GI:27544745
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Nadkarni, A., Sakaguchi, T., Takaku, H., Gorakshakar, A.,
Phanagaokar, S., Colah, R., Mohanty, D. and Kiyama, R.
TITLE Three novel polymorphisms found in the Indian Thalassemia patients
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 21)
AUTHORS Nadkarni, A., Sakaguchi, T., Takaku, H., Gorakshakar, A.,
Phanagaokar, S., Colah, R., Mohanty, D. and Kiyama, R.
TITLE Direct Submission
JOURNAL Submitted (05-JUL-2002) Ryoiti Kiyama, National Institute of
Advanced Industrial Science and Technology, Research Center for
Glycoscience; AIST Central 6, 1-1-1 Higashi, Tsukuba, Ibaraki
305-8566, Japan (E-mail:kiyama.romaist.go.jp, Tel:81-298-61-6189,
Fax:81-298-61-6190)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/isolate="Indian Thalassemia patient"
/db_xref="taxon:9606"
<1..>21
/note="Sequence containing a CTTT deletion at IVS 2
#200-203 from an Indian Thalassemia patient
beta-globin"
intron
Query Match 0.5%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. NO. 1.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2413 GAAAAATAAAGCAGAAGT 2431
|||||
Db 21 GAAAAATAAAGCAGAATT 3

RESULT 106
BOVDIK31
LOCUS BOVDIK31 22 bp DNA linear MAM 09-FEB-1999
DEFINITION Bovine DNA, microsatellite DIK054 PCR sense primer.
ACCESSION D44532
VERSION D44532.1 GI:624822
KEYWORDS microsatellite.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
REFERENCE 1 (sites)
AUTHORS Hirano, T., Nakane, S., Mizoshita, K., Yamakuchi, H.,
Inoue-Murayama, M., Watanabe, T., Barendse, W. and Sugimoto, Y.
TITLE Characterization of 42 highly polymorphic bovine microsatellite
markers
JOURNAL Anim. Genet. 27 (5), 365-368 (1996)
MEDLINE 97083737
PUBMED 8930081
REFERENCE 2 (bases 1 to 22)

AUTHORS Inoue, M., Watanabe, T., Hirano, T., Yamakuchi, H., Teukazawa, H.,
Watanabe, E., Morita, M. and Sugimoto, Y.
TITLE Isolation of microsatellites from Japanese black cattle (Wagyu) and
their application to individual identification and paternity
exclusion
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 22)
AUTHORS Sugimoto, Y.
TITLE Direct Submission
JOURNAL Submitted (21-DEC-1994) Yoshikazu Sugimoto, Japan Live Stock
Technology Association, Shirokawa Institute of Animal Genetics;
Nishigo Odakura, Nishishirakawa, Fukushima 961, Japan
(E-mail:LDI03222@niftyserve.or.jp, Tel:0248-25-5641,
Fax:0248-25-5725)
FEATURES
source Location/Qualifiers
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/organism="Bos taurus"
/mol_type="genomic DNA"
/db_xref="taxon:9913"
<1..22
/note="microsatellite DIK054 PCR sense primer"
misc_feature
Query Match 0.5%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. NO. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2750 GGATTTCGTATTAGAGTAT 2768
|||||
Db 1 GGATTTCGTATTAGGTAT 19

RESULT 107
A91051/c
LOCUS A91051 22 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 14 from Patent WO9828431.
ACCESSION A91051
VERSION A91051.1 GI:6740047
KEYWORDS
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dirks, R. and Jones, J.D.
TITLE TRANSCRIPTIONAL REGULATION IN PLANTS
JOURNAL Patent: WO 9828431-A 14 02-JUL-1998;
DIRKS ROBERT (BE); INNES JOHN CENTRE INNOV LTD (GB)
FEATURES
source Location/Qualifiers
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.5%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. NO. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 830 TATGTGAGGCAAAAGTTGA 848
|||||
Db 19 TATCTGAGGCCAAAGTTGA 1

RESULT 108
AR279060/c
LOCUS AR279060 22 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 193 from patent US 6514694.
ACCESSION AR279060
VERSION AR279060.1 GI:29713703
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Milhausen, M.J.

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TITLE Methods for the detection of encysted parasites

JOURNAL Patent: US 6514694-A 193 04-FEB-2003;

FEATURES Location/Qualifiers

source

1..22

/organism="unknown"

/mol_type="genomic DNA"

Query Match 0.5%; Score 15.8; DB 1; Length 22;

Best Local Similarity 89.5%; Pred. No. 1.5e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3132 TGCTTTTCACTTCCCAAGG 3150

Db 21 TGCTTCTGCACCTTCCCAAGG 3

RESULT 109

AX598303

LOCUS

DEFINITION

Accession

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..22

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

Query Match

Best Local Similarity

Matches

17; Conservative

0.5%; Score 15.8; DB 1; Length 22;

Pred. No. 1.5e+02;

Mismatches 2; Indels

0; Gaps

0;

QY 1130 GTCTGCATCCACAGCTT 1148

Db 1 GTCTGCTTCTCACAGCTT 19

RESULT 110

AR027263

LOCUS

DEFINITION

Accession

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..22

/organism="unknown"

/mol_type="unassigned DNA"

Query Match

Best Local Similarity

Matches

18; Conservative

0.5%; Score 15.6; DB 1; Length 22;

Pred. No. 1.6e+02;

Mismatches 4; Indels

0; Gaps

0;

TITLE Methods for the detection of encysted parasites

JOURNAL Patent: US 6514694-A 193 04-FEB-2003;

FEATURES Location/Qualifiers

source

1..22

/organism="unknown"

/mol_type="genomic DNA"

Query Match 0.5%; Score 15.8; DB 1; Length 22;

Best Local Similarity 89.5%; Pred. No. 1.5e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3132 TGCTTTTCACTTCCCAAGG 3150

Db 21 TGCTTCTGCACCTTCCCAAGG 3

RESULT 109

AX598303

LOCUS

DEFINITION

Accession

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..22

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

Query Match

Best Local Similarity

Matches

17; Conservative

0.5%; Score 15.8; DB 1; Length 22;

Pred. No. 1.5e+02;

Mismatches 2; Indels

0; Gaps

0;

QY 1130 GTCTGCATCCACAGCTT 1148

Db 1 GTCTGCTTCTCACAGCTT 19

RESULT 110

AR027263

LOCUS

DEFINITION

Accession

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..22

/organism="unknown"

/mol_type="unassigned DNA"

Query Match

Best Local Similarity

Matches

18; Conservative

0.5%; Score 15.6; DB 1; Length 22;

Pred. No. 1.6e+02;

Mismatches 4; Indels

0; Gaps

0;

QY 384 AGCTTCAGCTGCAGGCTCTTCA 405

Db 1 AGCTTAGGCTGCAGGCGCTGCA 22

RESULT 111

AR080307/c

LOCUS

DEFINITION

Accession

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..22

/organism="unknown"

/mol_type="unassigned DNA"

Query Match

Best Local Similarity

Matches

18; Conservative

0.5%; Score 15.6; DB 1; Length 22;

Pred. No. 1.6e+02;

Mismatches 4; Indels

0; Gaps

0;

QY 391 GCTCAGGCTCTTCAGCAAAAT 412

Db 22 GCAGCAGGCTCTGCACCCACAT 1

RESULT 112

AR111407

LOCUS

DEFINITION

Accession

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..22

/organism="unknown"

/mol_type="unassigned DNA"

Query Match

Best Local Similarity

Matches

18; Conservative

0.5%; Score 15.6; DB 1; Length 22;

Pred. No. 1.6e+02;

Mismatches 4; Indels

0; Gaps

0;

QY 384 AGCTTCAGCTGCAGGCTCTTCA 405

Db 1 AGCTTAGGCTGCAGGCGCTGCA 22

RESULT 113

AX217230

LOCUS

DEFINITION

Accession

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..22

/organism="unknown"

/mol_type="unassigned DNA"

Query Match

Best Local Similarity

Matches

18; Conservative

0.5%; Score 15.6; DB 1; Length 22;

Pred. No. 1.6e+02;

Mismatches 4; Indels

0; Gaps

0;

QY 384 AGCTTCAGCTGCAGGCTCTTCA 405

Db 1 AGCTTAGGCTGCAGGCGCTGCA 22

RESULT 111

AR080307/c

LOCUS

DEFINITION

Accession

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..22

/organism="unknown"

/mol_type="unassigned DNA"

Query Match

Best Local Similarity

Matches

18; Conservative

0.5%; Score 15.6; DB 1; Length 22;

Pred. No. 1.6e+02;

Mismatches 4; Indels

0; Gaps

0;

QY 391 GCTCAGGCTCTTCAGCAAAAT 412

Db 22 GCAGCAGGCTCTGCACCCACAT 1

RESULT 112

AR111407

LOCUS

DEFINITION

Accession

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..22

/organism="unknown"

/mol_type="unassigned DNA"

Query Match

Best Local Similarity

Matches

18; Conservative

0.5%; Score 15.6; DB 1; Length 22;

Pred. No. 1.6e+02;

Mismatches 4; Indels

0; Gaps

0;

QY 384 AGCTTCAGCTGCAGGCTCTTCA 405

Db 1 AGCTTAGGCTGCAGGCGCTGCA 22

RESULT 113

AX217230

LOCUS

DEFINITION

Accession

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..22

/organism="unknown"

/mol_type="unassigned DNA"

Query Match

Best Local Similarity

Matches

18; Conservative

0.5%; Score 15.6; DB 1; Length 22;

Pred. No. 1.6e+02;

Mismatches 4; Indels

0; Gaps

0;

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artificial sequences.
1
REFERENCE
AUTHORS
TITLE
Blatt,L., McSwiggen,J. and Chowrira,B.M.
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL
PATENT: WO 0159103-A 2672 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match
Best Local Similarity 0.5%; Score 15.4; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1491 TCTTTAAAGGGGAATT 1507
Db 1 TCTTTAAAGGGGAATT 17

RESULT 114
AX217231 17 bp RNA linear PAT 07-SEP-2001
LOCUS
DEFINITION
Sequence 2673 from Patent WO0159103.
ACCESSION
AX217231
VERSION
AX217231.1 GI:15527292
KEYWORDS
synthetic construct
synthetic construct
artificial sequences.
ORGANISM
Homo sapiens (human)
REFERENCE
AUTHORS
Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL
PATENT: WO 0159103-A 2673 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match
Best Local Similarity 0.5%; Score 15.4; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1492 CTTTAAAGGGGAATTC 1508
Db 1 CTTTAAAGGGGAATTC 17

RESULT 115
AX734885 17 bp DNA linear PAT 08-MAY-2003
LOCUS
DEFINITION
Sequence 475 from Patent WO03025177.
ACCESSION
AX734885
VERSION
AX734885.1 GI:30514162
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
Telerman,A., Anson,R. and Tuijnder,M.
TITLE
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments

artificial sequences.
1
JOURNAL
PATENT: WO 03025177-A 475 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.5%; Score 15.4; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2666 GCCAAGGAGAGGAGCATC 2682
Db 17 GCCAAGGAGAGGAGCATC 1

RESULT 116
AX759478 17 bp DNA linear PAT 25-JUN-2003
LOCUS
DEFINITION
Sequence 2799 from Patent WO03040369.
ACCESSION
AX759478
VERSION
AX759478.1 GI:32254094
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
Telerman,A., Anson,R. and Tuijnder,M.
TITLE
Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL
PATENT: WO 03040369-A 2799 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.5%; Score 15.4; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 358 ACAAGAAATTCAGATC 374
Db 17 ACAAGAAATTCAGATC 1

RESULT 117
AR048184 18 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION
Sequence 2 from patent US 5821062.
ACCESSION
AR048184
VERSION
AR048184.1 GI:5970527
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
AUTHORS
Komai,K., Kaneko,H. and Nakatsuka,I.
TITLE
Oligonucleotide for use in checking presence or absence of mutation
in human-derived cytochrome P45011C18 gene
JOURNAL
PATENT: US 5821062-A 2 13-OCT-1998;
FEATURES
source
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.5%; Score 15.4; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1516 CCAGTGGATGAAAAAGT 1532
 |||||
 Db 18 CCAGTGGCTGAAAAAGT 2

RESULT 118

E10137/c
 LOCUS 18 bp DNA linear PAT 29-SEP-1997
 DEFINITION PCR primer to amplify mutated genes encoding human cytochrome
 P45011C18.
 ACCESSION E10137
 VERSION E10137.1 GI:22026765
 KEYWORDS JP 1995285987-A/2.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Komai,K., Kaneko,H. and Nakatsuka,I.
 TITLE OLIGONUCLEOTIDE FOR AMPLIFYING MUTATION TYPE GENE OF HUMAN DERIVED
 CYTOCHROME P45011C18
 JOURNAL Patent: JP 1995285987-A 2 31-OCT-1995;
 SUMITOMO CHEM CO LTD
 COMMENT OS None
 OC Artificial sequences.
 PN JP 1995285987-A/2
 PD 31-OCT-1995
 PF 29-MAR-1994 JP 1994059386
 PI KOWAI KOICHIRO, KANEKO HIDEO, NAKATSUKA IWAO
 PC C07H21/04,C12Q1/68//C12N15/09;
 CC strandedness: Single;
 CC topology: Linear;
 FH Key Location/Qualifiers
 FT source 1..18
 FT /organism='Artificial sequences'.

FEATURES

source
 1..18 Location/Qualifiers
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

Query Match 0.5%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1516 CCAGTGGATGAAAAAGT 1532
 |||||
 Db 18 CCAGTGGCTGAAAAAGT 2

RESULT 119

AR294697
 LOCUS 18 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 6432 from patent US 6537751.
 ACCESSION AR294697
 VERSION AR294697.1 GI:31681981
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
 TITLE Biallelic markers for use in constructing a high density
 map of the human genome
 JOURNAL Patent: US 6537751-A 6432 25-MAR-2003;
 FEATURES Location/Qualifiers
 source 1..18
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 0.5%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 598 GGAAAGCTGGAGTCTG 614
 |||||
 Db 2 GGAAAGCTGGAGTCTG 18

RESULT 120

AX193676
 LOCUS 20 bp DNA linear PAT 15-AUG-2001
 DEFINITION Sequence 98 from Patent WO0140291.
 ACCESSION AX193676
 VERSION AX193676.1 GI:15211542
 KEYWORDS .
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1
 AUTHORS Burgess,C.E., Prayaga,S.K., Shimkets,R.A., Rastelli,L.,
 Zerhusen,B.D. and Mezes,P.S.
 TITLE Proteins and nucleic acids encoding the same
 JOURNAL Patent: WO 0140291-A 98 07-JUN-2001;
 Curagen Corporation (US)
 FEATURES Location/Qualifiers
 source 1..20
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="chemically synthesized"

Query Match 0.5%; Score 15.4; DB 1; Length 20;
 Best Local Similarity 94.1%; Pred. No. 1.3e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 381 TCAGCTTCAGTGCAG 397
 |||||
 Db 1 TGAAGCTTCAGTGCAG 17

RESULT 121

BD015688
 LOCUS 20 bp DNA linear PAT 27-AUG-2002
 DEFINITION Novel protein and DNA thereof.
 ACCESSION BD015688
 VERSION BD015688.1 GI:22556825
 KEYWORDS JP 2001204480-A/3.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Nakanishi,A. and Morita,S.
 TITLE Novel protein and DNA thereof
 JOURNAL Patent: JP 2001204480-A 3 31-JUL-2001;
 TAKEDA CHEMICAL INDUSTRIES LTD
 COMMENT OS Artificial Sequence
 PN JP 2001204480-A/3
 PD 31-JUL-2001
 PF 14-NOV-2000 JP 2000347107
 PI ATSUSHI NAKANISHI,SHIGERU MORITA
 PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P11/00,A61P11/06,
 PC A61P31/04,
 PC A61P31/06,A61P31/12,A61P31/18,A61P37/02,A61P37/08,A61P43/00,
 PC C07K16/40,
 PC C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/34,G01N33/15,G01N33/50//
 PC C12P21/08,C12N15/00,A61K37/02,C12N5/00
 CC Primer
 FH Key Location/Qualifiers
 FT source 1..20
 /organism='Artificial Sequence'.

FEATURES

source
 1..20 Location/Qualifiers
 /organism="synthetic construct"

1 (bases 1 to 20)
Nakanishi,A. and Morita,S.
Novel protein and its DNA
Patent: WO 0136633-A 3 25-MAY-2001;
TAKEDA CHEMICAL INDUSTRIES LTD,ATSUSHI NAKANISHI,SHIGERU MORITA
OS Artificial Sequence
PN WO 0136633-A/3
PD 25-MAY-2001

Matches 16; Conservative 0;

QV 81 GTGATCTTGGCTCACAG 97

```

Db      18 GTGATCTTGGCTCACTG 2
|||||
RESULT 125
AX085751
LOCUS      21 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION Sequence 3 from patent US 5985264.
ACCESSION  AR085751
VERSION     AR085751.1 GI:10012517
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 21)
AUTHORS    Metzger,D.W. and Arulanandam,B.P.
TITLE      IL-12 Stimulation of Neonatal Immunity
JOURNAL    Patent: US 5985264-A 3 16-NOV-1999;
FEATURES   Location/Qualifiers
            source
            1..21
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.5%; Score 15.4; DB 1; Length 21;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2373 TTGTCATCTCGTCACTTC 2389
|||||
Db      2 TTGTCATCTCGTCTTC 18

RESULT 126
AX097058
LOCUS      21 bp      DNA      linear      PAT 30-MAR-2001
DEFINITION Sequence 2326 from Patent WO0118250.
ACCESSION  AX097058
VERSION     AX097058.1 GI:13513326
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS    Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            McCarty,J.J.
TITLE      Single nucleotide polymorphisms in genes
JOURNAL    Patent: WO 0118250-A 2236 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES   Location/Qualifiers
            source
            1..21
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.5%; Score 15.4; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2916 GACAGTGCTCGGAAGTGG 2934
|||||
Db      2 GTCAGTGTGCGGAAGTGG 20

RESULT 127
AX487994
LOCUS      22 bp      DNA      linear      PAT 16-AUG-2002
DEFINITION Sequence 5294 from Patent WO02053728.
ACCESSION  AX487994
VERSION     AX487994.1 GI:22322074
KEYWORDS
SOURCE      Candida albicans

ORGANISM    Candida albicans
REFERENCE   1
AUTHORS    Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlseen,K.L.
TITLE      Gene disruption methodologies for drug target discovery
JOURNAL    Patent: WO 02053728-A 5294 11-JUL-2002;
            Elitra Pharmaceuticals, Inc. (US)
FEATURES   Location/Qualifiers
            source
            1..22
            /organism="Candida albicans"
            /mol_type="unassigned DNA"
            /db_xref="taxon:5476"

Query Match      0.5%; Score 15.4; DB 1; Length 22;
Best Local Similarity 94.1%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2480 CCAGGATTCCAAACAC 2496
|||||
Db      4 CAAGGATTCCAAACAC 20

RESULT 128
BOVINE44
LOCUS      20 bp      DNA      linear      MAM 06-FEB-1999
DEFINITION Bovine DNA for microsatellite marker, 3' terminus.
ACCESSION  D83324
VERSION     D83324.1 GI:1199741
KEYWORDS
SOURCE      Bos taurus (cow)
ORGANISM    Bos taurus
REFERENCE   1 (sites)
AUTHORS    Hirano,T., Nakane,S., Mizoshita,K., Yamakuchi,H.,
            Inoue-Murayama,M., Watanabe,T., Barendse,W. and Sugimoto,Y.
TITLE      Characterization of 42 highly polymorphic bovine microsatellite
            markers
JOURNAL    Anim. Genet. 27 (5), 365-368 (1996)
MEDLINE    97083737
PubMed     8930081
REFERENCE   2 (bases 1 to 20)
AUTHORS    Hirano,T., Nakane,S., Mizoshita,K., Inoue-Murayama,M., Watanabe,T.,
            Barendse,W. and Sugimoto,Y.
TITLE      Unpublished
REFERENCE   3 (bases 1 to 20)
AUTHORS    Sugimoto,Y.
JOURNAL    Submitted (29-JAN-1996) Yoshikazu Sugimoto, Japan Live Stock
            Technology Association, Shirakawa Institute of Animal Genetics,
            Nishigo Odakura, Nishishirakawa, Fukushima 961, Japan
            (E-mail:LDI03222@niftyserve.or.jp, Tel:0248-25-5641,
            Fax:0248-25-5725)
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="Bos taurus"
            /mol_type="genomic DNA"
            /db_xref="taxon:9913"
            <1..20
            /note="microsatellite DIK106 PCR antisense primer"

Query Match      0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2312 CCCCCTGTTTCCATATGGCT 2331
|||||
Db      1 CCCCCTCTTTCCATCTGTCT 20

```



```
RESULT 129
AR117759
LOCUS AR117759 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 67 from patent US 6140126.
ACCESSION AR117759
VERSION AR117759.1 GI:14098665
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
AUTHORS Bennett, C. Frank, and Cowser, L. M.
TITLE Antisense modulation of Y-box binding protein 1 expression
JOURNAL Patent: US 6140126-A 67 31-OCT-2000;
FEATURES
source
/mol_type="unassigned DNA"
Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2139 TCTCCTTGAATTTCTTCTGTC 2158
Dbb 1 TCTCCTTGAATTTCTTCTTATC 20

RESULT 130
AR122465/c
LOCUS AR122465 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 19 from patent US 6165728.
ACCESSION AR122465
VERSION AR122465.1 GI:14106782
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
AUTHORS Ward, D. T. and Cowser, L. M.
TITLE Antisense modulation of NCK-2 expression
JOURNAL Patent: US 6165728-A 19 26-DEC-2000;
FEATURES
source
/mol_type="unassigned DNA"
Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1290 CTAATGAAGGATTCATGAA 1309
Dbb 20 CCAGAAGAGGACTCCATGAA 1

RESULT 131
AR242914/c
LOCUS AR242914 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 60 from patent US 6475739.
ACCESSION AR242914
VERSION AR242914.1 GI:27289576
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
AUTHORS Brunkow, M. E., Proll, S., Paepfer, B. and Staehling-Hampton, K.
TITLE Methods for identifying genomic deletions
JOURNAL Patent: US 6475739-A 60 05-NOV-2002;
FEATURES
source
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1303 CCATGAAGCTGTGGGAAA 1322
Dbb 1 CCACGAATCTCTGGGAAA 20

RESULT 132
AR294853/c
LOCUS AR294853 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6588 from patent US 6537751.
ACCESSION AR294853
VERSION AR294853.1 GI:31682137
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 6588 25-MAR-2003;
FEATURES
source
/mol_type="genomic DNA"
Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1042 GTTCTTTGATCTGTGTC 1061
Dbb 20 GTTCTATGATTTGTAGTC 1

RESULT 133
AR310764
LOCUS AR310764 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 1301 from patent US 6559294.
ACCESSION AR310764
VERSION AR310764.1 GI:31704190
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
AUTHORS Griffais, R., Hoiseth, S. K., Zagursky, R. J., Metcalf, B. J., Peek, J. A.,
Sankaran, B. and Fletcher, L. D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 1301 06-MAY-2003;
FEATURES
source
/mol_type="genomic DNA"
Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1303 CCATGAAGCTGTGGGAAA 1322
Dbb 1 CCACGAATCTCTGGGAAA 20

RESULT 134
AR312610
LOCUS AR312610 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 3147 from patent US 6559294.
FEATURES
source
/mol_type="unassigned DNA"
Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1303 CCATGAAGCTGTGGGAAA 1322
Dbb 1 CCACGAATCTCTGGGAAA 20
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ACCESSION      AR312610
VERSION        AR312610.1  GI:31706036
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS        Griffais,R., Holseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
                Saukaran,B. and Fletcher,L.D.
TITLE          Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL        Patent: US 6559294-A 3147 06-MAY-2003;
FEATURES       Location/Qualifiers
                source
                1..20
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match    0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 475 CACCATCTACAGTACTGGAA 494
      ||||| ||||| ||||| |||||
Db 1 CACCACCTACAGTAATGGCA 20

RESULT 135
AX048431/c
LOCUS          AX048431          20 bp DNA linear PAT 12-JAN-2001
DEFINITION     Sequence 30 from Patent WO0071747.
ACCESSION      AX048431
VERSION        AX048431.1  GI:12225595
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1
AUTHORS        Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE          Detection system for separating constituents of a sample and
                production and use of the same
JOURNAL        Patent: WO 0071747-A 30 30-NOV-2000;
                Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES       Location/Qualifiers
                source
                1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Beschreibung der kunstlichen
                Sequenz:Erkennungssystem"

Query Match    0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3386 ACACACTCAAAAAAAAAA 3405
      ||||| ||||| ||||| |||||
Db 20 ACACCTTAAAAAAAAAAAAA 1

RESULT 136
AX293913
LOCUS          AX293913          20 bp DNA linear PAT 21-NOV-2001
DEFINITION     Sequence 5675 from Patent WO0179548.
ACCESSION      AX293913
VERSION        AX293913.1  GI:17055596
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1
AUTHORS        Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE          Method of designing addressable array for detection of nucleic acid
                sequence differences using ligase detection reaction
JOURNAL        Patent: WO 0179548-A 5675 25-OCT-2001;

ACCESSION      AR312610
VERSION        AR312610.1  GI:31706036
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS        Griffais,R., Holseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
                Saukaran,B. and Fletcher,L.D.
TITLE          Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL        Patent: US 6559294-A 3147 06-MAY-2003;
FEATURES       Location/Qualifiers
                source
                1..20
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match    0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 475 CACCATCTACAGTACTGGAA 494
      ||||| ||||| ||||| |||||
Db 1 CACCACCTACAGTAATGGCA 20

RESULT 135
AX048431/c
LOCUS          AX048431          20 bp DNA linear PAT 12-JAN-2001
DEFINITION     Sequence 30 from Patent WO0071747.
ACCESSION      AX048431
VERSION        AX048431.1  GI:12225595
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1
AUTHORS        Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE          Detection system for separating constituents of a sample and
                production and use of the same
JOURNAL        Patent: WO 0071747-A 30 30-NOV-2000;
                Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES       Location/Qualifiers
                source
                1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Beschreibung der kunstlichen
                Sequenz:Erkennungssystem"

Query Match    0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3386 ACACACTCAAAAAAAAAA 3405
      ||||| ||||| ||||| |||||
Db 20 ACACCTTAAAAAAAAAAAAA 1

RESULT 136
AX293913
LOCUS          AX293913          20 bp DNA linear PAT 21-NOV-2001
DEFINITION     Sequence 5675 from Patent WO0179548.
ACCESSION      AX293913
VERSION        AX293913.1  GI:17055596
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1
AUTHORS        Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE          Method of designing addressable array for detection of nucleic acid
                sequence differences using ligase detection reaction
JOURNAL        Patent: WO 0179548-A 5675 25-OCT-2001;

FEATURES       Location/Qualifiers
                source
                1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Hypothetical Probe Sequence"

Query Match    0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1095 CCATGCTAACGGACCCAGGA 1114
      ||||| ||||| ||||| |||||
Db 1 CCATGATGACGGTCCAGGA 20

RESULT 138
AX384966/c
LOCUS          AX384966          20 bp DNA linear PAT 19-MAR-2002
DEFINITION     Sequence 60 from Patent WO0210455.
ACCESSION      AX384966
VERSION        AX384966.1  GI:19578094
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1
AUTHORS        Brunkow,M.B., Proll,S. and Paepfer,B.
TITLE          Methods for identifying genomic deletions
JOURNAL        Patent: WO 0210455-A 60 07-FEB-2002;
                Celltech R & D, Inc. (US); Straehling-Hampton, Karen (US)
FEATURES       Location/Qualifiers
                source
                1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="PCR primer"

Query Match    0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1095 CCATGCTAACGGACCCAGGA 1114
      ||||| ||||| ||||| |||||
Db 1 CCATGATGACGGTCCAGGA 20

RESULT 138
AX384966/c
LOCUS          AX384966          20 bp DNA linear PAT 19-MAR-2002
DEFINITION     Sequence 60 from Patent WO0210455.
ACCESSION      AX384966
VERSION        AX384966.1  GI:19578094
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1
AUTHORS        Brunkow,M.B., Proll,S. and Paepfer,B.
TITLE          Methods for identifying genomic deletions
JOURNAL        Patent: WO 0210455-A 60 07-FEB-2002;
                Celltech R & D, Inc. (US); Straehling-Hampton, Karen (US)
FEATURES       Location/Qualifiers
                source
                1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="PCR primer"

Query Match    0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1095 CCATGCTAACGGACCCAGGA 1114
      ||||| ||||| ||||| |||||
Db 1 CCATGATGACGGTCCAGGA 20

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RESULT 141	AR098417/C	AR098417	21 bp	DNA	linear	PAT 14-FEB-2000
LOCUS		Sequence 24 from patent US 6075125.				
DEFINITION		AR098417				
ACCESSION		AR098417.1	GI:12807674			
VERSION						
KEYWORDS						
SOURCE		Unknown.				
ORGANISM		Unknown.				
REFERENCE		Unclassified.				
AUTHORS		1 (bases 1 to 21)				
TITLE		Bacon,L.D., Hunt,H.D. and Fulton,J.E.				
JOURNAL		Production of antisera specific to major histocompatibility complex				
FEATURES		molecules in chickens				
source		Patent: US 6075125-A 24 13-JUN-2000;				
		Location/Qualifiers				
		1. .21				
		/organism="unknown"				
		/mol_type="unassigned DNA"				
Query Match		0.4%;	Score 15.2;	DB 1;	Length 21;	
Best Local Similarity		85.0%;	Pred. No. 1.6e+02;			
Matches		17; Conservative	0; Mismatches	3; Indels	0; Gaps	0;
Qy	815	GAACATCTTCATGCCTATGT	834			
Db	21	GAACGTCTTCATGCTTTGT	2			
RESULT 142	AR098419	AR098419	21 bp	DNA	linear	PAT 14-FEB-2000
LOCUS		Sequence 26 from patent US 6075125.				
DEFINITION		AR098419				
ACCESSION		AR098419.1	GI:12807676			
VERSION						
KEYWORDS		Unknown.				
SOURCE		Unknown.				
ORGANISM		Unknown.				
REFERENCE		Unclassified.				
AUTHORS		1 (bases 1 to 21)				
TITLE		Bacon,L.D., Hunt,H.D. and Fulton,J.E.				
JOURNAL		Production of antisera specific to major histocompatibility complex				
FEATURES		molecules in chickens				
source		Patent: US 6075125-A 26 13-JUN-2000;				
		Location/Qualifiers				
		1. .21				
		/organism="unknown"				
		/mol_type="unassigned DNA"				
Query Match		0.4%;	Score 15.2;	DB 1;	Length 21;	
Best Local Similarity		85.0%;	Pred. No. 1.6e+02;			
Matches		17; Conservative	0; Mismatches	3; Indels	0; Gaps	0;
Qy	815	GAACATCTTCATGCCTATGT	834			
Db	1	GAACGTCTTCATGCTTTGT	20			
RESULT 143	AR294416	AR294416	21 bp	DNA	linear	PAT 12-JUN-2000
LOCUS		Sequence 6151 from patent US 6537751.				
DEFINITION		AR294416				
ACCESSION		AR294416.1	GI:31681700			
VERSION						
KEYWORDS		Unknown.				
SOURCE		Unknown.				
ORGANISM		Unknown.				
REFERENCE		Unclassified.				
AUTHORS		1 (bases 1 to 21)				
TITLE		Cohen,D., Chumakov,I. and Blumenfeld,M.				
JOURNAL		Biallelic markers for use in constructing a high density				
		disequilibrium map of the human genome				
		Patent: US 6537751-A 6151 25-MAR-2003;				

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FEATURES
  source      Location/Qualifiers
  1..21      /organism="unknown"
             /mol_type="genomic DNA"

Query Match
  Best Local Similarity 0.4%; Score 15.2; DB 1; Length 21;
  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 181 GACATTTTGGACAGTTTA 200
      |||||
Db 1 GACATTTTGAACAGTATA 20

RESULT 144
AR297593/3
LOCUS      AR297593      21 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 9328 from patent US 6537751.
ACCESSION AR297593
VERSION AR297593.1 GI:31684877
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
PATENT: US 6537751-A 9328 25-MAR-2003;
FEATURES
  source      Location/Qualifiers
  1..21      /organism="unknown"
             /mol_type="genomic DNA"

Query Match
  Best Local Similarity 0.4%; Score 15.2; DB 1; Length 21;
  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2699 TCAGTATTATTCTGTCTC 2718
      |||||
Db 20 TCACAAATTATTCTGTCTC 1

RESULT 145
AR298617
LOCUS      AR298617      21 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 10352 from patent US 6537751.
ACCESSION AR298617
VERSION AR298617.1 GI:31685901
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
PATENT: US 6537751-A 10352 25-MAR-2003;
FEATURES
  source      Location/Qualifiers
  1..21      /organism="unknown"
             /mol_type="genomic DNA"

Query Match
  Best Local Similarity 0.4%; Score 15.2; DB 1; Length 21;
  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3144 TCCAGGTGCTTCATCAACA 3163
      |||||
Db 1 TCCAGGTGCTTCATCAACA 20

RESULT 146
AR297593
LOCUS      AR297593      21 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 10665 from patent US 6537751.
ACCESSION AR297593
VERSION AR297593.1 GI:31686214
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
PATENT: US 6537751-A 10665 25-MAR-2003;
FEATURES
  source      Location/Qualifiers
  1..21      /organism="unknown"
             /mol_type="genomic DNA"

Query Match
  Best Local Similarity 0.4%; Score 15.2; DB 1; Length 21;
  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2628 GACTCTCTTCAGAAAAA 2647
      |||||
Db 1 GACTCTCATCAGAGAAAAA 20

RESULT 147
AX456787/C
LOCUS      AX456787      21 bp      DNA      linear      PAT 06-JUL-2002
DEFINITION Sequence 11 from Patent WO0230967.
ACCESSION AX456787
VERSION AX456787.1 GI:21715674
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Thonnard,J.G.
TITLE Novel compounds
JOURNAL Patent: WO 0230967-A 11 18-APR-2002;
SmithKline Beecham Biologics SA (BE)
FEATURES
  source      Location/Qualifiers
  1..21      /organism="synthetic construct"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"
             /note="Primer"

Query Match
  Best Local Similarity 0.4%; Score 15.2; DB 1; Length 21;
  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1680 AAGAAGCACTTTGTCAAGCA 1699
      |||||
Db 21 AACAGCACTTCGTCAAGAA 2

RESULT 148
AX766066
LOCUS      AX766066      21 bp      DNA      linear      PAT 25-JUN-2003
DEFINITION Sequence 10 from Patent WO03008573.
ACCESSION AX766066
VERSION AX766066.1 GI:32260139
KEYWORDS
SOURCE Human papillomavirus type 16
ORGANISM Human papillomavirus type 16
REFERENCE 1
AUTHORS Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
TITLE Papillomavirus.
Milner,A.J.
Silenccing of gene expression

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JOURNAL Patent: WO 0308573-A 10 30-JAN-2003;
Milner, Anne Josephine (GB)
FEATURES
  source
    Location/Qualifiers
      /organism="Human papillomavirus type 16"
      /mol_type="unassigned DNA"
      /db_xref="taxon:10581"

Query Match
Best Local Similarity 0.4%; Score 15.2; DB 1; Length 21;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3119 AGGTAGGACATTCCTTTT 3138
Db ||||| ||||| ||||| ||||| |||||
2 AGGTATATGACTTTCCTTTT 21

RESULT 149
AX692528/c
LOCUS AX692528 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5260 from Patent EP1281758.
ACCESSION AX692528
VERSION AX692528.1 GI:29415486
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5260 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
  source
    Location/Qualifiers
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 15; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3391 CTCAAAAAAAAAAAAA 3405
Db ||||| ||||| ||||| ||||| |||||
17 CTCAAAAAAAAAAAAA 3

RESULT 150
AX692529/c
LOCUS AX692529 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5261 from Patent EP1281758.
ACCESSION AX692529
VERSION AX692529.1 GI:29415487
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5261 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
  source
    Location/Qualifiers
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 15; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3391 CTCAAAAAAAAAAAAA 3405
Db ||||| ||||| ||||| ||||| |||||
17 CTCAAAAAAAAAAAAA 3

RESULT 151
AX692530/c
LOCUS AX692530 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5262 from Patent EP1281758.
ACCESSION AX692530
VERSION AX692530.1 GI:29415488
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5262 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
  source
    Location/Qualifiers
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 15; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3391 CTCAAAAAAAAAAAAA 3405
Db ||||| ||||| ||||| ||||| |||||
16 CTCAAAAAAAAAAAAA 2

RESULT 152
AX730294/c
LOCUS AX730294 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1928 from Patent WO03025175.
ACCESSION AX730294
VERSION AX730294.1 GI:30509637
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 1928 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
  source
    Location/Qualifiers
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 15; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2845 GTTGAAACACAGGAT 2859
Db ||||| ||||| ||||| ||||| |||||
16 GTTGAAACACAGGAT 2

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RESULT 153
AX762231/c
LOCUS AX762231 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 5552 from Patent WO03040369.
ACCESSION AX762231
VERSION AX762231.1 GI:32256847
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 5552 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2123 AATTGGAACCAAGA 2137
Db |||||

RESULT 154
AX129263/c
LOCUS AX129263 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 481 from Patent WO0130362.
ACCESSION AX129263
VERSION AX129263.1 GI:14135568
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: WO 0130362-A 481 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source
Location/Qualifiers
1..19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="Cdk4 ribozyme binding site"

Query Match 0.4%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2281 GATACGCCCACT 2295
Db |||||

RESULT 155
AR134331
LOCUS AR134331 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 14 from patent US 6194151.
ACCESSION AR134331
VERSION AR134331.1 GI:14123236
KEYWORDS

Query Match 0.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3166 TCCTGACAAACAA 3180
Db |||||

RESULT 156
AR136313/c
LOCUS AR136313 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 116 from patent US 6136603.
ACCESSION AR136313
VERSION AR136313.1 GI:14476985
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
AUTHORS Dean,N.M., Karras,J.G. and McKay,R.
TITLE Antisense modulation of interleukin-5 signal transduction
JOURNAL Patent: US 6136603-A 116 24-OCT-2000;
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1005 CCTGGGATGCACAGA 1019
Db |||||

RESULT 157
BD247768/c
LOCUS BD247768 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense modulation of interleukin-5 signal transduction.
ACCESSION BD247768
VERSION BD247768.1 GI:33057538
KEYWORDS JP 2002539846-A/116.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Dean,N.M., Karras,J.G. and McKay,R.
TITLE Antisense modulation of interleukin-5 signal transduction
JOURNAL Patent: JP 2002539846-A 116 26-NOV-2002;
ISIS PHARMACEUTICALS INC
COMMENT
OS Artificial Sequence
FN JP 2002539846-A/116
PD 26-NOV-2002
PF 17-MAR-2000 JP 2000608790
PR 26-MAR-1999 US 09/280799
PI NICHOLAS M DEAN,JAMES G KARRAS,ROBERT MCKAY
PC C12N15/09,A61K31/711,A61K48/00,A61P11/06,A61P29/00,A61P35/00,
PC A61P43/00,
PC A61P43/00,C12N5/02,C12N15/00

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CC Description of Artificial Sequence:Synthetic
FH Key Location/Qualifiers
FT source 1..20
   /organism='Artificial Sequence'.

FEATURES
   source
       Location/Qualifiers
       1..20
       /organism="synthetic construct"
       /mol_type="genomic DNA"
       /db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1005 CCTGGGATGCACAGA 1019
Db 15 CCTGGGATGCACAGA 1

RESULT 158
LOCUS AX048438/c
DEFINITION Sequence 37 from Patent WO0071747.
ACCESSION AX048438
VERSION AX048438.1 GI:12225602
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE Detection system for separating constituents of a sample and
        production and use of the same
JOURNAL Patent: WO 0071747-A 37 30-NOV-2000;
        Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES
   source
       Location/Qualifiers
       1..20
       /organism="synthetic construct"
       /mol_type="unassigned DNA"
       /db_xref="taxon:32630"
       /note="Beschreibung der kunstlichen
        Sequenz:Erkennungssystem"

Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3391 CTCAAAAAATAAAAA 3405
Db 16 CTCAAAAAATAAAAA 2

RESULT 159
LOCUS AX057886
DEFINITION Sequence 24 from Patent WO0077252.
ACCESSION AX057886
VERSION AX057886.1 GI:12310526
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Melkin,B.D., Gabra,H., Sellar,G.C., Watson,J.E. and Porteous,D.J.
TITLE Diagnosis, prognosis and treatment of cancer related to the barx2
        gene
JOURNAL Patent: WO 0077252-A 24 21-DEC-2000;
        IMPERIAL CANCER RESEARCH TECHNOLOGY LIMITED (GB) ; THE JOHNS
        HOPKINS UNIVERSITY (US)
FEATURES
   source
       Location/Qualifiers
       1..20
       /organism="synthetic construct"
       /mol_type="unassigned DNA"

/db_xref="taxon:32630"
/note="PCR primer"

Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2914 AGGACAGTGCCTGGG 2928
Db 1 AGGACAGTGCCTGGG 15

RESULT 160
LOCUS BD076487
DEFINITION Novel molecules of TNF receptor super family and utilization
        thereof.
ACCESSION BD076487
VERSION BD076487.1 GI:22622090
KEYWORDS JP 2001517443-A/5.
SOURCE unidentified
ORGANISM unidentified
          unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Busfield,S.J.
TITLE Novel molecules of TNF receptor super family and utilization
        thereof
JOURNAL Patent: JP 2001517443-A 5 09-OCT-2001;
        MILLENNIUM PHARMACEUTICALS INC
COMMENT OS Unidentified
        PN JP 2001517443-A/5
        PD 09-OCT-2001
        PF 25-SEP-1998 JP 2000512955
        PR 26-SEP-1997 US 08/938896,17-MAR-1998 US 09/042785 PI
        PC C12N15/09,C07K16/28,C12N5/10,C12P21/02,C12Q1/68,G01N33/53, PC
        GO1N33/53,
        PC G01N33/566,C12N15/00,C12N5/00
        CC Strandedness: Single;
        CC Topology: Linear;
        CC Novel molecules of TNF receptor super family and utilization
        thereof
        FH Key Location/Qualifiers
        FT source 1..20
           /organism='Unidentified'.
FEATURES
   source
       Location/Qualifiers
       1..20
       /organism="unidentified"
       /mol_type="genomic DNA"
       /db_xref="taxon:32644"

Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3166 TCCTGTGACACACAA 3180
Db 1 TCCTGTGACACACAA 15

RESULT 161
LOCUS AX825120/c
DEFINITION Sequence 18 from Patent WO03072818.
ACCESSION AX825120
VERSION AX825120.1 GI:39750849
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids

```

JOURNAL Patent: WO 03072818-A 18 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES Location/Qualifiers

source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding
1
/bound_moiety="Biotin"
modified_base
3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
6
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
9
/note="LNA-T (Locked Nucleic Acid)"
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12
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 0.4%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3391 CTCAAAAAATAAAAA 3405

Db 21 CTCAAAAAATAAAAA 7

RESULT 162
AR016102/c 18 bp DNA linear PAT 05-DEC-1998
LOCUS
DEFINITION Sequence 30 from patent US 5776680.
ACCESSION AR016102
VERSION AR016102.1 GI:3972379
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Leibowitz, M.J. and Liu, Y.
TITLE Diagnostic probes for pneumocystis carini
JOURNAL Patent: US 5776680-A 30 07-JUL-1998;
FEATURES Location/Qualifiers
source
1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 429 CAGAAGACAAGACAAAC 446

Db 18 CAGAAGACAAGACAAAC 1

RESULT 163
AR065086/c 18 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 30 from patent US 5849484.
ACCESSION AR065086
VERSION AR065086.1 GI:5995302

KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 18)
AUTHORS Leibowitz, M.J. and Liu, Y.
TITLE In vitro assay for inhibitors of the intron self-splicing reaction
in Pneumocystis carinii
JOURNAL Patent: US 5849484-A 30 15-DEC-1998;
FEATURES Location/Qualifiers
source
1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 429 CAGAAGACAAGACAAAC 446

Db 18 CAGAAGACAAGACAAAC 1

RESULT 164
AR106912/c 18 bp DNA linear PAT 14-FEB-2001
LOCUS
DEFINITION Sequence 73 from patent US 6107092.
ACCESSION AR106912
VERSION AR106912.1 GI:12821442
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 18)
AUTHORS Cowsett, L.M.; Bennett, C.Frank. and O'Malley, B.W.
TITLE Antisense modulation of SRA expression
JOURNAL Patent: US 6107092-A 73 22-AUG-2000;
FEATURES Location/Qualifiers
source
1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1334 TCTGCAGCCACACCTAAG 1351

Db 18 TCTGCAGCCACACCTGAG 1

RESULT 165
AR130053/c 18 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 45 from patent US 6187586.
ACCESSION AR130053
VERSION AR130053.1 GI:14117950
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 18)
AUTHORS Monia, B.P.; Cowsett, L.M. and Roth, R.A.
TITLE Antisense modulation of AKT-3 expression
JOURNAL Patent: US 6187586-A 45 13-FEB-2001;
FEATURES Location/Qualifiers
source
1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


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Qy 2423 GCAGAGTGGAGAAAT 2440
|||||
Db 18 GCAAGAAGAGAGAGAAAT 1

RESULT 166
LOCUS ARI138016 18 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 26 from patent US 6197584.
ACCESSION ARI138016
VERSION ARI138016.1 GI:14479525
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett,C.Frank. and Cowser,L.M.
TITLE Antisense modulation of CD40 expression
JOURNAL Patent: US 6197584-A 26 06-MAR-2001;
FEATURES
    source
        Location/Qualifiers
            1..18
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1608 CTCGTGTTCCAGTTTCTA 1625
|||||
Db 1 CTCGTGTTCCAGTTGCTA 18

RESULT 168
LOCUS ARI196080 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 545 from patent US 6350934.
ACCESSION ARI196080
VERSION ARI196080.1 GI:20245517
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens.,
        Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
TITLE Nucleic acid encoding delta-9 desaturase
JOURNAL Patent: US 6350934-A 545 26-FEB-2002;
FEATURES
    source
        Location/Qualifiers
            1..18
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 150 CTGCTCAGTCACCATTTG 167
|||||
Db 1 CTGCTCCGTCACCATGTG 18

RESULT 169
LOCUS AR373429/c 18 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 6 from patent US 6602712.
ACCESSION AR373429
VERSION AR373429.1 GI:40075557
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Handelsman,J. and Klimowicz,A.K.
TITLE Enterotoxin-deficient bacillus
JOURNAL Patent: US 6602712-A 6 05-AUG-2003;
FEATURES
    source
        Location/Qualifiers
            1..18
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1543 GAAGCGAGAGATAGTTGG 1560
|||||
Db 18 GCAGCGAAAGATAGTTGG 1

RESULT 170
LOCUS AX003420 18 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 37 from Patent WO9928449.
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Qy 2423 GCAGAGTGGAGAAAT 2440
|||||
Db 18 GCAAGAAGAGAGAGAAAT 1

RESULT 166
LOCUS ARI138016 18 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 26 from patent US 6197584.
ACCESSION ARI138016
VERSION ARI138016.1 GI:14479525
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett,C.Frank. and Cowser,L.M.
TITLE Antisense modulation of CD40 expression
JOURNAL Patent: US 6197584-A 26 06-MAR-2001;
FEATURES
    source
        Location/Qualifiers
            1..18
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1608 CTCGTGTTCCAGTTTCTA 1625
|||||
Db 1 CTCGTGTTCCAGTTGCTA 18

RESULT 168
LOCUS ARI196080 18 bp DNA linear PAT 20-JUL-2003
DEFINITION Identification of genetic targets for modulation by
        oligonucleotides and generation of oligonucleotides for gene
        modulation.
ACCESSION BD250472
VERSION BD250472.1 GI:33060242
KEYWORDS JP 2002511276-A/26.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cowser,L.M., Baker,B.F., McNeill,J., Freier,S.M., Sasnor,H.M.,
        Brooks,D.G., Ohasi,C., Wyatt,J.R., Borchers,A.H. and Vikkars,T.A.
TITLE Identification of genetic targets for modulation by
        oligonucleotides and generation of oligonucleotides for gene
        modulation
JOURNAL Patent: JP 2002511276-A 26 16-APR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002511276-A/26
PD 16-APR-2002
PF 13-APR-1999 JP 2000543647
PR 13-APR-1998 US 60/081483,28-APR-1998 US 09/067638 PI
LEX M COWSERT,BRENDA F BAKER,JOHN MCNEIL,SUSAN M FREIER,HENRI PI
M SASMOR,
PI DOUGLAS G BROOKS,CARA OHASI,JACQUELINE R WYATT,ALEXANDER H PI
BORCHERS,
PI TIMOTHY A VIKKARS
PC C12N15/09,C07B61/00,C07B61/30,G06F17/50, G06F17/50, PC
C12N15/00
CC Antisense Oligonucleotide
FH Key Location/Qualifiers
FT source 1..18
    /organism="Artificial Sequence".
    Location/Qualifiers
        1..18
            /organism="synthetic construct"
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ACCESSION AX003420
VERSION AX003420.1 GI:9927224
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
TITLE Schedl, A. and Harmar, A.J.
JOURNAL Patent: WO 9928449-A 37 10-JUN-1999;
FEATURES SCHEDL ANDREAS (DE); HARMAR ANTHONY JOHN (GB)
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Primer"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 236 CTTGCTCTTGGGATTAT 253
Db 18 CTTGCCTCTTGGGATTAT 1

RESULT 171
AX838044/c
LOCUS AX838044
DEFINITION Sequence 5168 from Patent EPI347046.
ACCESSION AX838044
VERSION AX838044.1 GI:39921736
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S.,
Yamanoto, J.I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R.,
Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and
Masuho, Y.
TITLE Full-length cDNA sequences
JOURNAL Patent: EP 1347046-A 5168 24-SEP-2003;
FEATURES Research Association for Biotechnology (JP)
source Location/Qualifiers
1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/notes="Description of Artificial Sequence: an artificially
synthesized primer se q"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3105 AGAATCCAGGGAACAGGT 3122
Db 1 AGAAGCCAGGGAACAGGT 18

RESULT 173
BD086284/c
LOCUS BD086284
DEFINITION Vector.
ACCESSION BD086284
VERSION BD086284.1 GI:22631894
KEYWORDS JP 2001525168-A/37.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Shen, S., Schedl, A. and Harmar, A.J.
TITLE Vector
JOURNAL Patent: JP 2001525168-A 37 11-DEC-2001;
COMMENT MEDICAL RESEARCH COUNCIL
OS Artificial Sequence
FN JP 2001525168-A/37
PD 11-DEC-2001
PF 27-NOV-1998 JP 2000523326
PR 28-NOV-1997 GB 9725311.6, 28-NOV-1997 GB 9725313.2 PR
20-MAR-1998 GB 9806072.6, 05-NOV-1998 GB 9824275.3 PI
SANBING SHEN, ANDREAS SCHEDL, ANTHONY JOHN HARMAR PC
CI2N15/09, CI2N15/00
CC Description of Artificial Sequence: Primer
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence'.
FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 236 CTTGCTCTTGGGATTAT 253
Db 18 CTTGCCTCTTGGGATTAT 1

RESULT 174
BD226567
LOCUS BD226567
DEFINITION Antisense modulation of CD40 expression.
ACCESSION BD226567
VERSION BD226567.1 GI:33036337
KEYWORDS JP 2002513593-A/26.

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SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1 (bases 1 to 18)
AUTHORS     Bennett,C.F. and Cowsett,L.M.
TITLE       Antisense modulation of CD40 expression
JOURNAL     Patent: JP 2002513593-A 26 14-MAY-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS Unidentified
            PN JP 2002513593-A/26
            PD 14-MAY-2002
            PF 22-APR-1999 JP 2000547271
            PR 01-MAY-1998 US 09/071433
            PI C FRANK BENNETT,LEX M COWSETT
            PC C12N15/09,A61K37/02,A61K48/00,A61P1/00,A61P11/06, PC
               A61P17/06,
            PC A61P29/00,A61P35/00,A61P37/02,A61P37/06,A61P43/00,C12P19/34,
            PC C12Q1/68,
            PC C12N15/00
            CC Strandedness: Single;
            CC Topology: Linear;
            CC Antisense modulation of CD40 expression
            FH Key Location/Qualifiers
            FT source 1..18 /organism='Unidentified'.
FEATURES    Location/Qualifiers
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            1..18
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"
Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1608 CTCCTGTCATGTTCTA 1625
Db 1 CTCCTGTCAGCTGTCTA 18

RESULT 175
AR123684
LOCUS      Sequence 22 from patent US 6171788.
DEFINITION AR123684
ACCESSION  AR123684
VERSION    AR123684.1 GI:14109045
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 19)
AUTHORS     Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.
TITLE       Methods for the diagnosis, prognosis and treatment of glaucoma and
            related disorders
JOURNAL     Patent: US 6171788-A 22 09-JAN-2001;
FEATURES    Location/Qualifiers
            source
            1..19
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 124 CCTTCTCAGCCTTGTC 141
Db 1 CCTTCTCAGCCTTGCTAC 18

RESULT 176
AR123684
LOCUS      Sequence 22 from patent US 6171788.
DEFINITION AR123684
ACCESSION  AR123684
VERSION    AR123684.1 GI:14109045
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 19)
AUTHORS     Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.
TITLE       Methods for the diagnosis, prognosis and treatment of glaucoma and
            related disorders
JOURNAL     Patent: US 6171788-A 22 09-JAN-2001;
FEATURES    Location/Qualifiers
            source
            1..19
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 124 CCTTCTCAGCCTTGTC 141
Db 1 CCTTCTCAGCCTTGCTAC 18

RESULT 176
BD237955
LOCUS      Nucleic acids, kits, and methods for the diagnosis, prognosis and
DEFINITION

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treatment of glaucoma and related disorders.
BD237955
VERSION    1 GI:33047725
KEYWORDS   JP 2002534135-A/22.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 19)
AUTHORS     Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.
TITLE       Nucleic acids, kits, and methods for the diagnosis, prognosis and
            treatment of glaucoma and related disorders
JOURNAL     Patent: JP 2002534135-A 22 15-OCT-2002;
            THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
COMMENT     OS Homo sapiens (human)
            PN JP 2002534135-A/22
            PD 15-OCT-2002
            PF 11-JAN-2000 JP 2000593777
            PR 11-JAN-1999 US 09/227881,07-MAY-1999 US 09/306828 PI
            THAI D NGUYEN,JON R POLANSKY,PU CHEN,HUA CHEN PC
            C12N15/09,A61K31/573,A61K45/00,A61P27/06,C12N1/15,C12N1/19, PC
            C12N1/21,
            PC C12N5/10,C12Q1/68,G01N33/53,G01N33/566,C12N15/00,C12N5/00 CC
            Nucleic acids, kits, and methods for the diagnosis, prognosis CC
            and
            CC treatment of glaucoma and related disorders
            FH Key Location/Qualifiers
            FT source 1..19 /organism='Homo sapiens (human)'.
FEATURES    Location/Qualifiers
            source
            1..19
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
Query Match 0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 124 CCTTCTCAGCCTTGTC 141
Db 1 CCTTCTCAGCCTTGCTAC 18

RESULT 177
AR241724/c
LOCUS      Sequence 12 from patent US 6472154.
DEFINITION AR241724
ACCESSION  AR241724
VERSION    AR241724.1 GI:27287536
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 19)
AUTHORS     Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE       Polymorphic repeats in human genes
JOURNAL     Patent: US 6472154-A 12 29-OCT-2002;
FEATURES    Location/Qualifiers
            source
            1..19
            /organism="unknown"
            /mol_type="genomic DNA"
Query Match 0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2412 AGAATAAATAAGCAAGAA 2429
Db 19 AGAAAAAGAAAGAAAGAA 2

RESULT 178

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AR242765
LOCUS AR242765 19 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 22 from patent US 6475724.
ACCESSION AR242765
VERSION AR242765.1 GI:27289404
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.
TITLE Nucleic acids, kits, and methods for the diagnosis, prognosis and treatment of glaucoma and related disorders
JOURNAL Patent: US 6475724-A 22 05-NOV-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 124 CCTTCTCAGCCTTGTC 141
|||||
Db 1 CCTTCTCAGCCTTGCTAC 18

RESULT 179
AX128874/c
LOCUS AX128874 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 92 from Patent WO0130362.
ACCESSION AX128874
VERSION AX128874.1 GI:14135179
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 92 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES Location/Qualifiers
source 1..19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cdk1 ribozyme binding site"

Query Match 0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3347 TGCTGACCAACAGCAGA 3364
|||||
Db 19 TGCTGACCAACAGCAGA 2

RESULT 180
AX352895/c
LOCUS AX352895 19 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 101 from Patent EP1174518.
ACCESSION AX352895
VERSION AX352895.1 GI:18617977
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Loukachov,V.V., van Gemen,B. and Goudsmit,J.

TITLE Collection of binding molecules
JOURNAL Patent: EP 1174518-A 101 23-JAN-2002;
Amsterdam Support Diagnostics B.V. (NL)
FEATURES Location/Qualifiers
source 1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="position 65"

Query Match 0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2731 CTGTTCTGTTTCTTAATA 2748
|||||
Db 19 CTGTTCTGTTTCTTTATA 2

RESULT 181
AX353089
LOCUS AX353089 19 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 295 from Patent EP1174518.
ACCESSION AX353089
VERSION AX353089.1 GI:18618171
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Loukachov,V.V., van Gemen,B. and Goudsmit,J.
TITLE Collection of binding molecules
JOURNAL Patent: EP 1174518-A 295 23-JAN-2002;
Amsterdam Support Diagnostics B.V. (NL)
FEATURES Location/Qualifiers
source 1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="position 103"

Query Match 0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2069 TTAAGAGTAAAAATCAG 2086
|||||
Db 1 TAAAGAGGAAAAATCAG 18

RESULT 182
AX362740/c
LOCUS AX362740 19 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 101 from Patent WO0208463.
ACCESSION AX362740
VERSION AX362740.1 GI:18694880
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Loukachov,V.V., Goudsmit,J. and van Gemen,B.
TITLE Collection of binding molecules
JOURNAL Patent: WO 0208463-A 101 31-JAN-2002;
Amsterdam Support Diagnostics B.V. (NL)
FEATURES Location/Qualifiers
source 1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="position 65"

Query Match 0.4%; Score 14.8; DB 1; Length 19;

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Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2731 CTGTTCTGTTTCTTAATA 2748
Db 19 CTGTTCTTTTCTTTATA 2

RESULT 183
AX362934
LOCUS AX362934 19 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 295 from Patent WO0208463.
ACCESSION AX362934
VERSION AX362934.1 GI:18695074
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Loukachov,V.V., Goudsmit,J. and van Gemen,B.
TITLE Collection of binding molecules
JOURNAL Patent: WO 0208463-A 295 31-JAN-2002;
Amsterdam Support Diagnostics B.V. (NL)
FEATURES
    source
    1..19
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="position 103"

Query Match 0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2069 TTAAGAAGTAAAAATCAG 2086
Db 1 TAAAAAGGAAAAATCAG 18

RESULT 184
BD065060
LOCUS BD065060 19 bp DNA linear PAT 27-AUG-2002
DEFINITION Methods for the diagnosis, prognosis and treatment of glaucoma and
related disorders.
ACCESSION BD065060
VERSION BD065060.1 GI:22610663
KEYWORDS JP 2001509669-A/22.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.
TITLE Methods for the diagnosis, prognosis and treatment of glaucoma and
related disorders
JOURNAL Patent: JP 2001509669-A 22 24-JUL-2001;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
COMMENT OS Unidentified
PN JP 2001509669-A/22
PD 24-JUL-2001
PF 09-JAN-1998 JP 1998532017
PR 28-JAN-1997 US 08/791154,26-SEP-1997 US
THAI D NGUYEN,JON R POLANSKY,PU CHEN,HUA CHEN PC
C12N15/12,C12Q1/68,C07K14/47,A61K31/70
CC Strandedness: Single;
CC Topology: Linear;
CC Methods for the diagnosis, prognosis and
treatment of glaucoma
CC disorders and related
CC disorders
CC Key Location/Qualifiers
FH Key 1..19
FT source /organism='Unidentified'.
FEATURES
    Location/Qualifiers

1..19
/organism='Unidentified'
/mol_type='genomic DNA'
/db_xref="taxon:32644"

source
1..19
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 124 CCTTCTCAGCCTTGTGC 141
Db 1 CCTTCTCAGCCTTGTCTAC 18

RESULT 185
BD171906
LOCUS BD171906 19 bp DNA linear PAT 18-FEB-2003
DEFINITION Novel clock gene Bmal2.
ACCESSION BD171906
VERSION BD171906.1 GI:28413202
KEYWORDS JP 2002238567-A/32.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Fukada,Y. and Okano,T.
TITLE Novel clock gene Bmal2
JOURNAL Patent: JP 2002238567-A 32 27-AUG-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Artificial Sequence
PN JP 2002238567-A/32
PD 27-AUG-2002
PF 13-FEB-2001 JP 2001035743
PI YOSHITAKA FUKADA,TOSHIYUKI OKANO
PC C12N15/09,A01K67/027,A61K45/00,A61P25/00,A61P43/00,C07K14/465,
C07K14/47,
PC C07K16/18,C07K19/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/
02,C12Q1/68.
PC G01N33/15,G01N33/50/C12P21/08,C12N15/00,C12N5/00 CC
Description of Artificial Sequence:cqCF862-primer FH Key
FEATURES
    source
    1..19
    Location/Qualifiers
    FT source /organism='Artificial Sequence'.
    FT Location/Qualifiers
    1..19
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"

Query Match 0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 85 TCTTGGCTCACAGGGGAC 102
Db 2 TCTTGGATCACAGGGGAC 19

RESULT 186
BD173560
LOCUS BD173560 19 bp DNA linear PAT 18-FEB-2003
DEFINITION Novel clock gene Bmal2.
ACCESSION BD173560
VERSION BD173560.1 GI:28414891
KEYWORDS WO 02064785-A/32.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 19)
AUTHORS Fukada,Y. and Okano,T.
TITLE Novel clock gene Bmal2
JOURNAL Patent: WO 02064785-A 32 22-AUG-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP,YOSHITAKA FUKADA,TOSHIYUKI OKANO

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[illegible]

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RESULT 191
AR095050          AR095050          20 bp      DNA      linear      PAT 08-SEP-2000
DEFINITION        Sequence 3 from patent US 6001992.
ACCESSION          AR095050
VERSION            AR095050.1  GI:10022551
KEYWORDS           .
SOURCE             Unknown.
ORGANISM            Unknown.
REFERENCE           1 (bases 1 to 20)
AUTHORS            Ackermann,E.J., Bennett,C.Frank., Dean,N.M. and Marcusson,E.G.
TITLE              Antisense modulation of novel anti-apoptotic bcl-2-related proteins
JOURNAL            Patent: US 6001992-A 3 14-DEC-1999;
FEATURES            Location/Qualifiers
                     source
                     1..20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Query Match        0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1306 TGAAGCTGTGGGAAAT 1323
Db 2 TGAAGCTGTGGGCAAT 19

RESULT 192
AR100077/c        AR100077          20 bp      DNA      linear      PAT 14-FEB-2001
LOCUS              AR100077
DEFINITION        Sequence 34 from patent US 6080546.
ACCESSION          AR100077
VERSION            AR100077.1  GI:12810525
KEYWORDS           .
SOURCE             Unknown.
ORGANISM            Unknown.
REFERENCE           1 (bases 1 to 20)
AUTHORS            Monia,B.P., Gaarde,W. and Cowseert,L.M.
TITLE              Antisense modulation of MEK5 expression
JOURNAL            Patent: US 6080546-A 34 27-JUN-2000;
FEATURES            Location/Qualifiers
                     source
                     1..20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Query Match        0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 969 CAAACATAGATGTTACTG 986
Db 18 CAAAGACAGATGTACTG 1

RESULT 193
AR106248/c        AR106248          20 bp      DNA      linear      PAT 14-FEB-2001
LOCUS              AR106248
DEFINITION        Sequence 10 from patent US 6106832.
ACCESSION          AR106248
VERSION            AR106248.1  GI:12820778
KEYWORDS           .
SOURCE             Unknown.
ORGANISM            Unknown.
REFERENCE           1 (bases 1 to 20)
AUTHORS            Spriggs,M.K., Armitage,R.J., Fanslow,W.C. III and Widmer,M.B.
TITLE              Treatment of individuals exhibiting defective CD40L
JOURNAL            Patent: US 6106832-A 10 22-AUG-2000;
FEATURES            Location/Qualifiers
                     source
                     1..20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Query Match        0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 384 AGCTTCAGCTGCAGGCTC 401
Db 19 AGCTTCAGCTCCTGGCTC 2

RESULT 196
AR136443/c        AR136443          20 bp      DNA      linear      PAT 16-JUN-2001
LOCUS              AR136443
DEFINITION        Sequence 38 from patent US 6136604.
ACCESSION          AR136443
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match        0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 395 CAGGCTCTTCAGCAAAAT 412
Db 19 CAAGCTCTTCAGCAATAT 2

RESULT 194
AR118956/c        AR118956          20 bp      DNA      linear      PAT 16-MAY-2001
LOCUS              AR118956
DEFINITION        Sequence 82 from patent US 6150092.
ACCESSION          AR118956
VERSION            AR118956.1  GI:14100866
KEYWORDS           .
SOURCE             Unknown.
ORGANISM            Unknown.
REFERENCE           1 (bases 1 to 20)
AUTHORS            Uchida,K., Uchida,T., Tanaka,Y., Matsuda,Y. and Kondo,S.
TITLE              Antisense nucleic acid compound targeted to VEGF
JOURNAL            Patent: US 6150092-A 82 21-NOV-2000;
FEATURES            Location/Qualifiers
                     source
                     1..20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Query Match        0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2411 AAGAAAAATAAGCAAGA 2428
Db 20 AAGAAAGATAGAGCAAGA 3

RESULT 195
AR126706/c        AR126706          20 bp      DNA      linear      PAT 16-MAY-2001
LOCUS              AR126706
DEFINITION        Sequence 135 from patent US 6180353.
ACCESSION          AR126706
VERSION            AR126706.1  GI:14113299
KEYWORDS           .
SOURCE             Unknown.
ORGANISM            Unknown.
REFERENCE           1 (bases 1 to 20)
AUTHORS            Dean,N.M. and Cowseert,L.M.
TITLE              Antisense modulation of daxx expression
JOURNAL            Patent: US 6180353-A 135 30-JAN-2001;
FEATURES            Location/Qualifiers
                     source
                     1..20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Query Match        0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 384 AGCTTCAGCTGCAGGCTC 401
Db 19 AGCTTCAGCTCCTGGCTC 2

RESULT 196
AR136443/c        AR136443          20 bp      DNA      linear      PAT 16-JUN-2001
LOCUS              AR136443
DEFINITION        Sequence 38 from patent US 6136604.
ACCESSION          AR136443
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VERSION AR136443.1 GI:14477115
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Wyatt,J.
TITLE Antisense inhibition of methionine aminopeptidase 2 expression
JOURNAL Patent: US 6136604-A 38 24-OCT-2000;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 996 TGGACCAAGCCTGGGATG 1013
|||||
Db 19 TGGATCAAGCCTGGGATG 2
RESULT 197
AR150424/c
LOCUS AR150424 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 500 from patent US 6228642.
ACCESSION AR150424
VERSION AR150424.1 GI:15115015
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Baker,B.F., Bennett,C.Frank., Butler,M.M. and Shanahan,W.R. Jr.
TITLE Antisense oligonucleotide modulation of tumor necrosis factor-(.alpha.) (TNF-.alpha.) expression
JOURNAL Patent: US 6228642-A 500 08-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3353 GCACAAAGCAGACACTCA 3370
|||||
Db 18 GCACACAGAAGACACTCA 1
RESULT 198
AR158979/c
LOCUS AR158979 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 601 from patent US 6251588.
ACCESSION AR158979
VERSION AR158979.1 GI:16221427
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and Kincaid,R.H.
TITLE Method for evaluating oligonucleotide probe sequences
JOURNAL Patent: US 6251588-A 601 26-JUN-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1073 ACTCAAGGATTCGGGAA 1090
|||||
Db 20 ACTCAAGACTTCGGGAA 3
RESULT 199
AR158980/c
LOCUS AR158980 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 602 from patent US 6251588.
ACCESSION AR158980
VERSION AR158980.1 GI:16221429
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and Kincaid,R.H.
TITLE Method for evaluating oligonucleotide probe sequences
JOURNAL Patent: US 6251588-A 602 26-JUN-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1073 ACTCAAGGATTCGGGAA 1090
|||||
Db 19 ACTCAAGACTTCGGGAA 2
RESULT 200
AR158981/c
LOCUS AR158981 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 603 from patent US 6251588.
ACCESSION AR158981
VERSION AR158981.1 GI:16221431
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Shannon,K.W., Wolber,P.K., Delenstarr,G.C., Webb,P.G. and Kincaid,R.H.
TITLE Method for evaluating oligonucleotide probe sequences
JOURNAL Patent: US 6251588-A 603 26-JUN-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1073 ACTCAAGGATTCGGGAA 1090
|||||
Db 18 ACTCAAGACTTCGGGAA 1
RESULT 201
AR175921
LOCUS AR175921 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 4 from patent US 6309879.
ACCESSION AR175921
VERSION AR175921.1 GI:17917220
KEYWORDS

FEATURES
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 FT source Location/Qualifiers
 1..20 /organism="Artificial Sequence",
 Location/Qualifiers
 1..20 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1306 TGAAGCTGTTGGGAAAT 1323
 |||||
 Db 2 TGAAGCTGTTGAGGCAAT 19
 |||||

RESULT 205
 E06910
 LOCUS 20 bp DNA linear PAT 29-SEP-1997
 DEFINITION Synthetic DNA for hybridization probe.
 ACCESSION E06910
 VERSION E06910.1 GI:2175065
 KEYWORDS JP 1994070799-A/1.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Hashimoto, K., Miwa, K., Goto, M. and Ishimori, Y.
 TITLE HYBRIDIZATION METHOD
 JOURNAL Patent: JP 1994070799-A 1 15-MAR-1994;
 TOSHIBA CORP

COMMENT
 OS Artificial gene
 OC Artificial sequence; Genes.
 OS Avian myelocytomatosis virus 29
 PN JP 1994070799-A/1
 PD 15-MAR-1994
 PF 26-AUG-1992 JP 1992227189
 PI HASHIMOTO KOJI, MIWA KEIKO, GOTO MASASHIKI, ISHIMORI YOSHIO PC
 C12Q1/68;
 CC strandedness: Single;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No.

FEATURES
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 1..20 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2404 TCGGAAGACGAAATAA 2421
 |||||
 Db 3 TCGGAAGACGAAACAAGA 20
 |||||

RESULT 206
 I17259
 LOCUS 20 bp DNA linear PAT 03-APR-1996
 DEFINITION Sequence 25 from patent US 5486599.
 ACCESSION I17259
 VERSION I17259.1 GI:1252167
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Saunders, S., Bernfield, M. and Kato, M.
 TITLE Construction and use of synthetic constructs encoding syndecan

JOURNAL Patent: US 5486599-A 25 23-JAN-1996;
 FEATURES
 source
 1..20 Location/Qualifiers
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 194 AAGTTTAACACGAGGCC 211
 |||||
 Db 3 AAGCTTATCCACGAGGCC 20
 |||||

RESULT 207
 I20025/c
 LOCUS 20 bp DNA linear PAT 07-OCT-1996
 DEFINITION Sequence 11 from patent US 5512545.
 ACCESSION I20025
 VERSION I20025.1 GI:1600380
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Brown, D., Edwards, R.M., Craig, S., Cook, A.L. and Clements, J.M.
 TITLE PDGF-B analogues
 JOURNAL Patent: US 5512545-A 11 30-APR-1996;
 FEATURES
 source
 1..20 Location/Qualifiers
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2736 CTGTTTCTTAATAGGAT 2753
 |||||
 Db 18 CTGTTACTTAGTAAGGAT 1
 |||||

RESULT 208
 I27347/c
 LOCUS 20 bp DNA linear PAT 06-FEB-1997
 DEFINITION Sequence 10 from patent US 5565321.
 ACCESSION I27347
 VERSION I27347.1 GI:1818123
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Spriggs, M.K., Armitage, R.J. and Fanslow, W.C. III.
 TITLE Detection of mutations in a CD40 ligand gene
 JOURNAL Patent: US 5565321-A 10 15-OCT-1996;
 FEATURES
 source
 1..20 Location/Qualifiers
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 395 CAGGCTCTTCAGCAAAAT 412
 |||||
 Db 19 CAGGCTCTTCAGCAATAT 2
 |||||

RESULT 209
 AR198673/c

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LOCUS AR198673 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 26 from patent US 6355237.
ACCESSION AR198673
VERSION AR198673.1 GI:20248747
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 20)
AUTHORS Snodgrass,H.Ralph., Cioffi,J., Zupanic,T.Joel. and Shafer,A.Wayne.
TITLE Methods for using the obese gene and its gene product to stimulate
  hematopoietic development
JOURNAL Patent: US 6355237-A 26 12-MAR-2002;
FEATURES
  source
    1..20
    /organism="unknown"
    /mol_type="unassigned DNA"
  Query Match 0.4%; Score 14.8; DB 1; Length 20;
  Best Local Similarity 88.9%; Pred. No. 1.6e+02;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 595 TTGGGAAGCTGGGATC 612
Db 20 TTGAGAAAGCTGGGATC 3

RESULT 210
LOCUS AR208806 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 15 from patent US 6383809.
ACCESSION AR208806
VERSION AR208806.1 GI:21510056
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 20)
AUTHORS Bennett,C.Frank. and Cowser,L.M.
TITLE Antisense inhibition of cytohesin-1 expression
JOURNAL Patent: US 6383809-A 15 07-MAY-2002;
FEATURES
  source
    1..20
    /organism="unknown"
    /mol_type="unassigned DNA"
  Query Match 0.4%; Score 14.8; DB 1; Length 20;
  Best Local Similarity 88.9%; Pred. No. 1.6e+02;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1005 CTGGGATCCACAGAA 1022
Db 18 CTTGGATCCACAGAGGA 1

RESULT 211
LOCUS AR230897 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 157 from patent US 6451602.
ACCESSION AR230897
VERSION AR230897.1 GI:27271684
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 20)
AUTHORS Popoff,I. and Cowser,L.M.
TITLE Antisense modulation of PARP expression
JOURNAL Patent: US 6451602-A 157 17-SEP-2002;
FEATURES
  source
    1..20
    /organism="unknown"
    /mol_type="genomic DNA"
  Query Match 0.4%; Score 14.8; DB 1; Length 20;
  Best Local Similarity 88.9%; Pred. No. 1.6e+02;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

LOCUS AR198673 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 26 from patent US 6355237.
ACCESSION AR198673
VERSION AR198673.1 GI:20248747
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 20)
AUTHORS Snodgrass,H.Ralph., Cioffi,J., Zupanic,T.Joel. and Shafer,A.Wayne.
TITLE Methods for using the obese gene and its gene product to stimulate
  hematopoietic development
JOURNAL Patent: US 6355237-A 26 12-MAR-2002;
FEATURES
  source
    1..20
    /organism="unknown"
    /mol_type="unassigned DNA"
  Query Match 0.4%; Score 14.8; DB 1; Length 20;
  Best Local Similarity 88.9%; Pred. No. 1.6e+02;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1474 GAAGTGGAGTGGATGGT 1491
Db 18 GAAGTGGAGAGGATGGT 1

RESULT 212
LOCUS AR240902 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 69 from patent US 6468791.
ACCESSION AR240902
VERSION AR240902.1 GI:27286103
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 20)
AUTHORS Tanzi,R.E., Schellenberg,G.D., Wasco,W., Levy-Lahad,E., Bird,T.D.
  and Galas,D.J.
TITLE Chromosome 1 gene and gene products related to Alzheimer's Disease
JOURNAL Patent: US 6468791-A 69 22-OCT-2002;
FEATURES
  source
    1..20
    /organism="unknown"
    /mol_type="genomic DNA"
  Query Match 0.4%; Score 14.8; DB 1; Length 20;
  Best Local Similarity 88.9%; Pred. No. 1.6e+02;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3203 GAATCCCGAGCATGCC 3220
Db 18 GAGCTCTCAGAGCATGCC 1

RESULT 213
LOCUS AR314252 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 4789 from patent US 6559294.
ACCESSION AR314252
VERSION AR314252.1 GI:31707678
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
  Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 4789 06-MAY-2003;
FEATURES
  source
    1..20
    /organism="unknown"
    /mol_type="genomic DNA"
  Query Match 0.4%; Score 14.8; DB 1; Length 20;
  Best Local Similarity 88.9%; Pred. No. 1.6e+02;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 951 TTCCCTTTGGACAGAAC 968
Db 20 TTCTCTTTGGACAGAGAC 3

RESULT 214
LOCUS AR359600 20 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 193 from patent US 6593305.
ACCESSION AR359600
```

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VERSION AR359600.1 GI:33766323
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Wright,J.A.
TITLE Antitumor antisense sequences directed against R1 and R2 components
JOURNAL Patent: US 6593305-A 193 15-JUL-2003;
FEATURES
source Location/Qualifiers
1..20
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 277 TGTCCTCAAAACATGAATAA 294
Db 19 TGTCCTCAAAACATGAATAA 2

RESULT 215
AR359663/c
LOCUS AR359663 20 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 33 from patent US 6593456.
ACCESSION AR359663
VERSION AR359663.1 GI:33766407
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Gatanaga,T. and Granger,G.A.
TITLE Tumor necrosis factor receptor releasing enzyme
JOURNAL Patent: US 6593456-A 33 15-JUL-2003;
FEATURES
source Location/Qualifiers
1..20
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 589 CTGGGCTTGGGAAGCTG 606
Db 20 CTGGGCTTGGAGAGCTG 3

RESULT 216
AR374938
LOCUS AR374938 20 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 4 from patent US 6605700.
ACCESSION AR374938
VERSION AR374938.1 GI:40078102
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Bumcrot,D.A.
TITLE Human patched genes and proteins, and uses related thereto
JOURNAL Patent: US 6605700-A 4 12-AUG-2003;
FEATURES
source Location/Qualifiers
1..20
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;

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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 203 CACGAAGCCGAAGACCTG 220
Db 1 CACAAAGCCCAAGACCTG 18

RESULT 217
AX083857
LOCUS AX083857 20 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 17 from Patent WO0112852.
ACCESSION AX083857
VERSION AX083857.1 GI:13185498
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE
AUTHORS Egholm,M. and Chen,C.
TITLE Polymerase extension at 3' terminus of pna-dna chimera
JOURNAL Patent: WO 0112852-A 17 22-FEB-2001;
FEATURES
source Location/Qualifiers
1..20
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1006 CTGGGATGCACAGAGAT 1023
Db 2 CTGGGATGCAGAGCAT 19

RESULT 218
AX092609/c
LOCUS AX092609 20 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 21 from Patent WO0115676.
ACCESSION AX092609
VERSION AX092609.1 GI:13444666
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Hayden,M.R., Brooks-Wilson,A.R., Pimstone,S.N. and Clee,S.M.
TITLE Compositions and methods for modulating hdl cholesterol and triglyceride levels
JOURNAL Patent: WO 0115676-A 21 08-MAR-2001;
FEATURES
source Location/Qualifiers
1..20
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 78 GATGTGATCTTGGCTCAC 95
Db 18 GGTGTGATCTGGGCTCAC 1

RESULT 219
AX184029
LOCUS AX184029 20 bp DNA linear PAT 06-AUG-2001

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DEFINITION Sequence 1782 from Patent WO0142511.
ACCESSION AX184029
VERSION AX184029.1 GI:15135365
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
TITLE Ibd-related polymorphisms
JOURNAL Patent: WO 0142511-A 1782 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
Biotherapeutics Corporation (CA)
FEATURES
source
1..20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2408 AAGAAGAAAATAAAGCAA 2426
Db 1 AAAAAGAAAANAAGAAA 19

RESULT 220
LOCUS AX555158 20 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 30 from Patent WO02057466.
ACCESSION AX555158
VERSION AX555158.1 GI:25898686
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Eibl,C., Huang,F.C., Klaus,S., Muehlbauer,S., Herz,S. and Koop,H.U.
TITLE Processes and vectors for plasmid transformation of higher plants
JOURNAL Patent: WO 02057466-A 30 25-JUL-2002;
Icon Genetics AG (DE)
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer"
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 878 ATTGGATGCTCCCTGCT 895
Db 1 ATTGTTGCTCCCTGCT 18

RESULT 221
LOCUS AX708288 20 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 17 from Patent WO03004650.
ACCESSION AX708288
VERSION AX708288.1 GI:29564175
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Koop,H.U., Muehlbauer,S., Klaus,S., Eibl,C., Huang,F.C. and
Golds,T.J.

TITLE Gene expression in plastids based on replicating vectors
JOURNAL Patent: WO 03004658-A 17 16-JAN-2003;
Icon Genetics AG (DE)
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer"
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 878 ATTGGATGCTCCCTGCT 895
Db 1 ATTGTTGCTCCCTGCT 18

RESULT 222
LOCUS BD023431 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for detecting abnormality in chromosome.
ACCESSION BD023431
VERSION BD023431.1 GI:22564654
KEYWORDS JP 2001505428-A/176.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 20)
AUTHORS Parisgard,N. and Hukurando,P.
TITLE Method for detecting abnormality in chromosome
JOURNAL Patent: JP 2001505428-A 176 24-APR-2001;
NEILLS PARISGARD
COMMENT PN JP 2001505428-A/176
PD 24-APR-2001
PF 08-DEC-1997 JP 1998525090
PI NEILLS PARISGARD,PATER HOKURANDO
PC C12N15/09,C12Q1/68,G01N33/50,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES
source
1..20
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2788 TGGTCTCACAGGCTGTC 2805
Db 3 TGGTCTTCAGGCTGTC 20

RESULT 223
LOCUS BD088707/c 20 bp DNA linear PAT 27-AUG-2002
DEFINITION A method of arraying genome clone.
ACCESSION BD088707
VERSION BD088707.1 GI:22634317
KEYWORDS JP 2001321190-A/951.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 20)
AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 951 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA

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COMMENT
OS Artificial Sequence
PN JP 2001321190-A/951
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SORDA
PC C12N15/09,C12M15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/00
PC C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key
FT Location/Qualifiers
FT source 1..20
FEATURES
    source
    1..20
        /organism="Artificial Sequence"
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
Query Match
Best Local Similarity 88.9%; Pred. No. 1.6e+02; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 947 ACAGTTCCTTGGACAG 964
Db 19 ACAGTTCCTGTGCACAG 2
RESULT 224
BD138161/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
    1 (bases 1 to 20)
AUTHORS
    Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.
TITLE
    Antisense modulation of human MDM2 expression
JOURNAL
    Patent: JP 2002508944-A 87 26-MAR-2002;
    ISIS PHARMACEUTICALS INC
COMMENT
    OS Unidentified
    PN JP 2002508944-A/87
    PD 26-MAR-2002
    PF 26-MAR-1999 JP 2000538025
    PI LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M
    COWSERT
    PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
    PC C12Q1/68,
    PC C12N15/00
    CC Strandedness: Single;
    CC Topology: Linear;
    CC Antisense modulation of human MDM2 expression FH Key
    CC Location/Qualifiers
    FT source 1..20
    FT Location/Qualifiers
    1..20
        /organism="Unidentified"
        /organism="unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"
Query Match
Best Local Similarity 88.9%; Pred. No. 1.6e+02; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 799 GATTAACCATTTATGCA 816
Db 19 GACTAAACGATTATGCA 2
RESULT 225
BD178824
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
    1 (bases 1 to 20)
AUTHORS
    Yokoya,F., Okutsu,T., Mori,M., Yoshiyuki, Takahara, Fukuda,H.,
    Aburatani,H. and Sonaka,I.
TITLE
    Gene panel for genes involving liver regeneration
JOURNAL
    Patent: WO 02077222-A 162 03-OCT-2002;
    AJINOMOTO CO INC,FUMIHIKO YOKOYA,TOMOHIISA OKUTSU,MAIKO MORI,
    YOSHIYUKI TAKAHARA,HISAO FUKUDA,HIROYUKI ABURATANI,ICHIRO SONAKA
COMMENT
    OS Artificial Sequence
    PN WO 02077222-A/162
    PD 03-OCT-2002 WO 2002JP002372
    PF 13-MAR-2002 WO 2002JP002372
    PI FUMIHIKO YOKOYA,TOMOHIISA OKUTSU,MAIKO MORI,YOSHIYUKI PI
    TAKAHARA,HISAO FUKUDA,
    PI HIROYUKI ABURATANI,ICHIRO SONAKA
    PC C12N15/09,C12Q1/68,G01N33/15,G01N33/50,G01N37/00 CC
    Description of Artificial Sequence: primer
    FH Key Location/Qualifiers
    FT source 1..20
    FT Location/Qualifiers
    1..20
        /organism="Artificial Sequence"
FEATURES
    source
    1..20
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
Query Match
Best Local Similarity 88.9%; Pred. No. 1.6e+02; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 99 GGACGATGTCAGCTCTT 116
Db 2 GGACGCTGTCATGCTCTT 19
RESULT 226
AB068922/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
    1
AUTHORS
    Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
    Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
    Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
    and Soeda,E.
TITLE
    A BAC-based STS-content map spanning a 35-Mb region of human
    chromosome 1p35-p36
JOURNAL
    Genomics 74 (1), 55-70 (2001)
MEDLINE
    21269192
PUBMED
    11374902
REFERENCE
    2 (bases 1 to 20)
AUTHORS
    Horii,A.
TITLE
    Direct Submission
JOURNAL
    Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
    Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,

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Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
Tel: 81-22-717-8042, Fax: 81-22-717-8047)

FEATURES

source 1. .20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
misc_feature 1. .20
/note="forward primer for human STS sts-R22M1R at lp36
sts-R22M1R obtained from clones B306H4, B362F4, Human BAC
library RPCI-11"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 947 ACAGTTCCTTTGGACAG 964
|||||
Db 19 ACAGTTCCTGTGCACAG 2

RESULT 227
AR103620
LOCUS AR103620 21 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 144 from patent US 6087485.
ACCESSION AR103620
VERSION AR103620.1 GI:12815208
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 21)
AUTHORS Brooks-Wilson, A.R., Buckler, A., Cardon, L., Carey, A.H., Galvin, M.,
Miller, A. and North, M.
TITLE Asthma related genes
JOURNAL Patent: US 6087485-A 144 11-JUL-2000;
FEATURES Location/Qualifiers
source 1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3357 AAAGCAGCACTCAATAAAT 3376
|||||
Db 1 ACAGCAGGCAVTCACAAAT 20

RESULT 228
AR298562/c
LOCUS AR298562 21 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 10297 from patent US 6537751.
ACCESSION AR298562
VERSION AR298562.1 GI:31685846
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 21)
AUTHORS Cohen, D., Chunakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 10297 25-MAR-2003;
FEATURES Location/Qualifiers
source 1. .21
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1961 GTGAGGATAGCCATAAA 1978
|||||
Db 20 GTAAGGAAGCCATAAA 3

RESULT 229
AR307355
LOCUS AR307355 21 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 54 from patent US 6551775.
ACCESSION AR307355
VERSION AR307355.1 GI:31697882
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 21)
AUTHORS Lifton, R.P., Chang, S.S. and Rossier, B.C.
TITLE Method to diagnose and treat pathological conditions resulting from
deficient ion transport such as pseudohypoaldosteronism type-1
JOURNAL Patent: US 6551775-A 54 22-APR-2003;
FEATURES Location/Qualifiers
source 1. .21
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2300 CCTCCTAACACGCCCTCT 2317
|||||
Db 3 CCCCTTAACACGCCCTCT 20

RESULT 230
AX096868
LOCUS AX096868 21 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 2046 from Patent WO0118250.
ACCESSION AX096868
VERSION AX096868.1 GI:13513136
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Lander, E.S., Gargill, M., Ireland, J.S., Bolck, S., Daley, G.O. and
McCarthy, J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 2046 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source 1. .21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1120 TCAGAAAGCAGTCTGCCATC 1139
|||||
Db 2 TCATGAGAGMTCTGCCATC 21

RESULT 231
AX101420/c
LOCUS AX101420 21 bp DNA linear PAT 10-APR-2001
DEFINITION Sequence 112 from Patent WO0121795.
ACCESSION AX101420

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VERSION      AX101420.1  GI:13620152
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus

REFERENCE    1
AUTHORS      Stahl,A., Hirsch,D.J., Lodish,H.F., Gimeno,R.E. and Tartaglia,L.A.
TITLE       Patty acid transport proteins
JOURNAL     Patent: WO 0121795-A 112 29-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES
  source
    1. .21
      /organism="Mus musculus"
      /mol_type="unassigned DNA"
      /db_xref="taxon:10090"

Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1559 GGGGTGTGGTGAACCTGTG 1576
Db 18 GGGGCGGGGGAACCTGTG 1

RESULT 232
AX133218/c
LOCUS      AX133218      21 bp      DNA      linear      PAT 15-MAY-2001
DEFINITION Sequence 4436 from Patent WO0130362.
ACCESSION  AX133218
VERSION    AX133218.1  GI:14139528
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens

REFERENCE   1
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE      Robbins,J.M. and Tritz,R.
JOURNAL    Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
PATENT     Patent: WO 0130362-A 4436 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES
  source
    1. .21
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"
      /notes="IL6 ribozyme recognition site"

Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1504 AATTCCCAAGACACAGTG 1521
Db 21 AACTCCCAAGACACAGTG 4

RESULT 233
AX326788
LOCUS      AX326788      21 bp      DNA      linear      PAT 07-JAN-2002
DEFINITION Sequence 49 from Patent WO0172995.
ACCESSION  AX326788
VERSION    AX326788.1  GI:18097505
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.

REFERENCE   1
AUTHORS     Zauderer,M. and Smith,E.S.
TITLE      Methods of producing a library and methods of selecting
            polynucleotides of interest

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JOURNAL     Patent: WO 0172995-A 49 04-OCT-2001;
            UNIVERSITY OF ROCHESTER (US)
FEATURES
  source
    1. .21
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Gus antisense"

Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 878 ATTGGATGCTCCCTGCT 895
Db 3 ATGTGTTGCTCCCTGCT 20

RESULT 234
AX658971
LOCUS      AX658971      21 bp      DNA      linear      PAT 22-MAR-2003
DEFINITION Sequence 95 from Patent WO02102855.
ACCESSION  AX658971
VERSION    AX658971.1  GI:29161212
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.

REFERENCE   1
AUTHORS     Zauderer,M. and Smith,E.S.
TITLE      In vitro methods of producing and identifying immunoglobulin
            molecules in eukaryotic cells
JOURNAL    Patent: WO 02102855-A 95 27-DEC-2002;
            UNIVERSITY OF ROCHESTER (US)
FEATURES
  source
    1. .21
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="primer"

Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 878 ATTGGATGCTCCCTGCT 895
Db 3 ATGTGTTGCTCCCTGCT 20

RESULT 235
AX698769/c
LOCUS      AX698769      21 bp      DNA      linear      PAT 02-APR-2003
DEFINITION Sequence 5 from Patent WO02088328.
ACCESSION  AX698769
VERSION    AX698769.1  GI:29499558
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.

REFERENCE   1
AUTHORS     Belardelli,F., Santini,S.M., Parlato,S., di Pucchio,T., Logozzi,M.,
            la Penta,C., Ferrantini,M., Santodonato,L. and D'Agostino,G.
TITLE      Method for generating highly active human dendritic cells from
            monocytes
JOURNAL    Patent: WO 02088328-A 5 07-NOV-2002;
            Istituto Superiore di Sanite (IT)
FEATURES
  source
    1. .21
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="PCR primer-Interleukin 12 5' amplification primer"

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Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 386 CTTGAGCTGGAGGCTCTT 403
Db 20 CTTGAGCTGGAGGCTCTT 3

RESULT 236
AX722193
LOCUS AX722193 21 bp DNA linear PAT 07-MAY-2003
DEFINITION Sequence 3 from Patent WO03025222.
ACCESSION AX722193
VERSION AX722193.1 GI:30422726
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
AUTHORS Del-Favero, J. and van Broeckhoven, C.
TITLE Brain expressed cap-2 gene and protein associated with bipolar disorder
JOURNAL Patent: WO 03025222-A 3 27-MAR-2003;
        Janssen Pharmaceutica N.V. (BE)
FEATURES
source Location/Qualifiers
      1..21
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="CAP2 - Exon3 Forward PCR primer"

Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2142 CTTTAATTCTTTGTCA 2159
Db 2 CTTTAATTCTTTGTCA 19

RESULT 237
AX798447/c
LOCUS AX798447 21 bp DNA linear PAT 08-OCT-2003
DEFINITION Sequence 5 from Patent WO03054551.
ACCESSION AX798447
VERSION AX798447.1 GI:37604686
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
AUTHORS van Beuningen, M.G.
TITLE Normalisation of microarray data based on hybridisation with an internal reference
JOURNAL Patent: WO 03054551-A 5 03-JUL-2003;
        PamGene B.V. (NL)
FEATURES
source Location/Qualifiers
      1..21
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Oligonucleotide"

Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 480 TCTACAGTACTGGAAG 497
Db 20 TGTACAGACTGGAAG 3

RESULT 240
AX811445
LOCUS AX811445 21 bp RNA linear PAT 02-DEC-2003
DEFINITION Sequence 2 from Patent WO03062432.
ACCESSION AX811445
VERSION AX811445.1 GI:38635667
KEYWORDS Homo sapiens (human)
SOURCE

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RESULT 238
AX798450
LOCUS AX798450 21 bp DNA linear PAT 08-OCT-2003
DEFINITION Sequence 8 from Patent WO03054551.
ACCESSION AX798450
VERSION AX798450.1 GI:37604689
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
AUTHORS van Beuningen, M.G.
TITLE Normalisation of microarray data based on hybridisation with an internal reference
JOURNAL Patent: WO 03054551-A 8 03-JUL-2003;
        PamGene B.V. (NL)
FEATURES
source Location/Qualifiers
      1..21
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Oligonucleotide"

Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 480 TCTACAGTACTGGAAG 497
Db 2 TGTACAGACTGGAAG 19

RESULT 239
AX798460/c
LOCUS AX798460 21 bp DNA linear PAT 08-OCT-2003
DEFINITION Sequence 18 from Patent WO03054551.
ACCESSION AX798460
VERSION AX798460.1 GI:37604699
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
AUTHORS van Beuningen, M.G.
TITLE Normalisation of microarray data based on hybridisation with an internal reference
JOURNAL Patent: WO 03054551-A 18 03-JUL-2003;
        PamGene B.V. (NL)
FEATURES
source Location/Qualifiers
      1..21
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Oligonucleotide"

Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 480 TCTACAGTACTGGAAG 497
Db 20 TGTACAGACTGGAAG 3

RESULT 240
AX811445
LOCUS AX811445 21 bp RNA linear PAT 02-DEC-2003
DEFINITION Sequence 2 from Patent WO03062432.
ACCESSION AX811445
VERSION AX811445.1 GI:38635667
KEYWORDS Homo sapiens (human)
SOURCE

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ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1
AUTHORS      Vornlocher,H.P., Limmer,S., Kreutzer,R., van der Kuip,H. and
Aulitzky,W.
TITLE        Method for increasing the efficiency of an inhibitor of tyrosine
              kinase activity
JOURNAL      Patent: WO 03062432-A 2 31-JUL-2003;
              Ribopharma AG (DE)
FEATURES     source
              1. .21
              Location/Qualifiers
                /organism="Homo sapiens"
                /mol_type="unassigned RNA"
                /db_xref="taxon:9606"

Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2200 AGTTGAAGGCCCTTCAG 2217
        |||||
        4 AGTTGAAGGCCCTTCAG 21

Db

RESULT 241
BD070796
LOCUS      BD070796
DEFINITION      21 bp DNA linear PAT 27-AUG-2002
                Method to diagnose and treat pathological conditions resulting from
                deficient ion transport such as Pseudohypoaldosteronism type-1.
ACCESSION      BD070796
VERSION        1 GI:22616399
KEYWORDS       JP 2001514521-A/35.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 21)
AUTHORS        Lifton,R.P., Chang,S.S. and Rossier,B.C.
TITLE          Method to diagnose and treat pathological conditions resulting from
                deficient ion transport such as Pseudohypoaldosteronism type-1
JOURNAL        Patent: JP 2001514521-A 35 11-SEP-2001;
                YALE UNIVERSITY
COMMENT        OS Unidentified
                PN JP 2001514521-A/35
                PD 11-SEP-2001
                PF 11-MAR-1998 JP 1998539716
                PR 11-MAR-1997 US 60/040171
                PI RICHARD P LIFTON,SUE S CHANG,BERNARD C ROSSIER PC
                C12Q1/68,C07K16/18,C12N15/12,C12N5/10,C07K14/47 CC Strandedness:
                Single;
                CC Topology: Linear;
                CC /desc = 'primer'
                FH Key Location/Qualifiers
                FT source 1. .21
                /organism='Unidentified'.

FEATURES     source
              1. .21
              Location/Qualifiers
                /organism="unidentified"
                /mol_type="genomic DNA"
                /db_xref="taxon:32644"

Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2300 CCTCCTAACCGCCCTCT 2317
        |||||
        3 CCTCCTAACCGCCCTCT 20

Db

RESULT 242
BD129850
LOCUS      BD129850
DEFINITION      21 bp DNA linear PAT 18-SEP-2002

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Asthma-associated gene.
BD129850
ACCESSION      BD129850.1 GI:23224795
VERSION        1
KEYWORDS       JP 2002500895-A/140.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 21)
AUTHORS        Wilton,A.R.B., Buckler,A., Cardon,L., Carey,A.H., Galvin,M.,
                Miller,A. and North,M.
TITLE          Asthma-associated gene
JOURNAL        Patent: JP 2002500895-A 140 15-JAN-2002;
                AXYS PHARMACEUTICALS INC
COMMENT        OS Unidentified
                PN JP 2002500895-A/140
                PD 15-JAN-2002
                PF 21-JAN-1998 JP 2000528715
                PI ANGELA R BROOKS WILSON,ALAN BUCKLER,LON
                CARDON,ALISOUN H CAREY,
                PI MARGARET GALVIN,ANDREW MILLER,MICHAEL NORTH
                PC C12Q1/68,A01K67/027,C07K14/47,C12N15/09,C12N15/00 CC
                Strandedness: Double;
                CC Topology: Linear;
                CC Asthma-associated gene
                FH Key Location/Qualifiers
                FT source 1. .21
                /organism='Unidentified'.

FEATURES     source
              1. .21
              Location/Qualifiers
                /organism="unidentified"
                /mol_type="genomic DNA"
                /db_xref="taxon:32644"

Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      3357 AAAGCAGACACTCAATAAAT 3376
        |||||
        1 ACAGCAGGCAYTCACAAAT 20

Db

RESULT 243
BD144854
LOCUS      BD144854/c
DEFINITION      21 bp DNA linear PAT 17-JAN-2003
                A method of detecting human phase I enzymes of drug-metabolizing
                and a probe and a kit therefor.
ACCESSION      BD144854
VERSION        1 GI:27850612
KEYWORDS       JP 2002142780-A/66.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1 (bases 1 to 21)
AUTHORS        Nishimura,M., Yaguchi,H., Naito,S. and Hiraoka,I.
TITLE          A method of detecting human phase I enzymes of drug-metabolizing
                and a probe and a kit therefor
JOURNAL        Patent: JP 2002142780-A 66 21-MAY-2002;
                OTSUKA PHARMACEUTICAL FACTORY INC
COMMENT        OS Homo sapiens (human)
                PN JP 2002142780-A/66
                PD 21-MAY-2002
                PF 28-AUG-2001 JP 2001257338
                PI MASUHIRO NISHIMURA,HIROSHI YAGUCHI,SHINSAKU NAITO,ISAO HIRAKA
                PC C12N15/09,C12Q1/68,C12N15/00
                CC human PTGS1 gene
                FH Key Location/Qualifiers
                FT source 1. .21
                /organism='Homo sapiens (human)'.

FEATURES     source
              1. .21
              Location/Qualifiers
                /organism="Homo sapiens"

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/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 380 GTCAAGCTTCAGCTGCAG 397
    ||||| ||||| |||||
Db 18 GTCAAAATTCAGCTGCAG 1

RESULT 244
AR391464/c 16 bp DNA linear PAT 18-DEC-2003
LOCUS AR391464
DEFINITION Sequence 76 from patent US 6613520.
ACCESSION AR391464
VERSION AR391464.1 GI:40114957
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Ashby,M.
TITLE Methods for the survey and genetic analysis of populations
JOURNAL Patent: US 6613520-A 76 02-SEP-2003;
FEATURES
    source
        Location/Qualifiers
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 98;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1144 AGCTTGGGACCTGGGG 1159
    ||||| ||||| |||||
Db 16 AGCTTGGGCCCTGGGG 1

RESULT 245
AX281944/c 16 bp DNA linear PAT 02-NOV-2001
LOCUS AX281944
DEFINITION Sequence 76 from Patent WO0177392.
ACCESSION AX281944
VERSION AX281944.1 GI:16609195
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Ashby,M.
TITLE Methods for the survey and genetic analysis of populations
JOURNAL Patent: WO 0177392-A 76 18-OCT-2001;
FEATURES
    source
        Location/Qualifiers
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
            /note="unidentified soil organism"

Query Match      0.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 98;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1144 AGCTTGGGACCTGGGG 1159
    ||||| ||||| |||||
Db 16 AGCTTGGGCCCTGGGG 1

RESULT 246
AR047222
LOCUS AR047222
DEFINITION Sequence 2015 from patent US 5817796.
ACCESSION AR047222
VERSION AR047222.1 GI:5968687
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb ribozymes having 2'-5'-linked adenylate residues
JOURNAL Patent: US 5817796-A 2015 06-OCT-1998;
FEATURES
    source
        Location/Qualifiers
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2544 GAGGTGATTTTGTGT 2559
    ||||| ||||| |||||
Db 1 GAGGAGATTTTGTGT 16

RESULT 247
BD255423/c 17 bp DNA linear PAT 17-JUL-2003
LOCUS BD255423
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255423
VERSION BD255423.1 GI:33065193
KEYWORDS JP 2002541795-A/3216.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 3216 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/3216
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC
C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source 1..17 Location/Qualifiers
FT /organism='Eukaryote'.
FEATURES
    source
        Location/Qualifiers
            1..17
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3389 CACTCAAAAAAAAAA 3404
    ||||| ||||| |||||
Db 17 CATTCAAAAAAAAAA 2

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RESULT 248
BD255424/c
LOCUS      BD255424      17 bp    DNA      linear      PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION  BD255424
VERSION    BD255424.1 GI:33065194
KEYWORDS   JP 2002541795-A/3217.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS   Blatt, L., Zwick, M., Pavco, P. and McSwiggen, J.
TITLE     Regulation of repressor genes using nucleic acid molecules
JOURNAL   Patent: JP 2002541795-A 3217 10-DEC-2002;
COMMENT   RIBOZYME PHARMACEUTICALS INC
          Eukaryote
          OS JP 2002541795-A/3217
          PD 10-DEC-2002
          PR 11-APR-2000 JP 2000611654
          PI 12-APR-1999 US 60/129390
          PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
          C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
          C12P21/02,
          PC C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
          C12R1:91),
          PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
          PC A61K37/02,
          PC (C12N5/00, C12R1:91)
          CC Regulation of repressor genes using nucleic acid molecules FH
          Key Location/Qualifiers
          FT source 1..17
          FT /organism='Eukaryote'.
          FEATURES
            source
            Location/Qualifiers
            1..17
            /organism='unidentified'
            /mol_type='genomic DNA'
            /db_xref='taxon:32644'
          Query Match 0.4%; Score 14.4; DB 1; Length 17;
          Best Local Similarity 93.8%; Pred. No. 1.2e+02;
          Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
          QY 3389 CACTCAAAAAAAAAA 3404
          Db 16 CATTCAAAAAAAAAA 1
          RESULT 249
          I54274
          LOCUS      I54274      17 bp    DNA      linear      PAT 07-OCT-1997
          DEFINITION Sequence 2015 from patent US 5646042.
          ACCESSION  I54274
          VERSION    I54274.1 GI:2475477
          KEYWORDS   .
          SOURCE     Unknown.
          ORGANISM   Unknown.
          UNCLASSIFIED.
          REFERENCE  1 (bases 1 to 17)
          AUTHORS   Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
          TITLE     C-myc targeted ribozymes
          JOURNAL   Patent: US 5646042-A 2015 08-JUL-1997;
          FEATURES   Location/Qualifiers
            source
            1..17
            /organism='unknown'
            /mol_type='unassigned DNA'
          Query Match 0.4%; Score 14.4; DB 1; Length 17;
          Best Local Similarity 93.8%; Pred. No. 1.2e+02;
          Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
          QY 2544 GAGGTGATTTTGTGT 2559
          RESULT 248
          BD255424/c
          LOCUS      BD255424      17 bp    DNA      linear      PAT 17-JUL-2003
          DEFINITION Regulation of repressor genes using nucleic acid molecules.
          ACCESSION  BD255424
          VERSION    BD255424.1 GI:33065194
          KEYWORDS   JP 2002541795-A/3217.
          SOURCE     unidentified
          ORGANISM   unclassified.
          REFERENCE  1 (bases 1 to 17)
          AUTHORS   Blatt, L., Zwick, M., Pavco, P. and McSwiggen, J.
          TITLE     Regulation of repressor genes using nucleic acid molecules
          JOURNAL   Patent: JP 2002541795-A 3217 10-DEC-2002;
          COMMENT   RIBOZYME PHARMACEUTICALS INC
          Eukaryote
          OS JP 2002541795-A/3217
          PD 10-DEC-2002
          PR 11-APR-2000 JP 2000611654
          PI 12-APR-1999 US 60/129390
          PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
          C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
          C12P21/02,
          PC C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
          C12R1:91),
          PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
          PC A61K37/02,
          PC (C12N5/00, C12R1:91)
          CC Regulation of repressor genes using nucleic acid molecules FH
          Key Location/Qualifiers
          FT source 1..17
          FT /organism='Eukaryote'.
          FEATURES
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            Location/Qualifiers
            1..17
            /organism='unidentified'
            /mol_type='genomic DNA'
            /db_xref='taxon:32644'
          Query Match 0.4%; Score 14.4; DB 1; Length 17;
          Best Local Similarity 93.8%; Pred. No. 1.2e+02;
          Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
          QY 3389 CACTCAAAAAAAAAA 3404
          Db 16 CATTCAAAAAAAAAA 1
          RESULT 249
          I54274
          LOCUS      I54274      17 bp    DNA      linear      PAT 07-OCT-1997
          DEFINITION Sequence 2015 from patent US 5646042.
          ACCESSION  I54274
          VERSION    I54274.1 GI:2475477
          KEYWORDS   .
          SOURCE     Unknown.
          ORGANISM   Unknown.
          UNCLASSIFIED.
          REFERENCE  1 (bases 1 to 17)
          AUTHORS   Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
          TITLE     C-myc targeted ribozymes
          JOURNAL   Patent: US 5646042-A 2015 08-JUL-1997;
          FEATURES   Location/Qualifiers
            source
            1..17
            /organism='unknown'
            /mol_type='unassigned DNA'
          Query Match 0.4%; Score 14.4; DB 1; Length 17;
          Best Local Similarity 93.8%; Pred. No. 1.2e+02;
          Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
          QY 2544 GAGGTGATTTTGTGT 2559
          RESULT 250
          AR326904/c
          LOCUS      AR326904      17 bp    RNA      linear      PAT 17-AUG-2003
          DEFINITION Sequence 4306 from patent US 6566127.
          ACCESSION  AR326904
          VERSION    AR326904.1 GI:33712712
          KEYWORDS   .
          SOURCE     Unknown.
          ORGANISM   Unknown.
          UNCLASSIFIED.
          REFERENCE  1 (bases 1 to 17)
          AUTHORS   Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
          TITLE     Method and reagent for the treatment of diseases or conditions
          JOURNAL   Patent: US 6566127-A 4306 20-MAY-2003;
          COMMENT   related to levels of vascular endothelial growth factor receptor
          FEATURES   Location/Qualifiers
            source
            1..17
            /organism='unknown'
            /mol_type='unassigned RNA'
          Query Match 0.4%; Score 14.4; DB 1; Length 17;
          Best Local Similarity 93.8%; Pred. No. 1.2e+02;
          Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
          QY 317 TTTTAAAGGACAGT 332
          Db 16 TTTTAAAGTACAGT 1
          RESULT 251
          AR401700/c
          LOCUS      AR401700      17 bp    DNA      linear      PAT 18-DEC-2003
          DEFINITION Sequence 40 from patent US 6623962.
          ACCESSION  AR401700
          VERSION    AR401700.1 GI:40149150
          KEYWORDS   .
          SOURCE     Unknown.
          ORGANISM   Unknown.
          UNCLASSIFIED.
          REFERENCE  1 (bases 1 to 17)
          AUTHORS   Akhtar, S., Fell, P. and McSwiggen, J.A.
          TITLE     Enzymatic nucleic acid treatment of diseases of conditions related
          JOURNAL   Patent: US 6623962-A 40 23-SEP-2003;
          FEATURES   Location/Qualifiers
            source
            1..17
            /organism='unknown'
            /mol_type='genomic DNA'
          Query Match 0.4%; Score 14.4; DB 1; Length 17;
          Best Local Similarity 93.8%; Pred. No. 1.2e+02;
          Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
          QY 1503 AAATCCCAAGACCA 1518
          Db 17 AAATCCCAAGACCA 2
          RESULT 252
          AX217232
          LOCUS      AX217232      17 bp    RNA      linear      PAT 07-SEP-2001
          DEFINITION Sequence 2674 from Patent WO0159103.
          ACCESSION  AX217232
          VERSION    AX217232.1 GI:15527293
          KEYWORDS   .
          SOURCE     synthetic construct
          ORGANISM   synthetic construct
          REFERENCE  1
          QY 2544 GAGGTGATTTTGTGT 2559
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AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 2674 16-AUG-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US); McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
 source 1..17
 /organism="synthetic construct"
 /mol_type="unassigned RNA"
 /db_xref="taxon:32630"
 /note="Nucleic Acid"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1493 TTTAAAGGGGAATTC 1508 17 bp DNA linear PAT 27-MAR-2003
 Db 1 TTTAAAGGGGATATTC 16
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 |||||

RESULT 253
 AX672501/c
 LOCUS AX672501 17 bp DNA linear PAT 27-MAR-2003
 DEFINITION Sequence 946 from Patent WO03004526.
 ACCESSION AX672501
 VERSION AX672501.1 GI:29330849
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 Telerman, A., Amson, R. and Tuijinder, M.
 Authors
 Title Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines
 Journal Patent: WO 03004526-A 946 16-JAN-2003;
 Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
 source 1..17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 1.2e+02;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1038 AGAAGTCTTCTGATC 1053 17 bp DNA linear PAT 27-MAR-2003
 Db 16 AGAAGTCTTCTGATC 1
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RESULT 254
 AX673385/c
 LOCUS AX673385 17 bp DNA linear PAT 27-MAR-2003
 DEFINITION Sequence 1830 from Patent WO03004526.
 ACCESSION AX673385
 VERSION AX673385.1 GI:29331733
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 Telerman, A., Amson, R. and Tuijinder, M.
 Authors
 Title Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines
 Journal Patent: WO 03004526-A 1830 16-JAN-2003;
 Molecular Engines Laboratories (FR)

FEATURES Location/Qualifiers
 source 1..17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1162 GGGCGACTTCAGATC 1177 17 bp DNA linear PAT 27-MAR-2003
 Db 16 GGGCGACTTCAGATC 1
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RESULT 255
 AX674057/c
 LOCUS AX674057 17 bp DNA linear PAT 27-MAR-2003
 DEFINITION Sequence 2502 from Patent WO03004526.
 ACCESSION AX674057
 VERSION AX674057.1 GI:29332405
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 Telerman, A., Amson, R. and Tuijinder, M.
 Authors
 Title Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines
 Journal Patent: WO 03004526-A 2502 16-JAN-2003;
 Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
 source 1..17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 657 TCTTGAAAAATGAGAT 672 17 bp DNA linear PAT 27-MAR-2003
 Db 17 TCTTGAAATATGAGAT 2
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 |||||

RESULT 256
 AX674146/c
 LOCUS AX674146 17 bp DNA linear PAT 27-MAR-2003
 DEFINITION Sequence 2591 from Patent WO03004526.
 ACCESSION AX674146
 VERSION AX674146.1 GI:29332494
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 Telerman, A., Amson, R. and Tuijinder, M.
 Authors
 Title Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines
 Journal Patent: WO 03004526-A 2591 16-JAN-2003;
 Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
 source 1..17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.4%; Score 14.4; DB 1; Length 17;

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Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 786 ATACCTTGAAGAGAT 801
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Db 17 ATACCTTGAAGAGAT 2

RESULT 257
AX688716
LOCUS AX688716 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1448 from Patent EP1281758.
ACCESSION AX688716
VERSION AX688716.1 GI:29411420
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL mdz12
Patent: EP 1281758-A 1448 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 384 AGCTTCAGCTGCAGGC 399
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Db 2 AGCTTCAGCTGCAGGC 17

RESULT 258
AX688717
LOCUS AX688717 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1449 from Patent EP1281758.
ACCESSION AX688717
VERSION AX688717.1 GI:29411421
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL mdz12
Patent: EP 1281758-A 1449 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 384 AGCTTCAGCTGCAGGC 399
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Db 1 AGCTTCAGCTGCAGGC 16

RESULT 259
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AX723929
LOCUS AX723929 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1616 from Patent WO03025176.
ACCESSION AX723929
VERSION AX723929.1 GI:30503272
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
JOURNAL medicines
Patent: WO 03025176-A 1616 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
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Location/Qualifiers
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1382 GATTTTCAGAGACA 1397
    ||||| ||||| |||||
Db 1 GATCTTCAAGAGACA 16

RESULT 260
AX724137
LOCUS AX724137 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1824 from Patent WO03025176.
ACCESSION AX724137
VERSION AX724137.1 GI:30503480
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
JOURNAL medicines
Patent: WO 03025176-A 1824 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
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Location/Qualifiers
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1174 GATCCTTATGTGCACA 1189
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Db 1 GATCCTTGTGTGCACA 16

RESULT 261
AX724362/c
LOCUS AX724362/c 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2049 from Patent WO03025176.
ACCESSION AX724362
VERSION AX724362.1 GI:30503705
KEYWORDS
SOURCE Mus musculus (house mouse)
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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE
AUTHORS
TITLE
Telerman, A., Amson, R. and Tuijnder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 2049 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1904 AATCTTTTGTGGGAT 1919
|||||
Db 17 AATACTTTTGTGGGAT 2
RESULT 262
AX726731/c
LOCUS AX726731 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4418 from Patent WO03025176.
ACCESSION AX726731
VERSION AX726731.1 GI:30506074
KEYWORDS Mus musculus (house mouse)
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE
AUTHORS
TITLE
Telerman, A., Amson, R. and Tuijnder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 4418 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
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1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2268 TAGAGTTTCTGGGGAT 2283
|||||
Db 17 TACAGTTTCTGGGGAT 2
RESULT 263
AX726856
LOCUS AX726856 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4543 from Patent WO03025176.
ACCESSION AX726856
VERSION AX726856.1 GI:30506199
KEYWORDS Mus musculus (house mouse)
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE
AUTHORS
TITLE
Telerman, A., Amson, R. and Tuijnder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as

medicines
JOURNAL Patent: WO 03025176-A 4543 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3315 ATCTTTTGTATTGCT 3330
|||||
Db 2 ATCTTTTGTATTGCT 17
RESULT 264
AX729319/c
LOCUS AX729319 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 953 from Patent WO03025175.
ACCESSION AX729319
VERSION AX729319.1 GI:30508662
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS
TITLE
Telerman, A., Amson, R. and Tuijnder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 953 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2591 ATAAGATGATAAGAT 2606
|||||
Db 17 ATAAATGATAAGAT 2
RESULT 265
AX730538/c
LOCUS AX730538 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2172 from Patent WO03025175.
ACCESSION AX730538
VERSION AX730538.1 GI:30509881
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS
TITLE
Telerman, A., Amson, R. and Tuijnder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 2172 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 657 TCTTGAATAATGAGAT 672

Db 17 TCTTGTAAATGAGAT 2

RESULT 266
AX730910/c
LOCUS AX730910 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2544 from Patent WO03025175.
ACCESSION AX730910
VERSION AX730910.1 GI:30510253

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines

JOURNAL Patent: WO 03025175-A 2544 27-MAR-2003;
Molecular Engines Laboratories (FR)

FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1527 AAAAGTGGTGGAGAT 1542

Db 17 AAAAGTGGGGGAGAT 2

RESULT 267
AX733396/c
LOCUS AX733396 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5030 from Patent WO03025175.
ACCESSION AX733396
VERSION AX733396.1 GI:30512739

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines

JOURNAL Patent: WO 03025175-A 5030 27-MAR-2003;
Molecular Engines Laboratories (FR)

FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 786 ATACCTTGAAGAT 801

||||| ||||| ||||| |||||

17 ATACCTCTGAAGAT 2

RESULT 268
AX738598/c
LOCUS AX738598 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4188 from Patent WO03025177.
ACCESSION AX738598
VERSION AX738598.1 GI:30517888

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments

JOURNAL Patent: WO 03025177-A 4188 27-MAR-2003;
Molecular Engines Laboratories (FR)

FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2582 ATAGAAAATATAAGAT 2597

Db 17 ATAGAAAATAAAGAT 2

RESULT 269
AX739835/c
LOCUS AX739835 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5425 from Patent WO03025177.
ACCESSION AX739835
VERSION AX739835.1 GI:30519132

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments

JOURNAL Patent: WO 03025177-A 5425 27-MAR-2003;
Molecular Engines Laboratories (FR)

FEATURES
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1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2073 AAGTAAATATCAGAT 2088

Db 17 AAGTAAATATCAGAT 2

RESULT 270
AX758569/c
LOCUS AX758569 17 bp DNA linear PAT 25-JUN-2003


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DEFINITION Sequence 1890 from Patent WO03040369.
ACCESSION AX758569
VERSION AX758569.1 GI:32253185
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 1890 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3209 CCAGAGCATGCTGAT 3224
Db 17 CCAGAGCATGCTGAT 2

RESULT 271
AX759037/c
LOCUS AX759037 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 2358 from Patent WO03040369.
ACCESSION AX759037
VERSION AX759037.1 GI:32253653
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 2358 15-MAY-2003;
Molecular Engines Laboratories (FR)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 657 TCTTGAATAATGAGAT 672
Db 17 TCTTGAATAATGAGAT 2

RESULT 272
AX759268/c
LOCUS AX759268 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 2589 from Patent WO03040369.
ACCESSION AX759268
VERSION AX759268.1 GI:32253884
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 2589 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2582 ATAGAAATATAAGAT 2597
Db 17 ATAGAAATATAAGAT 2

RESULT 273
AX762369/c
LOCUS AX762369 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 5690 from Patent WO03040369.
ACCESSION AX762369
VERSION AX762369.1 GI:32256985
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 5690 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2585 GAAATATAAGATGAT 2600
Db 17 GAAATATAAGATGAT 2

RESULT 274
BD067200/c
LOCUS BD067200 17 bp RNA linear PAT 27-AUG-2002
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors.
ACCESSION BD067200
VERSION BD067200.1 GI:22612803
KEYWORDS JP 2001511003-A/40.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Akhtar,S., Fell,P. and Mcswiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors
JOURNAL Patent: JP 2001511003-A 40 07-AUG-2001;
RIBOZYME PHARMACEUTICALS INC,ASTON UNIV

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COMMENT OS Unidentified
 PN JP 2001511003-A/40
 PD 07-AUG-2001
 PF 14-JAN-1998 JP 1998532913
 PR 31-JAN-1997 US 60/036476, 04-DEC-1997 US 08/985162 PI
 C12N9/00, C07K14/71
 SAGHIR AKHTAR, PATRICIA FELL, JAMES A MCSWIGGEN PC
 CC Strandedness: Single;
 CC Topology: Linear;
 CC Enzymatic nucleic acid treatment of diseases or conditions CC
 related to
 CC levels of epidermal growth factor receptors
 FH Key Location/Qualifiers
 FT source 1..17
 /organism='Unidentified'.
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unidentified"
 /mol_type="genomic RNA"
 /db_xref="taxon:32644"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1503 AAATTCCCAAGACCA 1518
 |||||
 Db 17 AAATTCCCAAGACCA 2

RESULT 275
 A89532/c
 LOCUS 18 bp DNA linear PAT 22-JAN-2000
 DEFINITION Sequence 1680 from Patent WO9833904.
 ACCESSION A89532
 VERSION A89532.1 GI:6738102
 KEYWORDS
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Brysch, W. and Schlingensiepen, K.
 TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
 JOURNAL Patent: WO 9833904-A 1680 06-AUG-1998;
 BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
 FEATURES Location/Qualifiers
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 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

Query Match 0.4%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2376 TCATCTCTGATCTTCA 2391
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 Db 16 TCATCTCTGATCTTCA 1

RESULT 276
 I17266
 LOCUS 18 bp DNA linear PAT 03-APR-1996
 DEFINITION Sequence 32 from patent US 5486599.
 ACCESSION I17266
 VERSION I17266.1 GI:1252174
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Saunders, S., Bernfield, M. and Kato, M.
 TITLE Construction and use of synthetic constructs encoding syndecan

JOURNAL Patent: US 5486599-A 32 23-JAN-1996;
 FEATURES Location/Qualifiers
 source 1..18
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2375 GTCATCTCTGATCTTCA 2390
 |||||
 Db 2 GCCATCTCTGATCTTCA 17

RESULT 277
 AR201812
 LOCUS 18 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 27 from patent US 6361941.
 ACCESSION AR201812
 VERSION AR201812.1 GI:20256351
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Todd, A.V., Fuery, C.J. and Cairns, M.J.
 TITLE Catalytic nucleic acid-based diagnostic methods
 JOURNAL Patent: US 6361941-A 27 26-MAR-2002;
 FEATURES Location/Qualifiers
 source 1..18
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 480 TGTACAGAAVTGGAAAAG 497
 |||||
 Db 1 TGTACAGAAVTGGAAAAG 18

RESULT 278
 AR201850/c
 LOCUS 18 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 65 from patent US 6361941.
 ACCESSION AR201850
 VERSION AR201850.1 GI:20256389
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Todd, A.V., Fuery, C.J. and Cairns, M.J.
 TITLE Catalytic nucleic acid-based diagnostic methods
 JOURNAL Patent: US 6361941-A 65 26-MAR-2002;
 FEATURES Location/Qualifiers
 source 1..18
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 480 TGTACAGAAVTGGAAAAG 497
 |||||
 Db 18 TGTACAGAAVTGGAAAAG 1

RESULT 279
 AR294083/c

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LOCUS       AR294083                               18 bp    DNA
DEFINITION   Sequence 5818 from patent US 6537751.
ACCESSION   AR294083
VERSION     AR294083.1  GI:31681367
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE       Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
JOURNAL     Patent: US 6537751-A 5818 25-MAR-2003;
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1607 TCTCTGTTCCATGTTT 1622
Db      17 TGTCTGTTCCATGTTT 2

RESULT 280
LOCUS       AX191826                               18 bp    DNA
DEFINITION   Sequence 108 from Patent WO0149775.
ACCESSION   AX191826
VERSION     AX191826.1  GI:15209995
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Iversen,P.L.
TITLE       Antisense antibacterial cell division composition and method
JOURNAL     Patent: WO 0149775-A 108 12-JUL-2001;
            Avi Biopharma, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="oligonucleotide"

Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2007 GGAACGACAAATGAAAT 2022
Db      18 GGAACGACAAATGAAAT 3

RESULT 281
LOCUS       AX352809                               18 bp    DNA
DEFINITION   Sequence 15 from Patent EP1174518.
ACCESSION   AX352809
VERSION     AX352809.1  GI:18617891
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Loukachov,V.V., van Gemen,B. and Goudsmit,J.
TITLE       Collection of binding molecules
JOURNAL     Patent: EP 1174518-A 15 23-JAN-2002;
            Amsterdam Support Diagnostics B.V. (NL)

LOCUS       AR294083                               18 bp    DNA
DEFINITION   Sequence 5818 from patent US 6537751.
ACCESSION   AR294083
VERSION     AR294083.1  GI:31681367
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE       Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
JOURNAL     Patent: US 6537751-A 5818 25-MAR-2003;
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1607 TCTCTGTTCCATGTTT 1622
Db      17 TGTCTGTTCCATGTTT 2

RESULT 280
LOCUS       AX191826                               18 bp    DNA
DEFINITION   Sequence 108 from Patent WO0149775.
ACCESSION   AX191826
VERSION     AX191826.1  GI:15209995
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Iversen,P.L.
TITLE       Antisense antibacterial cell division composition and method
JOURNAL     Patent: WO 0149775-A 108 12-JUL-2001;
            Avi Biopharma, Inc. (US)
FEATURES    Location/Qualifiers
            source
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="oligonucleotide"

Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2007 GGAACGACAAATGAAAT 2022
Db      18 GGAACGACAAATGAAAT 3

RESULT 281
LOCUS       AX352809                               18 bp    DNA
DEFINITION   Sequence 15 from Patent EP1174518.
ACCESSION   AX352809
VERSION     AX352809.1  GI:18617891
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Loukachov,V.V., van Gemen,B. and Goudsmit,J.
TITLE       Collection of binding molecules
JOURNAL     Patent: EP 1174518-A 15 23-JAN-2002;
            Amsterdam Support Diagnostics B.V. (NL)

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FEATURES    Location/Qualifiers
            source
            1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="position 41"

Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      482 TACAGTACTGGAAAAG 497
Db      2 TACAGAACTGGAAAAG 17

RESULT 282
LOCUS       AX362654                               18 bp    DNA
DEFINITION   Sequence 15 from Patent WO0208463.
ACCESSION   AX362654
VERSION     AX362654.1  GI:18694794
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Loukachov,V.V., Goudsmit,J. and van Gemen,B.
TITLE       Collection of binding molecules
JOURNAL     Patent: WO 0208463-A 15 31-JAN-2002;
            Amsterdam Support Diagnostics B.V. (NL)
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="position 41"

Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      482 TACAGTACTGGAAAAG 497
Db      2 TACAGAACTGGAAAAG 17

RESULT 283
LOCUS       AX822772                               18 bp    DNA
DEFINITION   Sequence 664 from Patent EP1340818.
ACCESSION   AX822772
VERSION     AX822772.1  GI:39749408
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
            Rujan,T. and Schmitt,A.
TITLE       Method and nucleic acids for the analysis of a colon cell
            proliferative disorder
JOURNAL     Patent: EP 1340818-A 664 03-SEP-2003;
            Epigenomics AG (DE)
FEATURES    Location/Qualifiers
            source
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="detection oligonucleotide for GTBP/MSH6"

Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;

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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1909 TTTTGTGGGATGGAGT 1924
      |||||
Db 1 TTTTGTGGGATGGAGT 16

RESULT 284
AX826412
LOCUS AX826412 18 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 664 from Patent WO03072821.
ACCESSION AX826412
VERSION AX826412.1 GI:39751926
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
TITLE Rujan,T. and Schmitt,A.
METHOD Method and nucleic acids for the analysis of a colon cell
Proliferative disorder
JOURNAL Patent: WO 03072821-A 664 04-SEP-2003;
EpiGenomics AG (DE)
FEATURES
source
location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for GTRP/MSH6"

Query Match 0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1909 TTTTGTGGGATGGAGT 1924
      |||||
Db 1 TTTTGTGGGATGGAGT 16

RESULT 285
BD067045/c
LOCUS BD067045 18 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD067045
VERSION BD067045.1 GI:22612648
KEYWORDS JP 2001511000-A/1680.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingsiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1680 07-AUG-2001;
BIOGENOSIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1680
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
FT source
FT source
location/Qualifiers
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/organism="Unknown"
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1909 TTTTGTGGGATGGAGT 1924
      |||||
Db 1 TTTTGTGGGATGGAGT 16

RESULT 286
AX297171/c
LOCUS AX297171 19 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 8906 from patent US 6537751.
ACCESSION AR297171
VERSION AR297171.1 GI:31684455
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 8906 25-MAR-2003;
FEATURES
source
location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 429 CAGAAGACACAGACAA 444
      |||||
Db 19 CAGAAGACACAGATCAA 4

RESULT 287
AX119429/c
LOCUS AX119429 19 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 86 from Patent WO0129251.
ACCESSION AX119429
VERSION AX119429.1 GI:14036348
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Messiaen,L. and Callens,T.
TITLE Improved mutation analysis of the nfi gene
JOURNAL Patent: WO 0129251-A 86 26-APR-2001;
UNIVERSITEIT GENT (BE)
FEATURES
source
location/Qualifiers
1..19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1493 TTTAAAGGGGAAATTC 1508
      |||||
Db 18 TTATACAGGGGAAATTC 3

RESULT 288
AX119529/c
LOCUS AX119529 19 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 186 from Patent WO0129251.
ACCESSION AX119529

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VERSION      AX119529.1  GI:14036448
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        1
JOURNAL      Messiaen,L. and Callens,T.
FEATURES     Improved mutation analysis of the nfi gene
SOURCE       UNIVERSITEIT GENT (BE)
              Location/Qualifiers
                source
                  1..19
                    /organism="Homo sapiens"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:9606"

Query Match      0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred.No.1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1493 TTTAAGGGGAAATTC 1508
        |||||
        18 TTTACAGGGGAAATTC 3

RESULT 289
ACE391671 19 bp DNA linear PLN 20-JUL-2000
LOCUS      Allium cepa STMS reverse primer sequence (AMS03-R) for germplasm
DEFINITION analysis.
ACCESSION  AJ391671
VERSION     AJ391671.1 GI:6911711
KEYWORDS    oligonucleotide; primer.
SOURCE      Allium cepa (onion)
ORGANISM    Allium cepa
REFERENCE    1 (bases 1 to 19)
AUTHORS      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE        Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
              Allium.
              Fischer,D. and Bachmann,K.
              Onion microsatellites for germplasm analysis and their use in
              assessing intra- and interspecific relatedness within the subgenus
              Rhizirideum
              Theor. Appl. Genet. 101, 153-164 (2000)
              2 (bases 1 to 19)
              Fischer,D. and Bachmann,K.
              Direct Submission
              Submitted (18-JAN-2000) Taxonomy, Institute of Plant Genetics and
              Crop Plant Research (IPK), Corrensstrasse 3, Gatersleben,
              Saxony-Anhalt 06466, Germany
              Location/Qualifiers
                source
                  1..19
                    /organism="Allium cepa"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:4679"

primer_bind    1..19
               /note="STMS reverse primer AMS03-R primer"

Query Match      0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred.No.1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2535 TTTCCTCTTGAGGTGA 2550
        |||||
        4 TTTCCTCTTGAGTGA 19

RESULT 290
A92156/c 20 bp DNA linear PAT 22-JAN-2000
LOCUS      Sequence 22 from Patent WO9820145.
DEFINITION
ACCESSION

VERSION      A92156.1  GI:14036448
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        1
JOURNAL      Messiaen,L. and Callens,T.
FEATURES     Improved mutation analysis of the nfi gene
SOURCE       UNIVERSITEIT GENT (BE)
              Location/Qualifiers
                source
                  1..19
                    /organism="Homo sapiens"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:9606"

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred.No.1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1806 TAGCATTGGAAAATGT 1821
        |||||
        18 TAGCATTGGAAAATGT 3

RESULT 291
A98716/c 20 bp DNA linear PAT 26-JAN-2000
LOCUS      Sequence 51 from Patent WO9910482.
DEFINITION
ACCESSION  A98716
VERSION     A98716.1 GI:6781754
KEYWORDS
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE    1 (bases 1 to 20)
AUTHORS      Lemieux,J. and Hekimi,S.
TITLE        THE C. ELEGANS GRO-1 GENE
JOURNAL      Patent: WO 9910482-A 51 04-MAR-1999;
              LEMIEUX JASON (CA); UNIV MCGILL (CA)
FEATURES     Location/Qualifiers
                source
                  1..20
                    /organism="unidentified"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32644"

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred.No.1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2135 AGAATCTCCTTTAATT 2150
        |||||
        16 AGAATCTCCTTTAATT 1

RESULT 292
AR067011 20 bp DNA linear PAT 29-SEP-1999
LOCUS      Sequence 359 from patent US 5851760.
DEFINITION
ACCESSION  AR067011
VERSION     AR067011.1 GI:5998233
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Evans,G.A. and Smith,M.W.
TITLE        Method for generation of sequence sampled maps of complex genomes
JOURNAL      Patent: US 5851760-A 359 22-DEC-1998;
FEATURES     Location/Qualifiers
                source
                  1..20
                    /organism="unknown"
                    /mol_type="unassigned DNA"

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ACCESSION AR226056
VERSION AR226056.1 GI:27264210
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Wyatt,J. and Freier,S.M.
TITLE Antisense modulation of Her-1 expression
JOURNAL Patent: US 6444465-A 119 03-SEP-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1503 AAATTCCTCCCAAGACCA 1518
Db 1 AAATTCCTCCCAAGACCA 16

RESULT 298
AR295538
LOCUS AR295538 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 7273 from patent US 6537751.
ACCESSION AR295538
VERSION AR295538.1 GI:31682822
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 7273 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3123 AGAGGACATTGCTTTT 3138
Db 4 AGAGTACATTGCTTTT 19

RESULT 299
AR311566/c
LOCUS AR311566 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 2103 from patent US 6559294.
ACCESSION AR311566
VERSION AR311566.1 GI:31704992
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Holiseth,S.K., Zagursky,R.J., Metcalfe,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 2103 06-MAY-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

ACCESSION AR226056
VERSION AR226056.1 GI:27264210
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Wyatt,J. and Freier,S.M.
TITLE Antisense modulation of Her-1 expression
JOURNAL Patent: US 6444465-A 119 03-SEP-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3254 TGGAGTGAATCGAAAT 3269
Db 20 TGGAGGGAATCGAAAT 5

RESULT 300
AX048436/c
LOCUS AX048436 20 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 35 from Patent WO0071747.
ACCESSION AX048436
VERSION AX048436.1 GI:12225600
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE Detection system for separating constituents of a sample and
production and use of the same
JOURNAL Patent: WO 0071747-A 35 30-NOV-2000;
Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kunstlichen
Sequenz:Erkennungssystem"

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3390 ACTCAAAAAAAAAAAAA 3405
Db 17 ACTTAAAAAAAAAAAAAA 2

RESULT 301
AX204955
LOCUS AX204955 20 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 2 from Patent WO0155362.
ACCESSION AX204955
VERSION AX204955.1 GI:15394236
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Zheng,C., O'Connell,B. and Baum,B.J.
TITLE Hybrid adeno-retroviral vector for the transfection of cells
JOURNAL Patent: WO 0155362-A 2 02-AUG-2001;
THE SECRETARY, DEPARTMENT OF HEALTH AND SOCIAL SERVICES (US)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR primer"

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3178 CAAACTAGAGCCAGG 3193
Db 2 CAAACTAGAGCCTGG 17
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RESULT 302
AX497581/c
LOCUS
DEFINITION Sequence 125 from Patent WO0233126.
ACCESSION AX497581
VERSION AX497581.1 GI:23342851
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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            /db_xref="taxon:32630"
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        modified_base
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            6-carboxyfluorescein (6-FAM)"
            /mod_base=OTHER
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    Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 949 AGTTCCTTTGGACAG 964
    |||||
    19 AGATCCCTTTGGACAG 4

RESULT 303
AX644862
LOCUS
DEFINITION Sequence 10 from Patent WO02061104.
ACCESSION AX644862
VERSION AX644862.1 GI:28610838
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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    Best Local Similarity 93.8%; Pred.No. 1.7e+02;
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QY 3178 CAAACTAGAGCCAGG 3193
    |||||
    2 CAAACTAGAGCCTGG 17

RESULT 304
AX795184/c
LOCUS
DEFINITION Sequence 14 from Patent EP1323825.
ACCESSION AX795184

```

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VERSION AX795184.1 GI:37515945
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Downstream primer used to detect the expression of
            the Carotene d esaturase gene by RT-PCR"
        primer_bind
            1. .20
                /note="Zds Downstream Primer"
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    Best Local Similarity 93.8%; Pred.No. 1.7e+02;
    Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2040 CTGTTGCATATGCTAT 2055
    |||||
    16 CTGTTGCATATGCTCT 1

Search completed: September 28, 2004, 08:31:07
Job time : 14 secs

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OM nucleic - nucleic search, using sw model

Run on: September 28, 2004, 08:34:37 ; Search time 14 Seconds
(without alignments)
3.723 Million cell updates/sec

Title: US-10-798-923A-4
Perfect score: 3405
Sequence: 1 cgcacacccaagtccaag.....acacactcaaaaaaaaaa 3405

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 355 seqs, 7653 residues

Total number of hits satisfying chosen parameters: 710

Minimum DB seq length: 8
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 355 summaries

Database : rng4.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	60	1.8	60	1	ABN35860
C 2	41	1.2	41	1	ABN35860
C 3	39.4	1.2	41	1	ABN35860
C 4	28	0.8	29	1	AAV09291
C 5	27	0.8	27	1	AAI12765
C 6	27	0.8	27	1	AAI12765
C 7	27	0.8	27	1	AAI12765
C 8	27	0.8	27	1	AAI12765
C 9	27	0.8	27	1	AAI12765
C 10	26	0.8	26	1	AAI12740
C 11	26	0.8	26	1	AAI12743
C 12	26	0.8	26	1	AAI12761
C 13	26	0.8	26	1	AAI12762
C 14	26	0.8	26	1	AAI12765
C 15	26	0.8	26	1	ABN35860
C 16	26	0.8	27	1	ABN35860
C 17	25.4	0.7	27	1	ABN35860
C 18	25	0.7	25	1	AAI12787
C 19	25	0.7	25	1	AAI12816
C 20	25	0.7	25	1	AAI12793
C 21	25	0.7	25	1	AAI12792
C 22	25	0.7	25	1	AAI12815
C 23	25	0.7	25	1	AAI12818
C 24	25	0.7	25	1	AAI12819
C 25	25	0.7	25	1	AAI12817
C 26	25	0.7	25	1	AAI12817
C 27	25	0.7	25	1	AAI12817
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C 29	25	0.7	25	1	AAI12817
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C 32	25	0.7	25	1	AAI12817
C 33	25	0.7	25	1	AAI12817

34	24.4	0.7	26	1	AAA12741	Nucleotide sequenc
35	24.4	0.7	26	1	AAI12741	Human ACE-2 DNA fr
36	24.4	0.7	26	1	AAI12741	Human ACE-2 exon 1
37	24	0.7	24	1	AAA12813	PCR primer ace2e18
C 38	24	0.7	24	1	AAA12772	PCR primer ace2e2c
C 39	24	0.7	24	1	AAA12788	PCR primer ace2e8c
C 40	24	0.7	24	1	AAA12784	PCR primer ace2e7c
C 41	24	0.7	24	1	AAA12738	Nucleotide sequenc
C 42	24	0.7	24	1	AAA12820	PCR primer ace2e18
C 43	24	0.7	24	1	AAA12771	PCR primer ace2e2b
C 44	24	0.7	24	1	AAI12771	ace2e8c PCR primer
C 45	24	0.7	24	1	AAI12771	ace2e18 PCR prime
C 46	24	0.7	24	1	AAI12771	ace2e18 PCR prime
C 47	24	0.7	24	1	AAI12771	ace2e2c PCR primer
C 48	24	0.7	24	1	AAI12771	ace2e2c PCR primer
C 49	24	0.7	24	1	AAI12771	ace2e7c PCR primer
C 50	24	0.7	24	1	AAI12771	Human genotyping p
C 51	23	0.7	23	1	AAI12771	PCR primer ace2e17
C 52	23	0.7	23	1	AAI12771	PCR primer ace2e9b
C 53	23	0.7	23	1	AAI12771	PCR primer ace2e1c
C 54	23	0.7	23	1	AAI12771	PCR primer used fo
C 55	23	0.7	23	1	AAI12771	PCR primer ace2e18
C 56	23	0.7	23	1	AAI12771	PCR primer ace2e17
C 57	23	0.7	23	1	AAI12771	ace2e18c PCR prime
C 58	23	0.7	23	1	AAI12771	Human ACE-2 exon 1
C 59	23	0.7	23	1	AAI12771	ace2e9b PCR primer
C 60	23	0.7	23	1	AAI12771	Human ACE-2 gene a
C 61	23	0.7	23	1	AAI12771	ace2e1c PCR primer
C 62	23	0.7	23	1	AAI12771	ace2e17c PCR prime
C 63	23	0.7	23	1	AAI12771	ace2e17b PCR prim
C 64	22.4	0.7	24	1	AAI12739	Nucleotide sequenc
C 65	22.4	0.7	24	1	AAI12739	Human ACE-2 exon 1
C 66	21	0.6	21	1	AAI12767	PCR primer ace2e1b
C 67	21	0.6	21	1	AAI12767	ace2e1b PCR primer
C 68	20.2	0.6	25	1	ABN13755	Human GDMPL-1 25-m
C 69	20	0.6	22	1	AAI12769	PCR primer ace2eld
C 70	20	0.6	22	1	AAI12769	ace2eld PCR primer
C 71	19.8	0.6	23	1	AAQ57377	Enzymatic RNA mole
C 72	19.8	0.6	28	1	ABK52626	Minority genome me
C 73	19.2	0.6	25	1	ABN13756	Human GDMPL-1 25-m
C 74	19.2	0.6	25	1	ABN13754	Human GDMPL-1 25-m
C 75	19	0.6	19	1	ABN13754	Human DNA represen
C 76	18.4	0.5	25	1	ABN13757	HLA HLA-A gene PCR
C 77	18.2	0.5	25	1	ABN13757	Human GDMPL-1 25-m
C 78	18.2	0.5	25	1	ABN13753	Human GDMPL-1 25-m
C 79	18	0.5	18	1	ABN13753	Human genotyping p
C 80	17.8	0.5	24	1	ACC69771	Mouse MOP transpor
C 81	17.8	0.5	25	1	ACC69771	HLA HLA-A gene PCR
C 82	17.8	0.5	25	1	ACC69771	HLA HLA-C gene PCR
C 83	17.8	0.5	25	1	ACC69771	Human microarray D
C 84	17.6	0.5	24	1	ACI02723	5' primer for RANB
C 85	17.6	0.5	24	1	ACI02723	Capture oligonucle
C 86	17.6	0.5	24	1	ACI02723	Capture oligonucle
C 87	17.6	0.5	25	1	ACI02723	HLA HLA-A gene PCR
C 88	17.6	0.5	25	1	ACI02723	HLA HLA-A gene PCR
C 89	17.6	0.5	25	1	ACI02723	Human GDMPL-1 25-m
C 90	17.6	0.5	25	1	ACI02723	Human GDMPL-1 25-m
C 91	17.6	0.5	25	1	ACI02723	Human microarray D
C 92	17.4	0.5	19	1	ABN13754	Human DNA represen
C 93	17.2	0.5	23	1	ABN13754	Escherichia coli S
C 94	17.2	0.5	24	1	ABN13754	Human ATP-dependen
C 95	17.2	0.5	24	1	ABN13754	Oligonucleotide ad
C 96	17.2	0.5	24	1	ABN13754	Oligonucleotide ad
C 97	17.2	0.5	24	1	ABN13754	Oligonucleotide ad
C 98	17.2	0.5	24	1	ABN13754	Analyte sorting ta
C 99	16.8	0.5	20	1	ABN13754	Human chromosome 1
C 100	16.8	0.5	21	1	ABN13754	Human gene single
C 101	16.8	0.5	22	1	ABN13754	Forward PCR primer
C 102	16.8	0.5	22	1	ABN13754	Human HKNG1 exon 4
C 103	16.8	0.5	22	1	ABN13754	Human IL4 gene PCR
C 104	16.8	0.5	24	1	ABN13754	Subtilisin 10 PCR
C 105	16.8	0.5	24	1	ABN13754	Human clathrin lig
C 106	16.8	0.5	24	1	ABN13754	Capture oligonucle

107	16.8	0.5	24	1	AB190378	Capture oligonucleotide	180	15.2	0.4	20	1	AA92000	PCR primer used to
108	16.6	0.5	23	1	AAQ34279	Upstream PCR prime	c 181	15.2	0.4	20	1	AA92000	Human biologic ma
109	16.6	0.5	23	1	Coffee alpha-D-gal	Primer #232, for N	c 182	15.2	0.4	20	1	AA92000	Fas ligand promote
110	16.4	0.5	20	1	AAQ38211	Primer #232, for N	c 183	15.2	0.4	20	1	AA92000	Oligonucleotide pr
111	16.4	0.5	20	1	AAQ38211	Primer #232, for N	c 184	15.2	0.4	20	1	AA92000	Human Y-box bindin
112	16.4	0.5	21	1	AAQ38211	Primer #232, for N	c 185	15.2	0.4	20	1	AA92000	Human beta-actin d
113	16.4	0.5	22	1	AAQ38211	Primer #232, for N	c 186	15.2	0.4	20	1	AA92000	Human Nck-2 phosph
114	16.4	0.5	22	1	AAQ38211	Primer #232, for N	c 187	15.2	0.4	20	1	AA92000	Human c-myc PCR pr
115	16.4	0.5	22	1	AAQ38211	Primer #232, for N	c 188	15.2	0.4	20	1	AA92000	Rat mOB gene RT-PC
116	16.4	0.5	22	1	AAQ38211	Primer #232, for N	c 189	15.2	0.4	20	1	AA92000	Zmax1 gene region
117	16.2	0.5	21	1	AAQ38211	Primer #232, for N	c 190	15.2	0.4	20	1	AA92000	Human ABC11 intro
118	16.2	0.5	21	1	AAQ38211	Primer #232, for N	c 191	15.2	0.4	20	1	AA92000	Human chromosome 1
119	16.2	0.5	21	1	AAQ38211	Primer #232, for N	c 192	15.2	0.4	20	1	AA92000	Mouse caspase 2 an
120	16.2	0.5	22	1	AAQ38211	Primer #232, for N	c 193	15.2	0.4	20	1	AA92000	Human Zmax1 CDNA f
121	16.2	0.5	22	1	AAQ38211	Primer #232, for N	c 194	15.2	0.4	20	1	AA92000	Human light chain
122	16.2	0.5	22	1	AAQ38211	Primer #232, for N	c 195	15.2	0.4	20	1	AA92000	Capture oligonucle
123	16.2	0.5	22	1	AAQ38211	Primer #232, for N	c 196	15.2	0.4	20	1	AA92000	Capture oligonucle
124	16.2	0.5	22	1	AAQ38211	Primer #232, for N	c 197	15.2	0.4	20	1	AA92000	Triple helix formi
125	16	0.5	19	1	AAQ38211	Primer #232, for N	c 198	15.2	0.4	20	1	AA92000	Triple helix formi
126	16	0.5	20	1	AAQ38211	Primer #232, for N	c 199	15.2	0.4	20	1	AA92000	Human oligonucleot
127	16	0.5	20	1	AAQ38211	Primer #232, for N	c 200	15.2	0.4	20	1	AA92000	Human IL4-R oligon
128	16	0.5	21	1	AAQ38211	Primer #232, for N	c 201	15.2	0.4	20	1	AA92000	Human oligonucleot
129	15.8	0.5	19	1	AAQ38211	Primer #232, for N	c 202	15.2	0.4	20	1	AA92000	Human oligonucleot
130	15.8	0.5	19	1	AAQ38211	Primer #232, for N	c 203	15.2	0.4	20	1	AA92000	Human HEM SPS mark
131	15.8	0.5	20	1	AAQ38211	Primer #232, for N	c 204	15.2	0.4	20	1	AA92000	DPP10 PCR primer #
132	15.8	0.5	20	1	AAQ38211	Primer #232, for N	c 205	15.2	0.4	20	1	AA92000	Human oligonucleot
133	15.8	0.5	20	1	AAQ38211	Primer #232, for N	c 206	15.2	0.4	20	1	AA92000	Mouse phospholipid
134	15.8	0.5	20	1	AAQ38211	Primer #232, for N	c 207	15.2	0.4	20	1	AA92000	Pathogen variant d
135	15.8	0.5	20	1	AAQ38211	Primer #232, for N	c 208	15.2	0.4	20	1	AA92000	Clone specific PCR
136	15.8	0.5	20	1	AAQ38211	Primer #232, for N	c 209	15.2	0.4	20	1	AA92000	Sequence tagged si
137	15.8	0.5	20	1	AAQ38211	Primer #232, for N	c 210	15.2	0.4	20	1	AA92000	Reverse transcript
138	15.8	0.5	20	1	AAQ38211	Primer #232, for N	c 211	15.2	0.4	20	1	AA92000	PCR primer B13M126
139	15.8	0.5	21	1	AAQ38211	Primer #232, for N	c 212	15.2	0.4	20	1	AA92000	PCR primer B13M126
140	15.8	0.5	21	1	AAQ38211	Primer #232, for N	c 213	15.2	0.4	20	1	AA92000	Human biologic ma
141	15.8	0.5	21	1	AAQ38211	Primer #232, for N	c 214	15.2	0.4	20	1	AA92000	Human biologic ma
142	15.8	0.5	21	1	AAQ38211	Primer #232, for N	c 215	15.2	0.4	20	1	AA92000	Single nucleotide
143	15.8	0.5	22	1	AAQ38211	Primer #232, for N	c 216	15.2	0.4	20	1	AA92000	Human gene single
144	15.8	0.5	22	1	AAQ38211	Primer #232, for N	c 217	15.2	0.4	20	1	AA92000	Human COL1A1 PCR p
145	15.8	0.5	22	1	AAQ38211	Primer #232, for N	c 218	15.2	0.4	20	1	AA92000	H influenzae BASB2
146	15.6	0.5	22	1	AAQ38211	Primer #232, for N	c 219	15.2	0.4	20	1	AA92000	Human mitochondria
147	15.6	0.5	22	1	AAQ38211	Primer #232, for N	c 220	15.2	0.4	20	1	AA92000	Candidate HPV16 E6
148	15.6	0.5	22	1	AAQ38211	Primer #232, for N	c 221	15.2	0.4	20	1	AA92000	Bovine lactate deh
149	15.6	0.5	22	1	AAQ38211	Primer #232, for N	c 222	15.2	0.4	20	1	AA92000	IGF-1 oligonucleot
150	15.6	0.5	22	1	AAQ38211	Primer #232, for N	c 223	15.2	0.4	20	1	AA92000	Tumour suppression
151	15.6	0.5	22	1	AAQ38211	Primer #232, for N	c 224	15.2	0.4	20	1	AA92000	Human MDZ7 scannin
152	15.6	0.5	22	1	AAQ38211	Primer #232, for N	c 225	15.2	0.4	20	1	AA92000	Human MDZ7 scannin
153	15.6	0.5	22	1	AAQ38211	Primer #232, for N	c 226	15.2	0.4	20	1	AA92000	Tumour suppression
154	15.4	0.5	22	1	AAQ38211	Primer #232, for N	c 227	15.2	0.4	20	1	AA92000	DPP10 related PSQ
155	15.4	0.5	22	1	AAQ38211	Primer #232, for N	c 228	15.2	0.4	20	1	AA92000	cdk4 ribozyme bind
156	15.4	0.5	22	1	AAQ38211	Primer #232, for N	c 229	15.2	0.4	20	1	AA92000	Cell-cycle depende
157	15.4	0.5	22	1	AAQ38211	Primer #232, for N	c 230	15.2	0.4	20	1	AA92000	Reverse transcript
158	15.4	0.5	22	1	AAQ38211	Primer #232, for N	c 231	15.2	0.4	20	1	AA92000	Human TNF receptor
159	15.4	0.5	22	1	AAQ38211	Primer #232, for N	c 232	15.2	0.4	20	1	AA92000	Nested gene-specif
160	15.4	0.5	22	1	AAQ38211	Primer #232, for N	c 233	15.2	0.4	20	1	AA92000	Mouse IL-5 recepto
161	15.4	0.5	22	1	AAQ38211	Primer #232, for N	c 234	15.2	0.4	20	1	AA92000	Primer used to amp
162	15.4	0.5	22	1	AAQ38211	Primer #232, for N	c 235	15.2	0.4	20	1	AA92000	Human beta-actin d
163	15.4	0.5	22	1	AAQ38211	Primer #232, for N	c 236	15.2	0.4	20	1	AA92000	Human oligonucleot
164	15.4	0.5	22	1	AAQ38211	Primer #232, for N	c 237	15.2	0.4	20	1	AA92000	Human oligonucleot
165	15.4	0.5	22	1	AAQ38211	Primer #232, for N	c 238	15.2	0.4	20	1	AA92000	Mouse interleukin
166	15.4	0.5	22	1	AAQ38211	Primer #232, for N	c 239	15.2	0.4	20	1	AA92000	Reverse transcript
167	15.4	0.5	22	1	AAQ38211	Primer #232, for N	c 240	15.2	0.4	20	1	AA92000	Reverse transcript
168	15.4	0.5	22	1	AAQ38211	Primer #232, for N	c 241	15.2	0.4	20	1	AA92000	Reverse transcript
169	15.4	0.5	22	1	AAQ38211	Primer #232, for N	c 242	15.2	0.4	20	1	AA92000	Selection and ampli
170	15.4	0.5	22	1	AAQ38211	Primer #232, for N	c 243	15.2	0.4	20	1	AA92000	Oligomer HIV18 fo
171	15.4	0.5	22	1	AAQ38211	Primer #232, for N	c 244	15.2	0.4	20	1	AA92000	Granule bound star
172	15.4	0.5	22	1	AAQ38211	Primer #232, for N	c 245	15.2	0.4	20	1	AA92000	Oligonucleotide us
173	15.4	0.5	22	1	AAQ38211	Primer #232, for N	c 246	15.2	0.4	20	1	AA92000	Primer used for am
174	15.4	0.5	22	1	AAQ38211	Primer #232, for N	c 247	15.2	0.4	20	1	AA92000	Human CD40 phospho
175	15.4	0.5	22	1	AAQ38211	Primer #232, for N	c 248	15.2	0.4	20	1	AA92000	PCR primer used in
176	15.4	0.5	22	1	AAQ38211	Primer #232, for N	c 249	15.2	0.4	20	1	AA92000	Bacillus cereus en
177	15.2	0.4	20	1	AAQ38211	Primer #232, for N	c 250	15.2	0.4	20	1	AA92000	
178	15.2	0.4	20	1	AAQ38211	Primer #232, for N	c 251	15.2	0.4	20	1	AA92000	
179	15.2	0.4	20	1	AAQ38211	Primer #232, for N	c 252	15.2	0.4	20	1	AA92000	

253	14.8	0.4	18	1	AAZ47710	Human CD40 antisense	102	14.8	0.4	20	1	ADD81528	HIV PRT antisense
c 254	14.8	0.4	18	1	AAZ92573	Antisense oligonucleotide	327	14.8	0.4	20	1	ADZ39777	Porcine CD 151 rel
c 255	14.8	0.4	18	1	AAH79637	Human Akt-3 antisense	c 328	14.8	0.4	21	1	AAZ77685	Wheat microsatellite
c 256	14.8	0.4	18	1	AAH19624	Complementary oligonucleotide	329	14.8	0.4	21	1	AAZ09125	Human biallelic polymorphism
c 257	14.8	0.4	18	1	AAZ85250	Reverse primer L5	330	14.8	0.4	21	1	AAZ57635	Exon 2 of an ENAC
c 258	14.8	0.4	18	1	AAZ11199	Oligonucleotide #2	331	14.8	0.4	21	1	AAZ26499	Human polymorphic
c 259	14.8	0.4	18	1	AAZ07721	Enterobacteria phage	332	14.8	0.4	21	1	AAZ26500	Human polymorphic
c 260	14.8	0.4	19	1	AAV10722	Human breast cancer	333	14.8	0.4	21	1	AAZ18494	Polymorphic fragile
c 261	14.8	0.4	19	1	AAV10742	Human breast cancer	334	14.8	0.4	21	1	AAZ75941	Human biallelic polymorphism
c 262	14.8	0.4	19	1	AAV51387	Human TIGR PCR primer	c 335	14.8	0.4	21	1	AAZ80401	Human ASTHLJ intro
c 263	14.8	0.4	19	1	AAZ82506	cdk1 ribozyme binding	336	14.8	0.4	21	1	AAZ60704	Oligonucleotide #2
c 264	14.8	0.4	19	1	AAZ57505	Primer used for SS	c 337	14.8	0.4	21	1	AAZ60705	Oligonucleotide #3
c 265	14.8	0.4	19	1	AAZ57668	Cell-cycle dependent	c 338	14.8	0.4	21	1	AAZ59588	Human gene single
c 266	14.8	0.4	19	1	AAZ88879	HIV-1 related binding	339	14.8	0.4	21	1	AAZ03024	PCR primer Gus ant
c 267	14.8	0.4	19	1	AAZ89073	HIV-1 related binding	c 340	14.8	0.4	21	1	AAZ62233	Zinc finger protein
c 268	14.8	0.4	19	1	AAZ88532	EST polymorphic DN	c 341	14.8	0.4	21	1	AAZ27174	Drug-resistance gene
c 269	14.8	0.4	19	1	AAZ79687	PCR primer #1 for	c 342	14.8	0.4	21	1	AAZ62012	IL6 hairpin/hammer
c 270	14.8	0.4	20	1	AAZ39509	Probe specific for	c 343	14.8	0.4	21	1	AAZ89051	GC box assay FATP5
c 271	14.8	0.4	20	1	AAZ58798	CD40 ligand gene m	344	14.8	0.4	21	1	AAZ97282	Human aryl hydroc
c 272	14.8	0.4	20	1	AAZ67125	Primer for exon 13	c 345	14.8	0.4	21	1	AAZ04600	Human PTGS1 gene p
c 273	14.8	0.4	20	1	AAZ23337	Human AD4 exon 8 p	346	14.8	0.4	21	1	AAZ68816	PCR primer, #2, us
c 274	14.8	0.4	20	1	AAZ51303	Mouse CD34 reverse	c 347	14.8	0.4	21	1	AAZ17461	GUS reporter gene
c 275	14.8	0.4	20	1	AAZ75184	Primer MYH11:1377L	c 348	14.8	0.4	21	1	AAZ69340	Human SL1A3 codi
c 276	14.8	0.4	20	1	AAZ41074	Primer #1 for exte	349	14.8	0.4	21	1	AAZ22424	Gus gene PCR prime
c 277	14.8	0.4	20	1	AAZ40467	Human ptc-2 PCR pr	c 350	14.8	0.4	21	1	AAZ00728	IL-12 p40 sense pr
c 278	14.8	0.4	20	1	AAZ89480	Human mdm2 phospho	351	14.8	0.4	21	1	AAZ00603	Human CAP2 gene ex
c 279	14.8	0.4	20	1	AAZ73557	PCR primer used to	c 352	14.8	0.4	21	1	AAZ84380	Fluorescein label
c 280	14.8	0.4	20	1	AAZ03775	PCR primer used to	c 353	14.8	0.4	21	1	AAZ84393	HIVpol7p41 target
c 281	14.8	0.4	20	1	AAZ95463	Probe for peripher	354	14.8	0.4	21	1	AAZ84383	Probe HIVpol7p41-4
c 282	14.8	0.4	20	1	AAZ37011	Human TNFalpha ant	c 355	14.8	0.4	21	1	AAZ04439	Bcr-abl fusion gen
c 283	14.8	0.4	20	1	AAZ41259	Human A1 anti-apop							
c 284	14.8	0.4	20	1	AAZ39069	Ribonucleotide red							
c 285	14.8	0.4	20	1	AAZ90847	Human MEK5 phosph							
c 286	14.8	0.4	20	1	AAZ61982	Interleukin 10 sho							
c 287	14.8	0.4	20	1	AAZ60942	Human dactx inhibit							
c 288	14.8	0.4	20	1	AAZ73034	Human PARP-2 antis							
c 289	14.8	0.4	20	1	AAZ45736	Human ABC1 transcr							
c 290	14.8	0.4	20	1	AAZ92850	PCR primer for a m							
c 291	14.8	0.4	20	1	AAZ27939	Human mdm2 phospho							
c 292	14.8	0.4	20	1	AAZ80711	Human hDPP PCR pri							
c 293	14.8	0.4	20	1	AAZ74765	Murine Xist gene p							
c 294	14.8	0.4	20	1	AAZ75704	Oligonucleotide #2							
c 295	14.8	0.4	20	1	AAZ67718	Human inflammatory							
c 296	14.8	0.4	20	1	AAZ91454	Human mdm2 antisense							
c 297	14.8	0.4	20	1	AAZ29326	Oligonucleotide hy							
c 298	14.8	0.4	20	1	AAZ80637	Oligonucleotide hy							
c 299	14.8	0.4	20	1	AAZ80639	Oligonucleotide hy							
c 300	14.8	0.4	20	1	AAZ80638	Plant vector PCR p							
c 301	14.8	0.4	20	1	AAZ52263	Human cytohesin-1							
c 302	14.8	0.4	20	1	AAZ73901	Human cytohesin-1							
c 303	14.8	0.4	20	1	AAZ43907	Human cytohesin-1							
c 304	14.8	0.4	20	1	AAZ66437	Porcine CD 151 cod							
c 305	14.8	0.4	20	1	AAZ49188	Human oligonucleot							
c 306	14.8	0.4	20	1	AAZ87594	Human oligonucleot							
c 307	14.8	0.4	20	1	AAZ88879	Human oligonucleot							
c 308	14.8	0.4	20	1	AAZ85771	Human oligonucleot							
c 309	14.8	0.4	20	1	AAZ94088	Human oligonucleot							
c 310	14.8	0.4	20	1	AAZ93102	Human oligonucleot							
c 311	14.8	0.4	20	1	AAZ92034	Human oligonucleot							
c 312	14.8	0.4	20	1	AAZ88937	Human oligonucleot							
c 313	14.8	0.4	20	1	AAZ93343	Human dual specific							
c 314	14.8	0.4	20	1	AAZ90985	Liver regeneration							
c 315	14.8	0.4	20	1	AAZ16110	NOVX related rever							
c 316	14.8	0.4	20	1	AAZ55467	Human FGFR-3 antis							
c 317	14.8	0.4	20	1	AAZ1748	Human PCTAIRE prot							
c 318	14.8	0.4	20	1	AAZ61748	Tumour necrosis fa							
c 319	14.8	0.4	20	1	AAZ05487	Matrix metalloprot							
c 320	14.8	0.4	20	1	AAZ79170	Human mdm2 antisense							
c 321	14.8	0.4	20	1	AAZ21522	Human Ship-1 antis							
c 322	14.8	0.4	20	1	AAZ61223	HIV PRT antisense							
c 323	14.8	0.4	20	1	AAZ81530	HIV PRT antisense							
c 324	14.8	0.4	20	1	AAZ81530	HIV PRT antisense							
c 325	14.8	0.4	20	1	AAZ81529	HIV PRT antisense							

ALIGNMENTS

RESULT 1

ABN35860

ID ABN35860 standard; DNA; 60 BP.

XX ABN35860;

AC ABN35860;

DT 15-JUL-2002 (first entry)

Human spliced transcript detection oligonucleotide SEQ ID NO:8608.

Human; mouse; rat; splice transcript; detection; RNA transcript;

splice variant; transcriptome; oligonucleotide library; ss.

OS Homo sapiens.

PN WO200210449-A2.

PD 07-FEB-2002.

PF 20-JUL-2001; 2001WO-IB001903.

PR 28-JUL-2000; 2000US-0221607P.

XX 02-MAY-2001; 2001US-0287724P.

(COMP-) COMPUGEN INC.

Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

WPI; 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which

selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-specific genes.

Example 1; SEQ ID NO 8608; 47bp; English.

The present invention describes oligonucleotide libraries for detecting

Claim 3; Page 790; 977pp; English.

The invention relates to an isolated nucleic acid from a human gene encoding aminopeptidase P (XPNPEP2), bradykinin receptor B1 (BDKBR1), tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein 1 (KLK1), bradykinin receptor B2 (BDKBR2), angiotensin converting enzyme 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one polymorphic position. Also included are (1) a probe that hybridises to a polymorphic position as provided in the detailed summary of single nucleotide polymorphisms comprising additional 5' and 3' flanking genomic sequence; (2) analysing (MI) at least one nucleic acid sample comprising obtaining the sample from one or more individuals and determining the nucleic acid sequence at one or more polymorphic positions in a gene

CC encoding a protein selected from the group above; (3) constructing (M2)
CC haplotypes using the genes comprising grouping at least two nucleic acids
CC identifying (M3) an individual at risk of developing a disorder
CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor
CC using the polymorphic data; (5) a library of nucleic acids, each of which
CC comprises one or more polymorphic positions within a gene encoding a
CC human protein selected from the group above; and (6) genotyping (M4) an
CC individual comprising obtaining a nucleic acid sample, determining the

leads one position with a known data set. The genes, (M1, M2, M3 and M4), and compositions are useful for detecting, diagnosing, treating, preventing various disorders such as angioedema and diseases which involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's disease, trachomas, and cardiovascular diseases like angina pectoris, hypertension, heart failure, myocardial infarction, ventricular hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary artery disease, arteriosclerosis and/or atherosclerosis, and

CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammation
CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
CC obstructive pulmonary disease (COPD) and enterocolitis (many other
CC diseases and disorders are listed in the specification). The
CC polynucleotides are also useful for chromosome identification. Antibodies
CC against the proteins may be utilised for immunophenotyping of cell lines
CC and biological samples. The present sequence represents or contains the
CC region surrounding a single-nucleotide polymorphism in one of the genes
CC encoding one of the proteins listed above
XX
SQ Sequence 41 BP; 15 A; 6 C; 9 G; 11 T; 0 U; 0 Other;

Query Match 1.2%; Score 41; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0

[illegible]

KW Amino peptidase P: XPNEP2: bradykinin receptor B1: ds: SNP: BDKRB1:

tachykinin receptor B1; TACR1; C1 esterase inhibitor; CLNH; kallikrein 1;
 KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
 angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
 polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
 cardiovascular disease; angina pectoris; hypertension; heart failure;
 myocardial infarction; ventricular hypertrophy; vascular disease;
 aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
 arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;
 autoimmune disease; inflammatory arthritis; cancer; wound;
 viral infection; bacterial infection; fungal infection; COPD;
 Chronic obstructive pulmonary disease; enterocolitis;
 single-nucleotide polymorphism.

Homo sapiens.

WO200261131-A2.

08-AUG-2002.

03-DEC-2001; 2001WO-US047235.

04-DEC-2000; 2000US-0251015P.

23-JAN-2001; 2001US-0263678P.

02-MAR-2001; 2001US-0273037P.

(BRIM) BRISTOL-MYERS SQUIBB CO.

(TSUC/) TSUCHIHASHI Z.

(HUIL/) HUI L.

Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;

Swanson BN, Powell JR;

WPI; 2002-619265/66.

New isolated nucleic acid with at least one polymorphic position, useful for detecting, diagnosing and treating disorders such as angioedema, cancer, viral, bacterial or fungal infection, cardiovascular and autoimmune diseases.

Claim 3; Page 795; 977pp; English.

The invention relates to an isolated nucleic acid from a human gene encoding aminopeptidase P (XPNEP2), bradykinin receptor B1 (BDKRB1), tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one polymorphic position. Also included are (1) a probe that hybridises to a nucleotide polymorphisms comprising additional 5' and 3' flanking genomic sequence; (2) analysing (M1) at least one nucleic acid sample comprising obtaining the sample from one or more individuals and determining the nucleic acid sequence at one or more polymorphic positions in a gene encoding a protein selected from the group above; (3) constructing (M2) haplotypes using the genes comprising grouping at least two nucleic acids; (4) identifying (M3) an individual at risk of developing a disorder upon administration of an ACE inhibitor and/or vasoconstrictor using the polymorphic data; (5) a library of nucleic acids, each of which comprises one or more polymorphic positions within a gene encoding a human protein selected from the group above; and (6) genotyping (M4) an individual comprising obtaining a nucleic acid sample, determining the nucleotide present in at least one polymorphic position, and comparing at least one position with a known data set. The genes, (M1, M2, M3 and M4) and compositions are useful for detecting, diagnosing, treating, preventing various disorders such as angioedema and diseases which involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's disease, trachomas, and cardiovascular diseases like angina pectoris, hypertension, heart failure, myocardial infarction, ventricular hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary artery disease, arteriosclerosis and/or atherosclerosis, and hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic obstructive pulmonary disease (COPD) and enterocolitis (many other diseases and disorders are listed in the specification). The

CC polynucleotides are also useful for chromosome identification. Antibodies
 CC against the proteins may be utilised for immunophenotyping of cell lines
 CC and biological samples. The present sequence represents or contains the
 CC region surrounding a single-nucleotide polymorphism in one of the genes
 CC encoding one of the proteins listed above

SQ Sequence 41 BP; 14 A; 6 C; 10 G; 11 T; 0 U; 0 Other;

Query Match 1.2%; Score 39.4; DB 1; Length 41;

Best Local Similarity 97.6%; Pred. No. 3.1;

Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2153 TTGTGCACTGCACCTAAATAATGTCTGATATCATTCCTAG 2193

DB 41 TTGTGCACTGCACCTAAATAATGTCTGATATCATTCCTAG 1

RESULT 4

AAV09291/c

ID AAV09291 standard; cDNA; 29 BP.

XX AAV09291;

XX 07-JUL-1998 (first entry)

XX Clone AU47_8 oligonucleotide probe.

XX AU47_8 protein; human adult testes cDNA library; nutritional activity;
 KW cytokine activity; cell proliferation/differentiation activity; probe;
 KW homology; pig vasolin-containing protein; VCP mRNA; hybridisation; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9748801-A2.

XX 24-DEC-1997.

XX 16-JUN-1997; 97WO-US010501.

XX 17-JUN-1996; 96US-00664596.

XX (GEMY) GENETICS INST INC.

XX Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;

XX Evans C, Spaulding V, Bowman M;

XX WPI; 1998-063142/06.

XX Poly-nucleotide(s) and proteins obtained from human PBMC, dendritic cell,
 PT adult brain, foetal brain and adult testes cDNA libraries - used in
 PT research, detection and therapy of, e.g. cytokine and cell proliferation
 PT or differentiation.

PS Disclosure; Page 64; 78pp; English.

XX This nucleotide sequence is the probe used in the isolation of the AU47_8
 CC clone, from a human adult testes cDNA library. The products of the
 CC isolated clone can be used in research, detection and therapy, as they
 CC may have nutritional activity, cytokine and cell
 CC proliferation/differentiation activity. A search against the Genbank
 CC database demonstrated at least some homology with pig vasolin-containing
 CC protein (VCP) mRNA

SQ Sequence 29 BP; 6 A; 4 C; 9 G; 9 T; 0 U; 1 Other;

Query Match 0.8%; Score 28; DB 1; Length 29;

Best Local Similarity 96.6%; Pred. No. 24;

Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 326 GAACAGTCCACACTTGCACCAATGTATCC 354

DB 29 GAACAGTCCACACTTGCACCAATGTATNC 1

```

RESULT 5
AA12765/c
ID AAA12765 standard; DNA; 27 BP.
XX
AC AAA12765;
XX
DT 25-JUL-2000 (first entry)
XX
DE PCR primer for cDNA encoding a human angiotensin converting enzyme-2.
XX
KW Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang. (1-9);
KW blood pressure; hypertension; congestive heart failure; atherosclerosis;
KW chronic heart failure; acute heart failure; myocardial infarction;
KW renal failure; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200018899-A2.
XX
PD 06-APR-2000.
XX
PF 29-SEP-1999; 99WO-US022976.
XX
PR 30-SEP-1998; 98US-00163648.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Acton LS, Robison KE, Hsieh FY;
XX
DR WPI; 2000-293140/25.
XX
PT Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
PT polypeptide useful for detecting an ACE-2 therapeutic for treating
PT hypertension, congestive heart failure, myocardial infarction,
PT atherosclerosis and renal failure.
XX
PS Example; Page 95; 138pp; English.
XX
CC The present PCR primer was used to amplify cDNA encoding a human
CC angiotensin converting enzyme-2 (ACE-2). ACE-2 is expressed predominantly
CC in kidneys and testis. The sequence of the full length ACE-2 cDNA was
CC determined from a clone obtained from a cDNA library prepared from mRNA
CC of a human heart of a subject who had congestive heart failure. ACE-2 has
CC significant sequence homologies with ACE enzymes, and has also been shown
CC to hydrolyse angiotensin I into Ang. (1-9). The ACE-2 therapeutics are
CC used to treat blood pressure related diseases and conditions, such as
CC hypertension, congestive heart failure, chronic heart failure, acute
CC heart failure, myocardial infarction, atherosclerosis and renal failure
XX
SQ Sequence 27 BP; 7 A; 13 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 0.8%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1550 GAGATAGTTGGGTGGTGGAACTGTG 1576
Db ||||||||||||||||||||||||||||
27 GAGATAGTTGGGTGGTGGAACTGTG 1

RESULT 6
AAD02759/c
ID AAD02759 standard; DNA; 27 BP.
XX
AC AAD02759;
XX
DT 31-MAY-2001 (first entry)
XX
DE Gene specific primer used for cloning and analysis of human ACE-2.
XX
KW Human; angiotensin converting enzyme-2; ACE-2; peptidyl dipeptidase A;

```

```

KW screening; therapy; hypertension; congestive heart failure; CHF;
KW inflammation; pain; RACE; primer; ss.
XX
OS Homo sapiens.
XX
PN US6194556-B1.
XX
PD 27-FEB-2001.
XX
PF 11-DEC-1997; 97US-00989299.
XX
PR 11-DEC-1997; 97US-00989299.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Acton SL, Robison KE;
XX
DR WPI; 2001-210604/21.
XX
PT Novel genes encoding angiotensin converting enzyme-2 useful as antisense
PT or antigen agents for therapeutics, diagnostics and screening assays.
XX
PS Example; Col 65; 76pp; English.
XX
CC The present sequence is a gene specific primer designed starting about
CC 400 bp downstream of the 5' end of the 1.6 kb human angiotensin
CC converting enzyme-2 (ACE-2) clone. This sequence is used in 5' RACE
CC (rapid amplification of cDNA ends) for cloning and analysis of human ACE-
CC 2. ACE is also referred as peptidyl dipeptidase A. Nucleic acid sequence
CC encoding ACE-2 is useful as antisense or antigen agents for sequence
CC specific modulation of gene expression or in the analysis of single base-
CC pair mutations in the gene. Nucleic acid sequence encoding ACE-2 is
CC useful in therapeutics, diagnostics and in screening assays. ACE-2
CC antagonist is used to treat hypertension or congestive heart failure
CC (CHF). ACE agonist is used to reduce the inflammation and pain resulting
CC from an insect sting or bite, which was accompanied by an injection of
CC bradykinin. Anti-ACE-2 antibodies are used to monitor ACE-2 protein
CC levels for determining the disease or condition associated with an
CC aberrant protein level
XX
SQ Sequence 27 BP; 7 A; 13 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 0.8%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1550 GAGATAGTTGGGTGGTGGAACTGTG 1576
Db ||||||||||||||||||||||||||||
27 GAGATAGTTGGGTGGTGGAACTGTG 1

RESULT 7
AAD32658
ID AAD32658 standard; DNA; 27 BP.
XX
AC AAD32658;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human ACE-2 exon 18 fragment.
XX
KW Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
KW myocardial infarction; heart failure; arrhythmia; renal failure;
KW inflammation; fertility; enzyme; exon 18; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(14, A) /*tag= a
XX
PN WO200212471-A2.

```


DR WPI; 2002-619265/66.

XX New isolated nucleic acid with at least one polymorphic position, useful

PT for detecting, diagnosing and treating disorders such as angioedema,

PT cancer, viral, bacterial or fungal infection, cardiovascular and

PT autoimmune diseases.

XX

PS Example 3; Page 915; 977pp; English.

XX

XX The invention relates to an isolated nucleic acid from a human gene

CC encoding aminopeptidase P (XPNPE2), bradykinin receptor B1 (BOKRBI),

CC tachykinin receptor B1 (TACRI), C1 esterase inhibitor (C1NH), kallikrein

CC 1 (KLK1), bradykinin receptor B2 (BKR2), angiotensin converting enzyme

CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one

CC polymorphic position. Also included are (1) a probe that hybridises to a

CC polymorphic position as provided in the detailed summary of single

CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic

CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising

CC obtaining the sample from one or more individuals and determining the

CC nucleic acid sequence at one or more polymorphic positions in a gene

CC encoding a protein selected from the group above; (3) constructing (M2)

CC haplotypes using the genes comprising grouping at least two nucleic acids

CC ; (4) identifying (M3) an individual at risk of developing a disorder

CC upon administration of an ACE inhibitor and/or vasoconstrictor inhibitor

CC using the polymorphic data; (5) a library of nucleic acids, each of which

CC comprises one or more polymorphic positions within a gene encoding a

CC human protein selected from the group above; and (6) genotyping (M4) an

CC individual comprising obtaining a nucleic acid sample, determining the

CC nucleotide present in at least one polymorphic position, and comparing at

CC least one position with a known data set. The genes, (M1, M2, M3 and M4)

CC and compositions are useful for detecting, diagnosing, treating,

CC preventing various disorders such as angioedema and diseases which

CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's

CC disease, trachomas, and cardiovascular diseases like angina pectoris,

CC hypertension, heart failure, myocardial infarction, ventricular

CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary

CC artery disease, arteriosclerosis and/or atherosclerosis, and

CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory

CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic

CC obstructive pulmonary disease (COPD) and enterocolitis (many other

CC diseases and disorders are listed in the specification). The

CC polynucleotides are also useful for chromosome identification. Antibodies

CC against the proteins may be utilised for immunophenotyping of cell lines

CC and biological samples. The present sequence is a genotyping PCR primer

CC for the gene encoding one of the proteins listed above

XX

SQ Sequence 27 BP; 9 A; 5 C; 2 G; 11 T; 0 U; 0 Other;

Query Match 0.8%; Score 27; DB 1; Length 27;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2125 TTGTGAACCAAGATCTCCTTTATTT 2151

DB 1 TTGTGAACCAAGATCTCCTTTATTT 27

RESULT 10

AA12740

ID AA12740 standard; DNA; 26 BP.

XX

AC AA12740;

XX

XX 25-JUL-2000 (first entry)

DE

DE Nucleotide sequence containing a polymorphism in 3' UTR of ACE-2.

XX

XX Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang. (1-9);

KW blood pressure; hypertension; congestive heart failure; atherosclerosis;

KW chronic heart failure; acute heart failure; myocardial infarction;

KW renal failure; ss.

XX

OS Homo sapiens.

XX WO200018899-A2.

XX

PD 06-APR-2000.

XX

PF 29-SEP-1999; 99WO-US022976.

XX

XX 30-SEP-1998; 98US-00163648.

XX

XX (MILL-) MILLENNIUM PHARM INC.

XX

XX Acton LS, Robison KE, Hsieh FY;

XX

XX WPI; 2000-293140/25.

XX

XX Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)

PT polypeptide useful for detecting an ACE-2 therapeutic for treating

PT hypertension, congestive heart failure, myocardial infarction,

PT atherosclerosis and renal failure.

XX

XX Example; Page 107; 138pp; English.

XX

XX AAA12740-41 represent nucleotide sequences containing a G to T

CC polymorphism in 3' UTR of human angiotensin converting enzyme-2 (ACE-2).

CC AAA12741 represents the variant sequence, with position 13 representing

CC the polymorphism. ACE-2 is expressed predominantly in kidneys and testis.

CC The sequence of the full length ACE-2 cDNA was determined from a clone

CC obtained from a cDNA library prepared from mRNA of a human heart of a

CC subject who had congestive heart failure. ACE-2 has significant sequence

CC homologies with ACE enzymes, and has also been shown to hydrolyse

CC angiotensin I into Ang. (1-9). The ACE-2 therapeutics are used to treat

CC blood pressure related diseases and conditions, such as hypertension,

CC congestive heart failure, chronic heart failure, acute heart failure,

CC myocardial infarction, atherosclerosis and renal failure

XX

SQ Sequence 26 BP; 11 A; 2 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 0.8%; Score 26; DB 1; Length 26;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2844 AGTTGAAAACAGGATATATCATTTGG 2869

DB 1 AGTTGAAAACAGGATATATCATTTGG 26

RESULT 11

AA12743/c

ID AA12743 standard; DNA; 26 BP.

XX

AC AA12743;

XX

XX 25-JUL-2000 (first entry)

DE

DE PCR primer used for chromosome localisation of human ACE-2.

XX

XX Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang. (1-9);

KW blood pressure; hypertension; congestive heart failure; atherosclerosis;

KW chronic heart failure; acute heart failure; myocardial infarction;

KW renal failure; PCR primer; ss.

XX

OS Homo sapiens.

XX

XX WO200018899-A2.

XX

XX 06-APR-2000.

XX

XX 29-SEP-1999; 99WO-US022976.

XX

XX 30-SEP-1998; 98US-00163648.

XX

XX (MILL-) MILLENNIUM PHARM INC.

XX

PI Acton LS, Robison KE, Hsieh FY;
 DR WPI; 2000-293140/25.
 XX
 PT Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
 PT polypeptide useful for detecting an ACE-2 therapeutic for treating
 PT hypertension, congestive heart failure, myocardial infarction,
 PT atherosclerosis and renal failure.
 XX
 PS Example; Page 111; 138pp; English.
 XX
 CC PCR primers AAA12742-43 were used for chromosome localisation of human
 CC angiotensin converting enzyme-2 (ACE-2). ACE-2 is expressed predominantly
 CC in kidneys and testis. The sequence of the full length ACE-2 cDNA was
 CC determined from a clone obtained from a cDNA library prepared from mRNA
 CC of a human heart of a subject who had congestive heart failure. ACE-2 has
 CC significant sequence homologies with ACE enzymes, and has also been shown
 CC to hydrolyse angiotensin I into Ang.(1-9). The ACE-2 therapeutics are
 CC used to treat blood pressure related diseases and conditions, such as
 CC hypertension, congestive heart failure, chronic heart failure, acute
 CC heart failure, myocardial infarction, atherosclerosis and renal failure
 XX
 SQ Sequence 26 BP; 8 A; 7 C; 5 G; 6 T; 0 U; 0 Other;

 Query Match 0.8%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 3045 GCCTACAGTGAGTTTGAATCGATC 3070
 Db 26 GCCTACAGTGAGTTTGAATCGATC 1

 RESULT 12
 AAD32661/c
 ID AAD32661 standard; DNA; 26 BP.
 AC AAD32661;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Human ACE-2 gene amplifying reverse PCR primer.
 XX
 KW Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
 KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
 KW myocardial infarction; heart failure; arrhythmia; renal failure;
 KW inflammation; fertility; enzyme; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200212471-A2.
 XX
 PD 14-FEB-2002.
 XX
 PF 09-AUG-2001; 2001WO-US025059.
 XX
 PR 09-AUG-2000; 2000US-00635501.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Acton S, Robison KE, Hsieh FY;
 XX
 DR WPI; 2002-257481/30.
 XX
 PT Isolated human polypeptide, known as angiotensin converting enzyme-2,
 PT useful for treating or preventing the development of an abnormal blood
 PT pressure or related diseases, e.g. hypertension, heart failure or
 PT myocardial infarction.
 XX
 PS Example 13; Page 123; 218pp; English.
 XX
 CC The invention relates to human angiotensin converting enzyme-2 (ACE-2)
 CC polypeptides and polynucleotides. ACE-2 is also known as peptidyl

CC dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
 CC treating or preventing the development of abnormal blood pressure and
 CC diseases or disorders associated with the protein in a subject. The
 CC diseases include hypertension, hypotension, congestive heart failure,
 CC chronic heart failure, acute heart failure, myocardial infarction,
 CC atherosclerosis, arrhythmia and renal failure. They are also useful for
 CC treating inflammatory conditions and diseases relating to fertility. The
 CC present sequence is a PCR primer used to amplify human ACE-2 gene
 XX
 SQ Sequence 26 BP; 8 A; 7 C; 5 G; 6 T; 0 U; 0 Other;

 Query Match 0.8%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 3045 GCCTACAGTGAGTTTGAATCGATC 3070
 Db 26 GCCTACAGTGAGTTTGAATCGATC 1

 RESULT 13
 AAD32652
 ID AAD32652 standard; DNA; 26 BP.
 XX
 AC AAD32652;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Human ACE-2 exon 18 fragment.
 XX
 KW Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
 KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
 KW myocardial infarction; heart failure; arrhythmia; renal failure;
 KW inflammation; fertility; enzyme; exon 18; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT variation replace(13, T)
 FT /*tag= a
 XX
 PN WO200212471-A2.
 XX
 PD 14-FEB-2002.
 XX
 PF 09-AUG-2001; 2001WO-US025059.
 XX
 PR 09-AUG-2000; 2000US-00635501.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Acton S, Robison KE, Hsieh FY;
 XX
 DR WPI; 2002-257481/30.
 XX
 PT Isolated human polypeptide, known as angiotensin converting enzyme-2,
 PT useful for treating or preventing the development of an abnormal blood
 PT pressure or related diseases, e.g. hypertension, heart failure or
 PT myocardial infarction.
 XX
 PS Example 10; Page 117; 218pp; English.
 XX
 CC The invention relates to human angiotensin converting enzyme-2 (ACE-2)
 CC polypeptides and polynucleotides. ACE-2 is also known as peptidyl
 CC dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
 CC treating or preventing the development of abnormal blood pressure and
 CC diseases or disorders associated with the protein in a subject. The
 CC diseases include hypertension, hypotension, congestive heart failure,
 CC chronic heart failure, acute heart failure, myocardial infarction,
 CC atherosclerosis, arrhythmia and renal failure. They are also useful for
 CC treating inflammatory conditions and diseases relating to fertility. The
 CC present sequence is human ACE-2 exon 18 fragment

SQ Sequence 26 BP; 11 A; 2 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 0.8%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2844 AGTTGAAACACAGGATATCATTTGG 2869
 |||||
 Db 1 AGTTGAAACACAGGATATCATTTGG 26

RESULT 14
 AAD32654
 ID AAD32654 standard; DNA; 26 BP.
 XX
 AC AAD32654;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Human ACE-2 DNA fragment.
 XX
 KW Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
 KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
 KW myocardial infarction; heart failure; arrhythmia; renal failure;
 KW inflammation; fertility; enzyme; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT variation replace(13, G)
 FT /*tag= a
 XX
 XX WO200212471-A2.
 XX
 PD 14-FEB-2002.
 XX
 PF 09-AUG-2001; 2001WO-US025059.
 XX
 XX 09-AUG-2000; 2000US-00635501.
 PR
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 XX Acton S, Robison KE, Hsieh FY;
 PI WPI; 2002-257481/30.
 DR
 XX Isolated human polypeptide, known as angiotensin converting enzyme-2,
 PT useful for treating or preventing the development of an abnormal blood
 PT pressure or related diseases, e.g. hypertension, heart failure or
 PT myocardial infarction.
 XX
 PS Example 10; Page 117; 218pp; English.
 XX
 CC The invention relates to human angiotensin converting enzyme-2 (ACE-2)
 CC polypeptides and polynucleotides. ACE-2 is also known as peptidyl
 CC dipeptidase A (BC 3.4.15.1). Polypeptides of the invention are useful for
 CC treating or preventing the development of abnormal blood pressure and
 CC diseases or disorders associated with the protein in a subject. The
 CC diseases include hypertension, hypotension, congestive heart failure,
 CC chronic heart failure, acute heart failure, myocardial infarction,
 CC atherosclerosis, arrhythmia and renal failure. They are also useful for
 CC treating inflammatory conditions and diseases relating to fertility. The
 CC present sequence is human ACE-2 DNA fragment.
 XX
 SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 0.8%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 CTAGGGAAGTCATTTCAGTGATGTG 83
 |||||
 Db 1 CTAGGGAAGTCATTTCAGTGATGTG 26

RESULT 15
 ABS61010
 ID ABS61010 standard; DNA; 26 BP.
 XX
 AC ABS61010;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Human genotyping PCR primer #163.
 XX
 KW Human; ss; aminopeptidase P; XPNEP2; bradykinin receptor B1; primer;
 KW BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;
 KW kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
 KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
 KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
 KW cardiovascular disease; angina pectoris; hypertension; heart failure;
 KW myocardial infarction; ventricular hypertrophy; vascular disease;
 KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
 KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;
 KW autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;
 KW viral infection; bacterial infection; fungal infection; COPD;
 KW Chronic obstructive pulmonary disease; enterocolitis.
 XX
 OS Homo sapiens.
 XX
 PN WO200261131-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 03-DEC-2001; 2001WO-US047235.
 XX
 XX 04-DEC-2000; 2000US-0251015P.
 PR
 PR 23-JAN-2001; 2001US-0263678P.
 PR
 PR 02-MAR-2001; 2001US-0273037P.
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA (TSUC/) TSUCHIHASHI Z.
 PA (HUI/) HUI L.
 XX
 XX Teuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
 PI Swanson BN, Powell JR;
 PI WPI; 2002-619265/66.
 DR
 XX New isolated nucleic acid with at least one polymorphic position, useful
 PT for detecting, diagnosing and treating disorders such as angioedema,
 PT cancer, viral, bacterial or fungal infection, cardiovascular and
 PT autoimmune diseases.
 XX
 PS Example 3; Page 914; 977pp; English.
 XX
 CC The invention relates to an isolated nucleic acid from a human gene
 CC encoding aminopeptidase P (XPNEP2), bradykinin receptor B1 (BDKRB1),
 CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
 CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
 CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
 CC polymorphic position. Also included are (1) a probe that hybridises to a
 CC polymorphic position as provided in the detailed summary of single
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
 CC obtaining the sample from one or more individuals and determining the
 CC nucleic acid sequence at one or more polymorphic positions in a gene
 CC encoding a protein selected from the group above; (3) constructing (M2)
 CC haplotypes using the genes comprising grouping at least two nucleic acids
 CC ; (4) identifying (M3) an individual at risk of developing a disorder
 CC upon administration of an ACE inhibitor and/or vasopressinase inhibitor
 CC using the polymorphic data; (5) a library of nucleic acids, each of which
 CC comprises one or more polymorphic positions within a gene encoding a
 CC human protein selected from the group above; and (6) genotyping (M4) an
 CC individual comprising obtaining a nucleic acid sample, determining the
 CC nucleotide present in at least one polymorphic position, and comparing at

CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
 CC and compositions are useful for detecting, diagnosing, treating,
 CC preventing various disorders such as angioedema and diseases which
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,
 CC hypertension, heart failure, myocardial infarction, ventricular
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
 CC artery disease, arteriosclerosis and/or atherosclerosis, and
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other
 CC diseases and disorders are listed in the specification). The
 CC polynucleotides are also useful for chromosome identification. Antibodies
 CC against the proteins may be utilised for immunophenotyping of cell lines
 CC and biological samples. The present sequence is a genotyping PCR primer
 CC for the gene encoding one of the proteins listed above
 XX
 SQ Sequence 26 BP; 10 A; 4 C; 5 G; 7 T; 0 U; 0 Other;
 Query Match 0.8%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 490 TGGAAAGCTTTGTACCCAGATAATC 515
 DB 1 TGGAAAGCTTTGTACCCAGATAATC 26
 RESULT 16
 ABS61101/c
 ID ABS61101 standard; DNA; 27 BP.
 AC ABS61101;
 DT 05-NOV-2002 (first entry)
 DE Human automated genomic bit analysis (GBA) PCR primer #78.
 XX Human; ss; aminopeptidase P; XPNP2; bradykinin receptor B1; primer;
 KW BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH;
 KW kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
 KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
 KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
 KW cardiovascular disease; angina pectoris; hypertension; heart failure;
 KW myocardial infarction; ventricular hypertrophy; vascular disease;
 KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
 KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;
 KW autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;
 KW viral infection; bacterial infection; fungal infection; COPD; GBA;
 KW Chronic obstructive pulmonary disease; enterocolitis;
 KW automated genetic bit analysis.
 XX
 OS Homo sapiens.
 XX WO200261131-A2.
 PN 08-AUG-2002.
 PD 03-DEC-2001; 2001WO-US047235.
 PF 04-DEC-2000; 2000US-0251015P.
 PR 23-JAN-2001; 2001US-0263678P.
 PR 02-MAR-2001; 2001US-0273037P.
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA (TSUC/) TSUCHIHASHI Z.
 PA (HUI/) HUI L.
 XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
 PI Swanson BN, Powell JR;
 XX WPI; 2002-619265/66.
 DR

PT New isolated nucleic acid with at least one polymorphic position, useful
 PT for detecting, diagnosing and treating disorders such as angioedema,
 PT cancer, viral, bacterial or fungal infection, cardiovascular and
 XX autoimmune diseases.
 PS Example 3; Page 936; 977pp; English.
 XX The invention relates to an isolated nucleic acid from a human gene
 CC encoding aminopeptidase P (XPNP2), bradykinin receptor B1 (BDKRB1),
 CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
 CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
 CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
 CC polymorphic position. Also included are (1) a probe that hybridises to a
 CC polymorphic position as provided in the detailed summary of single
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
 CC obtaining the sample from one or more individuals and determining the
 CC nucleic acid sequence at one or more polymorphic positions in a gene
 CC encoding a protein selected from the group above; (3) constructing (M2)
 CC haplotypes using the genes comprising grouping at least two nucleic acids
 CC upon administration of an ACE inhibitor and/or vasoconstrictor inhibitor
 CC using the polymorphic data; (5) a library of nucleic acids, each of which
 CC comprises one or more polymorphic positions within a gene encoding a
 CC human protein selected from the group above; and (6) genotyping (M4) an
 CC individual comprising obtaining a nucleic acid sample, determining the
 CC nucleotide present in at least one polymorphic position, and comparing at
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
 CC and compositions are useful for detecting, diagnosing, treating,
 CC preventing various disorders such as angioedema and diseases which
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,
 CC hypertension, heart failure, myocardial infarction, ventricular
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
 CC artery disease, arteriosclerosis and/or atherosclerosis, and
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other
 CC diseases and disorders are listed in the specification). The
 CC polynucleotides are also useful for chromosome identification. Antibodies
 CC against the proteins may be utilised for immunophenotyping of cell lines
 CC and biological samples. The present sequence is a genotyping PCR primer
 CC for the gene encoding one of the proteins listed above, using the method
 CC of automated genetic bit analysis, GBA
 XX
 SQ Sequence 27 BP; 9 A; 5 C; 4 G; 8 T; 0 U; 1 Other;
 Query Match 0.8%; Score 26; DB 1; Length 27;
 Best Local Similarity 96.3%; Pred. No. 33;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2174 GGTCTGATATCATTCCTAGAACTGAA 2200
 DB 27 GTGCTGATATNATTCCTAGAACTGAA 1
 RESULT 17
 AAD32659
 ID AAD32659 standard; DNA; 27 BP.
 XX AAD32659;
 AC AAD32659;
 XX 18-JUN-2002 (first entry)
 DT Human ACE-2 exon 18 fragment polymorphic variant.
 DE Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
 KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
 KW myocardial infarction; heart failure; arrhythmia; renal failure;
 KW inflammation; fertility; enzyme; exon 18; polymorphism; ds.
 XX Homo sapiens.
 OS

```

FH Key          Location/Qualifiers
FT variation    replace(14, G)
FT              /*tag= a
XX WO200212471-A2.
XX
XX
XX
XX 14-FEB-2002.
XX
XX 09-AUG-2001; 2001WO-US025059.
XX
XX 09-AUG-2000; 2000US-00635501.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Acton S, Robison KE, Hsieh FY;
XX WPI; 2002-257481/30.
XX
XX Isolated human polypeptide, known as angiotensin converting enzyme-2,
XX useful for treating or preventing the development of an abnormal blood
XX pressure or related diseases, e.g. hypertension, heart failure or
XX myocardial infarction.
XX
XX Example 10; Page 117; 218pp; English.
XX
XX The invention relates to human angiotensin converting enzyme-2 (ACE-2)
XX polypeptides and polynucleotides. ACE-2 is also known as peptidyl
XX dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
XX treating or preventing the development of abnormal blood pressure and
XX diseases or disorders associated with the protein in a subject. The
XX diseases include hypertension, hypotension, congestive heart failure,
XX chronic heart failure, acute heart failure, myocardial infarction,
XX atherosclerosis, arrhythmia and renal failure. They are also useful for
XX treating inflammatory conditions and diseases relating to fertility. The
XX present sequence is human ACE-2 exon 18 fragment polymorphic variant
XX
XX Sequence 27 BP; 9 A; 3 C; 7 G; 8 T; 0 U; 0 Other;
XX
XX Query Match          0.7%; Score 25.4; DB 1; Length 27;
XX Best Local Similarity 96.3%; Pred. No. 38;
XX Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 3242 GTTCTCTAACTGGAGTGTGAATGAAA 3268
XX      |||||
XX      1 GTTCTCTAACTGGAGTGTGAATGAAA 27
XX
XX Db
XX
XX RESULT 18
XX AAA12787
XX ID AAA12787 standard; DNA; 25 BP.
XX AC AAA12787;
XX XX
XX XX 25-JUL-2000 (first entry)
XX DT
XX DE
XX DE PCR primer ace2e8b used in SSCP analysis of human ACE-2.
XX KW Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang. (1-9);
XX KW blood pressure; hypertension; congestive heart failure; atherosclerosis;
XX KW chronic heart failure; acute heart failure; myocardial infarction;
XX KW renal failure; PCR primer; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200018899-A2.
XX XX
XX XX 06-APR-2000.
XX XX
XX XX 29-SEP-1999; 99WO-US022976.
XX PF
XX PR 30-SEP-1998; 98US-00163648.
XX PR
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PA
XX PI Acton LS, Robison KE, Hsieh FY;
XX PI WPI; 2000-293140/25.
XX DR
XX XX Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
XX PT polypeptide useful for detecting an ACE-2 therapeutic for treating
XX PT hypertension, congestive heart failure, myocardial infarction,
XX PT atherosclerosis and renal failure.
XX XX
XX Example; Page 106; 138pp; English.
XX
XX PCR primers AAA12766-A12821 were used for single strand conformation
XX polymorphism (SSCP) analysis of human angiotensin converting enzyme-2
XX (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
XX sequence of the full length ACE-2 cDNA was determined from a clone
XX obtained from a cDNA library prepared from mRNA of a human heart of a
XX subject who had congestive heart failure. ACE-2 has significant sequence
XX homologies with ACE enzymes, and has also been shown to hydrolyse
XX angiotensin I into Ang. (1-9). The ACE-2 therapeutics are used to treat
XX blood pressure related diseases and conditions, such as hypertension,
XX congestive heart failure, chronic heart failure, acute heart failure,
XX myocardial infarction, atherosclerosis and renal failure
XX
XX Sequence 25 BP; 9 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX Query Match          0.7%; Score 25; DB 1; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 36;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1088 GAAAATTCATGCTAAGGACCCAG 1112
XX      |||||
XX      1 GAAAATTCATGCTAAGGACCCAG 25
XX
XX Db
XX
XX RESULT 19
XX AAA12816/c
XX ID AAA12816 standard; DNA; 25 BP.
XX AC AAA12816;
XX XX
XX XX 25-JUL-2000 (first entry)
XX DT
XX DE
XX DE PCR primer ace2e18e used in SSCP analysis of human ACE-2.
XX KW Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang. (1-9);
XX KW blood pressure; hypertension; congestive heart failure; atherosclerosis;
XX KW chronic heart failure; acute heart failure; myocardial infarction;
XX KW renal failure; PCR primer; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200018899-A2.
XX XX
XX XX 06-APR-2000.
XX XX
XX XX 29-SEP-1999; 99WO-US022976.
XX PF
XX PR 30-SEP-1998; 98US-00163648.
XX PR
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PA
XX PI Acton LS, Robison KE, Hsieh FY;
XX PI WPI; 2000-293140/25.
XX DR
XX XX Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
XX PT polypeptide useful for detecting an ACE-2 therapeutic for treating
XX PT hypertension, congestive heart failure, myocardial infarction,
XX PT atherosclerosis and renal failure.
XX XX
XX Example; Page 106; 138pp; English.
XX
XX

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```

XX Acton LS, Robison KE, Hsieh FY;
XX WPI; 2000-293140/25.
XX
XX Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
XX polypeptide useful for detecting an ACE-2 therapeutic for treating
XX hypertension, congestive heart failure, myocardial infarction,
XX atherosclerosis and renal failure.
XX
XX Example; Page 105; 138pp; English.
XX
XX PCR primers AAA12766-A12821 were used for single strand conformation
XX polymorphism (SSCP) analysis of human angiotensin converting enzyme-2
XX (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
XX sequence of the full length ACE-2 cDNA was determined from a clone
XX obtained from a cDNA library prepared from mRNA of a human heart of a
XX subject who had congestive heart failure. ACE-2 has significant sequence
XX homologies with ACE enzymes, and has also been shown to hydrolyse
XX angiotensin I into Ang. (1-9). The ACE-2 therapeutics are used to treat
XX blood pressure related diseases and conditions, such as hypertension,
XX congestive heart failure, chronic heart failure, acute heart failure,
XX myocardial infarction, atherosclerosis and renal failure
XX
XX Sequence 25 BP; 9 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX Query Match          0.7%; Score 25; DB 1; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 36;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1088 GAAAATTCATGCTAAGGACCCAG 1112
XX      |||||
XX      1 GAAAATTCATGCTAAGGACCCAG 25
XX
XX Db
XX
XX RESULT 19
XX AAA12816/c
XX ID AAA12816 standard; DNA; 25 BP.
XX AC AAA12816;
XX XX
XX XX 25-JUL-2000 (first entry)
XX DT
XX DE
XX DE PCR primer ace2e18e used in SSCP analysis of human ACE-2.
XX KW Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang. (1-9);
XX KW blood pressure; hypertension; congestive heart failure; atherosclerosis;
XX KW chronic heart failure; acute heart failure; myocardial infarction;
XX KW renal failure; PCR primer; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200018899-A2.
XX XX
XX XX 06-APR-2000.
XX XX
XX XX 29-SEP-1999; 99WO-US022976.
XX PF
XX PR 30-SEP-1998; 98US-00163648.
XX PR
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PA
XX PI Acton LS, Robison KE, Hsieh FY;
XX PI WPI; 2000-293140/25.
XX DR
XX XX Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
XX PT polypeptide useful for detecting an ACE-2 therapeutic for treating
XX PT hypertension, congestive heart failure, myocardial infarction,
XX PT atherosclerosis and renal failure.
XX XX
XX Example; Page 106; 138pp; English.
XX
XX

```

CC PCR primers AAL12766-A12821 were used for single strand conformation
 CC polymorphism (SSCP) analysis of human angiotensin converting enzyme-2
 CC (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
 CC sequence of the full length ACE-2 cDNA was determined from a clone
 CC obtained from a cDNA library prepared from mRNA of a human heart of a
 CC subject who had congestive heart failure. ACE-2 has a significant sequence
 CC homologies with ACE enzymes, and has also been shown to hydrolyse
 CC angiotensin I into Ang.(1-9). The ACE-2 therapeutics are used to treat
 CC blood pressure related diseases and conditions, such as hypertension,
 CC congestive heart failure, chronic heart failure, acute heart failure,
 CC myocardial infarction, atherosclerosis and renal failure
 XX

SQ Sequence 25 BP; 8 A; 7 C; 3 G; 7 T; 0 U; 0 Other;
 Query Match 0.7%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3049 ACAGTCATGTTTGGATCGATCATG 3073
 Db 25 ACAGTCATGTTTGGATCGATCATG 1

RESULT 20
 AAL12783
 ID AAL12783 standard; DNA; 25 BP.
 XX
 AC AAL12783;
 XX
 DT 25-JUL-2000 (first entry)
 XX
 DE PCR primer ace2e7b used in SSCP analysis of human ACE-2.
 XX
 KW Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang.(1-9);
 KW blood pressure; hypertension; congestive heart failure; atherosclerosis;
 KW chronic heart failure; acute heart failure; myocardial infarction;
 KW renal failure; PCR primer; ss.
 OS Homo sapiens.
 OS
 PN WO200018899-A2.
 XX
 PD 06-APR-2000.
 XX
 PF 29-SEP-1999; 99WO-US022976.
 XX
 PR 30-SEP-1998; 98US-00163648.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Acton LS, Robison KE, Hsieh FY;
 XX
 DR WPI; 2000-293140/25.
 XX
 CC Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
 CC polypeptide useful for detecting an ACE-2 therapeutic for treating
 CC hypertension, congestive heart failure, myocardial infarction,
 CC atherosclerosis and renal failure.
 XX
 PS Example; Page 105; 138pp; English.
 XX

CC PCR primers AAL12766-A12821 were used for single strand conformation
 CC polymorphism (SSCP) analysis of human angiotensin converting enzyme-2
 CC (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
 CC sequence of the full length ACE-2 cDNA was determined from a clone
 CC obtained from a cDNA library prepared from mRNA of a human heart of a
 CC subject who had congestive heart failure. ACE-2 has a significant sequence
 CC homologies with ACE enzymes, and has also been shown to hydrolyse
 CC angiotensin I into Ang.(1-9). The ACE-2 therapeutics are used to treat
 CC blood pressure related diseases and conditions, such as hypertension,
 CC congestive heart failure, chronic heart failure, acute heart failure,
 CC myocardial infarction, atherosclerosis and renal failure
 XX

SQ Sequence 25 BP; 5 A; 0 C; 11 G; 9 T; 0 U; 0 Other;
 Query Match 0.7%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 905 GGTGATATGTGGGTAGATTTCGA 929
 Db 1 GGTGATATGTGGGTAGATTTCGA 25

RESULT 21
 AAL12792/c
 ID AAL12792 standard; DNA; 25 BP.
 XX
 AC AAL12792;
 XX
 DT 25-JUL-2000 (first entry)
 XX
 DE PCR primer ace2e9c used in SSCP analysis of human ACE-2.
 XX
 KW Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang.(1-9);
 KW blood pressure; hypertension; congestive heart failure; atherosclerosis;
 KW chronic heart failure; acute heart failure; myocardial infarction;
 KW renal failure; PCR primer; ss.
 OS Homo sapiens.
 OS
 PN WO200018899-A2.
 XX
 PD 06-APR-2000.
 XX
 PF 29-SEP-1999; 99WO-US022976.
 XX
 PR 30-SEP-1998; 98US-00163648.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Acton LS, Robison KE, Hsieh FY;
 XX
 DR WPI; 2000-293140/25.
 XX
 CC Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
 CC polypeptide useful for detecting an ACE-2 therapeutic for treating
 CC hypertension, congestive heart failure, myocardial infarction,
 CC atherosclerosis and renal failure.
 XX
 PS Example; Page 105; 138pp; English.
 XX

CC PCR primers AAL12766-A12821 were used for single strand conformation
 CC polymorphism (SSCP) analysis of human angiotensin converting enzyme-2
 CC (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
 CC sequence of the full length ACE-2 cDNA was determined from a clone
 CC obtained from a cDNA library prepared from mRNA of a human heart of a
 CC subject who had congestive heart failure. ACE-2 has a significant sequence
 CC homologies with ACE enzymes, and has also been shown to hydrolyse
 CC angiotensin I into Ang.(1-9). The ACE-2 therapeutics are used to treat
 CC blood pressure related diseases and conditions, such as hypertension,
 CC congestive heart failure, chronic heart failure, acute heart failure,
 CC myocardial infarction, atherosclerosis and renal failure
 XX

SQ Sequence 25 BP; 7 A; 9 C; 3 G; 6 T; 0 U; 0 Other;
 Query Match 0.7%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1294 TGAAGGATTCCATGAAGCTGTGGG 1318
 Db 25 TGAAGGATTCCATGAAGCTGTGGG 1

RESULT 22

```

AA12815
ID AAA12815 standard; DNA; 25 BP.
XX
AC
AA12815;
XX
25-JUL-2000 (first entry)
XX
DE PCR primer ace2e18d used in SSCP analysis of human ACE-2.
XX
XX Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang.(1-9);
KW blood pressure; hypertension; congestive heart failure; atherosclerosis;
KW chronic heart failure; acute heart failure; myocardial infarction;
KW renal failure; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200018899-A2.
XX
PD 06-APR-2000.
XX
PF 29-SEP-1999; 99WO-US022976.
XX
PR 30-SEP-1998; 98US-00163648.
XX
PR 30-SEP-1998; 98US-00163648.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
XX Acton LS, Robison KE, Heieh FY;
XX
DR WPI; 2000-293140/25.
XX
XX Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
PT polypeptide useful for detecting an ACE-2 therapeutic for treating
PT hypertension, congestive heart failure, myocardial infarction,
PT atherosclerosis and renal failure.
XX
XX Example; Page 106; 138pp; English.
XX
XX PCR primers AAA12766-A12821 were used for single strand conformation
CC polymorphism (SSCP) analysis of human angiotensin converting enzyme-2
CC (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
CC sequence of the full length ACE-2 cDNA was determined from a clone
CC obtained from a cDNA library prepared from mRNA of a human heart of a
CC subject who had congestive heart failure. ACE-2 has significant sequence
CC homologies with ACE enzymes, and has also been shown to hydrolyse
CC angiotensin I into Ang.(1-9). The ACE-2 therapeutics are used to treat
CC blood pressure related diseases and conditions, such as hypertension,
CC congestive heart failure, chronic heart failure, acute heart failure,
CC myocardial infarction, atherosclerosis and renal failure
XX
XX Sequence 25 BP; 6 A; 6 C; 5 G; 8 T; 0 U; 0 Other;
XX
Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred.No. 36;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2990 GTCAGGATGACATGCTTCTTCAC 3014
DB 1 GTCAGGATGACATGCTTCTTCAC 25
RESULT 23
AA12818/C
ID AAA12818 standard; DNA; 25 BP.
XX
AC AAA12818;
XX
XX 25-JUL-2000 (first entry)
XX
DE PCR primer ace2e18g used in SSCP analysis of human ACE-2.
XX
XX Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang.(1-9);
KW blood pressure; hypertension; congestive heart failure; atherosclerosis;
KW chronic heart failure; acute heart failure; myocardial infarction;
KW renal failure; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200018899-A2.
XX
PD 06-APR-2000.
XX
PF 29-SEP-1999; 99WO-US022976.
XX
PR 30-SEP-1998; 98US-00163648.
XX
PR 30-SEP-1998; 98US-00163648.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
XX Acton LS, Robison KE, Heieh FY;
XX
DR WPI; 2000-293140/25.
XX
XX Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
PT polypeptide useful for detecting an ACE-2 therapeutic for treating
PT hypertension, congestive heart failure, myocardial infarction,
PT atherosclerosis and renal failure.
XX
XX Example; Page 106; 138pp; English.
XX
XX PCR primers AAA12766-A12821 were used for single strand conformation
CC polymorphism (SSCP) analysis of human angiotensin converting enzyme-2
CC (ACE-2). The peptide is used to raise antibodies. ACE-2 is expressed
CC predominantly in kidneys and testis. The sequence of the full length ACE-
CC 2 cDNA was determined from a clone obtained from a cDNA library prepared
CC from mRNA of a human heart of a subject who had congestive heart failure.
CC ACE-2 has significant sequence homologies with ACE enzymes, and has also
CC been shown to hydrolyse angiotensin I into Ang.(1-9). The ACE-2
CC therapeutics are used to treat blood pressure related diseases and
CC conditions, such as hypertension, congestive heart failure, chronic heart
CC failure, acute heart failure, myocardial infarction, atherosclerosis and
CC renal failure
XX
XX Sequence 25 BP; 6 A; 6 C; 5 G; 8 T; 0 U; 0 Other;
XX
Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred.No. 36;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2776 AAAGTGATGATTGGTCTTCACAGGC 2800
DB 25 AAAGTGATGATTGGTCTTCACAGGC 1
RESULT 24
AA12819
ID AAA12819 standard; DNA; 25 BP.
XX
AC AAA12819;
XX
XX 25-JUL-2000 (first entry)
XX
DE PCR primer ace2e18h used in SSCP analysis of human ACE-2.
XX
XX Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang.(1-9);
KW blood pressure; hypertension; congestive heart failure; atherosclerosis;
KW chronic heart failure; acute heart failure; myocardial infarction;
KW renal failure; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200018899-A2.
XX
PD 06-APR-2000.
XX
PF 29-SEP-1999; 99WO-US022976.
XX
PR 30-SEP-1998; 98US-00163648.
XX
PR 30-SEP-1998; 98US-00163648.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
XX Acton LS, Robison KE, Heieh FY;
XX
DR WPI; 2000-293140/25.
XX
XX Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
PT polypeptide useful for detecting an ACE-2 therapeutic for treating
PT hypertension, congestive heart failure, myocardial infarction,
PT atherosclerosis and renal failure.
XX
XX Example; Page 106; 138pp; English.
XX
XX PCR primers AAA12766-A12821 were used for single strand conformation
CC polymorphism (SSCP) analysis of human angiotensin converting enzyme-2
CC (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
CC sequence of the full length ACE-2 cDNA was determined from a clone
CC obtained from a cDNA library prepared from mRNA of a human heart of a
CC subject who had congestive heart failure. ACE-2 has significant sequence
CC homologies with ACE enzymes, and has also been shown to hydrolyse
CC angiotensin I into Ang.(1-9). The ACE-2 therapeutics are used to treat
CC blood pressure related diseases and conditions, such as hypertension,
CC congestive heart failure, chronic heart failure, acute heart failure,
CC myocardial infarction, atherosclerosis and renal failure
XX
XX Sequence 25 BP; 8 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred.No. 36;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2776 AAAGTGATGATTGGTCTTCACAGGC 2800
DB 25 AAAGTGATGATTGGTCTTCACAGGC 1
RESULT 24
AA12819
ID AAA12819 standard; DNA; 25 BP.
XX
AC AAA12819;
XX
XX 25-JUL-2000 (first entry)
XX
DE PCR primer ace2e18h used in SSCP analysis of human ACE-2.
XX
XX Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang.(1-9);
KW blood pressure; hypertension; congestive heart failure; atherosclerosis;
KW chronic heart failure; acute heart failure; myocardial infarction;
KW renal failure; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200018899-A2.
XX
PD 06-APR-2000.
XX
PF 29-SEP-1999; 99WO-US022976.
XX
PR 30-SEP-1998; 98US-00163648.
XX
PR 30-SEP-1998; 98US-00163648.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
XX Acton LS, Robison KE, Heieh FY;
XX
DR WPI; 2000-293140/25.
XX
XX Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
PT polypeptide useful for detecting an ACE-2 therapeutic for treating
PT hypertension, congestive heart failure, myocardial infarction,
PT atherosclerosis and renal failure.
XX
XX Example; Page 106; 138pp; English.
XX
XX PCR primers AAA12766-A12821 were used for single strand conformation
CC polymorphism (SSCP) analysis of human angiotensin converting enzyme-2
CC (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
CC sequence of the full length ACE-2 cDNA was determined from a clone
CC obtained from a cDNA library prepared from mRNA of a human heart of a
CC subject who had congestive heart failure. ACE-2 has significant sequence
CC homologies with ACE enzymes, and has also been shown to hydrolyse
CC angiotensin I into Ang.(1-9). The ACE-2 therapeutics are used to treat
CC blood pressure related diseases and conditions, such as hypertension,
CC congestive heart failure, chronic heart failure, acute heart failure,
CC myocardial infarction, atherosclerosis and renal failure
XX
XX Sequence 25 BP; 8 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred.No. 36;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2776 AAAGTGATGATTGGTCTTCACAGGC 2800
DB 25 AAAGTGATGATTGGTCTTCACAGGC 1

```

```

XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Acton LS, Robison KE, Hsieh FY;
XX XX
XX DR WPI; 2000-293140/25.
XX XX
XX PT Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
XX PT polypeptide useful for detecting an ACE-2 therapeutic for treating
XX PT hypertension, congestive heart failure, myocardial infarction,
XX PT atherosclerosis and renal failure.
XX PS
XX PS Example; Page 106; 138pp; English.
XX CC
XX CC PCR primers AAA12766-A12821 were used for single strand conformation
XX CC polymorphism (SSCP) analysis of human angiotensin converting enzyme-2
XX CC (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
XX CC sequence of the full length ACE-2 cDNA was determined from a clone
XX CC obtained from a cDNA library prepared from mRNA of a human heart of a
XX CC subject who had congestive heart failure. ACE-2 has significant sequence
XX CC homologies with ACE enzymes, and has also been shown to hydrolyse
XX CC angiotensin I into Ang.(1-9). The ACE-2 therapeutics are used to treat
XX CC blood pressure related diseases and conditions, such as hypertension,
XX CC congestive heart failure, chronic heart failure, acute heart failure,
XX CC myocardial infarction, atherosclerosis and renal failure
XX XX
XX SQ Sequence 25 BP; 5 A; 7 C; 4 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 0.7%; Score 25; DB 1; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 36;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 2494 CACTGATGATGTTTCAGACCTCCTTT 2518
DB 1 CACTGATGATGTTTCAGACCTCCTTT 25
XX
RESULT 25
AAAA12817
ID AAA12817 standard; DNA; 25 BP.
AC AAA12817;
XX
XX 25-JUL-2000 (first entry)
XX
XX PCR primer ace2e18f used in SSCP analysis of human ACE-2.
XX
XX Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang.(1-9);
XX KW blood pressure; hypertension; congestive heart failure; atherosclerosis;
XX KW chronic heart failure; acute heart failure; myocardial infarction;
XX KW renal failure; PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PI WO20001899-A2.
XX PN
XX PD 06-APR-2000.
XX
XX PF 29-SEP-1999; 99WO-US022976.
XX
XX PR 30-SEP-1998; 98US-00163648.
XX
XX PA (MILL-) MILLENNIUM PHARM INC.
XX
XX PI Acton LS, Robison KE, Hsieh FY;
XX XX
XX DR WPI; 2000-293140/25.
XX
XX PT Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
XX PT polypeptide useful for detecting an ACE-2 therapeutic for treating
XX PT hypertension, congestive heart failure, myocardial infarction,
XX PT atherosclerosis and renal failure.
XX PS
XX PS Example; Page 106; 138pp; English.
XX CC
XX CC PCR primers AAA12766-A12821 were used for single strand conformation
XX CC polymorphism (SSCP) analysis of human angiotensin converting enzyme-2
XX CC (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
XX CC sequence of the full length ACE-2 cDNA was determined from a clone
XX CC obtained from a cDNA library prepared from mRNA of a human heart of a
XX CC subject who had congestive heart failure. ACE-2 has significant sequence
XX CC homologies with ACE enzymes, and has also been shown to hydrolyse
XX CC angiotensin I into Ang.(1-9). The ACE-2 therapeutics are used to treat
XX CC blood pressure related diseases and conditions, such as hypertension,
XX CC congestive heart failure, chronic heart failure, acute heart failure,
XX CC myocardial infarction, atherosclerosis and renal failure
XX XX
XX SQ Sequence 25 BP; 5 A; 7 C; 4 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 0.7%; Score 25; DB 1; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 36;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 2494 CACTGATGATGTTTCAGACCTCCTTT 2518
DB 1 CACTGATGATGTTTCAGACCTCCTTT 25
XX
RESULT 26
AAD32637
ID AAD32637 standard; DNA; 25 BP.
AC AAD32637;
XX
XX 18-JUN-2002 (first entry)
XX
XX ace2e18d PCR primer for SSCP analysis of human ACE-2 DNA.
XX
XX Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
XX KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
XX KW myocardial infarction; heart failure; arrhythmia; renal failure;
XX KW inflammation; fertility; enzyme; PCR; primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200212471-A2.
XX
XX PD 14-FEB-2002.
XX
XX PF 09-AUG-2001; 2001WO-US025059.
XX
XX PR 09-AUG-2000; 2000US-00635501.
XX
XX PA (MILL-) MILLENNIUM PHARM INC.
XX
XX PI Acton S, Robison KE, Hsieh FY;
XX
XX DR WPI; 2002-257481/30.
XX
XX PT Isolated human polypeptide, known as angiotensin converting enzyme-2,
XX PT useful for treating or preventing the development of an abnormal blood
XX PT pressure or related diseases, e.g. hypertension, heart failure or
XX PT myocardial infarction.
XX
XX PS Example 10; Page 115; 218pp; English.
XX
XX CC The invention relates to human angiotensin converting enzyme-2 (ACE-2)
XX CC polypeptides and polynucleotides. ACE-2 is also known as peptidyl
XX CC dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
XX CC treating or preventing the development of abnormal blood pressure and
XX CC diseases or disorders associated with the protein in a subject. The
XX CC diseases include hypertension, hypotension, congestive heart failure,
XX CC chronic heart failure, acute heart failure, myocardial infarction,
XX CC atherosclerosis, arrhythmia and renal failure. They are also useful for
XX CC treating inflammatory conditions and diseases relating to fertility. The
XX CC present sequence is a PCR primer used in single strand conformation

```


KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
 KW myocardial infarction; heart failure; arrhythmia; renal failure;
 XX inflammation; fertility; enzyme; PCR; primer; ss.
 OS Homo sapiens.
 XX WO200212471-A2.
 PN 14-FEB-2002.
 XX 09-AUG-2001; 2001WO-US025059.
 PF 09-AUG-2000; 2000US-00635501.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Acton S, Robison KE, Hsieh FY;
 PI WPI; 2002-257481/30.
 DR Isolated human polypeptide, known as angiotensin converting enzyme-2,
 XX useful for treating or preventing the development of an abnormal blood
 PT pressure or related diseases, e.g. hypertension, heart failure or
 PT myocardial infarction.
 XX Example 10; Page 115; 218pp; English.
 PS The invention relates to human angiotensin converting enzyme-2 (ACE-2)
 CC polypeptides and polynucleotides. ACE-2 is also known as peptidyl
 CC dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
 CC treating or preventing the development of abnormal blood pressure and
 CC diseases or disorders associated with the protein in a subject. The
 CC diseases include hypertension, hypotension, congestive heart failure,
 CC chronic heart failure, acute heart failure, myocardial infarction,
 CC atherosclerosis, arrhythmia and renal failure. They are also useful for
 CC treating inflammatory conditions and diseases relating to fertility. The
 CC present sequence is a PCR primer used in single strand conformation
 CC polymorphism (SSCP) analysis of human ACE-2 DNA
 XX Sequence 25 BP; 7 A; 9 C; 3 G; 6 T; 0 U; 0 Other;
 SQ Query Match 0.7%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1294 TGAAGGATTCATGAGCTGTTGGG 1318
 DB 25 TGAAGGATTCATGAGCTGTTGGG 1
 RESULT 30
 AAD32638/c
 ID AAD32638 standard; DNA; 25 BP.
 AC AAD32638;
 XX 18-JUN-2002 (first entry)
 DT ace218e PCR primer for SSCP analysis of human ACE-2 DNA.
 DE Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
 XX peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
 KW myocardial infarction; heart failure; arrhythmia; renal failure;
 KW inflammation; fertility; enzyme; PCR; primer; ss.
 OS Homo sapiens.
 XX WO200212471-A2.
 PN 14-FEB-2002.
 XX 09-AUG-2001; 2001WO-US025059.
 PF Isolated human polypeptide, known as angiotensin converting enzyme-2,
 XX useful for treating or preventing the development of an abnormal blood
 PT pressure or related diseases, e.g. hypertension, heart failure or
 PT myocardial infarction.

PR 09-AUG-2000; 2000US-00635501.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Acton S, Robison KE, Hsieh FY;
 PI WPI; 2002-257481/30.
 DR Isolated human polypeptide, known as angiotensin converting enzyme-2,
 XX useful for treating or preventing the development of an abnormal blood
 PT pressure or related diseases, e.g. hypertension, heart failure or
 PT myocardial infarction.
 XX Example 10; Page 115; 218pp; English.
 PS The invention relates to human angiotensin converting enzyme-2 (ACE-2)
 CC polypeptides and polynucleotides. ACE-2 is also known as peptidyl
 CC dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
 CC treating or preventing the development of abnormal blood pressure and
 CC diseases or disorders associated with the protein in a subject. The
 CC diseases include hypertension, hypotension, congestive heart failure,
 CC chronic heart failure, acute heart failure, myocardial infarction,
 CC atherosclerosis, arrhythmia and renal failure. They are also useful for
 CC treating inflammatory conditions and diseases relating to fertility. The
 CC present sequence is a PCR primer used in single strand conformation
 CC polymorphism (SSCP) analysis of human ACE-2 DNA
 XX Sequence 25 BP; 8 A; 7 C; 3 G; 7 T; 0 U; 0 Other;
 SQ Query Match 0.7%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3049 ACAGTGATGTTTGGATCGATCATG 3073
 DB 25 ACAGTGATGTTTGGATCGATCATG 1
 RESULT 31
 AAD32640/c
 ID AAD32640 standard; DNA; 25 BP.
 AC AAD32640;
 XX 18-JUN-2002 (first entry)
 DT ace218g PCR primer for SSCP analysis of human ACE-2 DNA.
 DE Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
 KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
 KW myocardial infarction; heart failure; arrhythmia; renal failure;
 KW inflammation; fertility; enzyme; PCR; primer; ss.
 OS Homo sapiens.
 XX WO200212471-A2.
 PN 14-FEB-2002.
 XX 09-AUG-2001; 2001WO-US025059.
 PF Isolated human polypeptide, known as angiotensin converting enzyme-2,
 XX useful for treating or preventing the development of an abnormal blood
 PT pressure or related diseases, e.g. hypertension, heart failure or
 PT myocardial infarction.

```
XX Example 10; Page 116; 218pp; English.
XX
CC The invention relates to human angiotensin converting enzyme-2 (ACE-2)
CC polypeptides and polynucleotides. ACE-2 is also known as peptidyl
CC dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
CC treating or preventing the development of abnormal blood pressure and
CC diseases or disorders associated with the protein in a subject. The
CC diseases include hypertension, hypotension, congestive heart failure,
CC chronic heart failure, acute heart failure, myocardial infarction,
CC atherosclerosis, arrhythmia and renal failure. They are also useful for
CC treating inflammatory conditions and diseases relating to fertility. The
CC present sequence is a PCR primer used in single strand conformation
CC polymorphism (SSCP) analysis of human ACE-2 DNA
XX
SQ Sequence 25 BP; 8 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2776 AAAGTGTGTTTGGTCTCAGGC 2800
Db 25 AAAGTGTGTTTGGTCTCAGGC 1
RESULT 32
AAD32605
ID AAD32605 standard; DNA; 25 BP.
AC AAD32605;
XX
XX 18-JUN-2002 (first entry)
XX
DE ace2e7b PCR primer for SSCP analysis of human ACE-2 DNA.
XX
KW Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
KW myocardial infarction; heart failure; arrhythmia; renal failure;
KW inflammation; fertility; enzyme; PCR; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200212471-A2.
XX
XX 14-FEB-2002.
XX
XX 09-AUG-2001; 2001WO-US025059.
XX
XX 09-AUG-2000; 2000US-00635501.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Acton S, Robison KE, Hsieh FY;
XX
XX WO200212471-A2.
XX
XX 14-FEB-2002.
XX
XX 09-AUG-2001; 2001WO-US025059.
XX
XX 09-AUG-2000; 2000US-00635501.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Acton S, Robison KE, Hsieh FY;
XX
XX WPI; 2002-257481/30.
XX
XX Isolated human polypeptide, known as angiotensin converting enzyme-2,
XX useful for treating or preventing the development of an abnormal blood
XX pressure or related diseases, e.g. hypertension, heart failure or
XX myocardial infarction.
XX
XX Example 10; Page 114; 218pp; English.
XX
CC The invention relates to human angiotensin converting enzyme-2 (ACE-2)
CC polypeptides and polynucleotides. ACE-2 is also known as peptidyl
CC dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
CC treating or preventing the development of abnormal blood pressure and
CC diseases or disorders associated with the protein in a subject. The
CC diseases include hypertension, hypotension, congestive heart failure,
CC chronic heart failure, acute heart failure, myocardial infarction,
CC atherosclerosis, arrhythmia and renal failure. They are also useful for
CC treating inflammatory conditions and diseases relating to fertility. The
CC present sequence is a PCR primer used in single strand conformation
CC polymorphism (SSCP) analysis of human ACE-2 DNA
XX
SQ Sequence 25 BP; 8 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2776 AAAGTGTGTTTGGTCTCAGGC 2800
Db 25 AAAGTGTGTTTGGTCTCAGGC 1
RESULT 32
AAD32605
ID AAD32605 standard; DNA; 25 BP.
AC AAD32605;
XX
XX 18-JUN-2002 (first entry)
XX
DE ace2e7b PCR primer for SSCP analysis of human ACE-2 DNA.
XX
KW Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
KW myocardial infarction; heart failure; arrhythmia; renal failure;
KW inflammation; fertility; enzyme; PCR; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200212471-A2.
XX
XX 14-FEB-2002.
XX
XX 09-AUG-2001; 2001WO-US025059.
XX
XX 09-AUG-2000; 2000US-00635501.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Acton S, Robison KE, Hsieh FY;
XX
XX WPI; 2002-257481/30.
XX
XX Isolated human polypeptide, known as angiotensin converting enzyme-2,
XX useful for treating or preventing the development of an abnormal blood
XX pressure or related diseases, e.g. hypertension, heart failure or
XX myocardial infarction.
XX
XX Example 10; Page 114; 218pp; English.
XX
CC The invention relates to human angiotensin converting enzyme-2 (ACE-2)
CC polypeptides and polynucleotides. ACE-2 is also known as peptidyl
CC dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
CC treating or preventing the development of abnormal blood pressure and
CC diseases or disorders associated with the protein in a subject. The
CC diseases include hypertension, hypotension, congestive heart failure,
CC chronic heart failure, acute heart failure, myocardial infarction,
CC atherosclerosis, arrhythmia and renal failure. They are also useful for
CC treating inflammatory conditions and diseases relating to fertility. The
CC present sequence is a PCR primer used in single strand conformation
CC polymorphism (SSCP) analysis of human ACE-2 DNA
XX
SQ Sequence 25 BP; 8 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2776 AAAGTGTGTTTGGTCTCAGGC 2800
Db 25 AAAGTGTGTTTGGTCTCAGGC 1
```

```
CC present sequence is a PCR primer used in single strand conformation
CC polymorphism (SSCP) analysis of human ACE-2 DNA
XX
SQ Sequence 25 BP; 5 A; 0 C; 11 G; 9 T; 0 U; 0 Other;
Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 905 GGTGATATGCGGTAGATTTCGA 929
Db 1 GGTGATATGCGGTAGATTTCGA 25
RESULT 33
AAD32639
ID AAD32639 standard; DNA; 25 BP.
XX
XX AAD32639;
XX
XX 18-JUN-2002 (first entry)
XX
XX ace2e18f PCR primer for SSCP analysis of human ACE-2 DNA.
XX
KW Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
KW myocardial infarction; heart failure; arrhythmia; renal failure;
KW inflammation; fertility; enzyme; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200212471-A2.
XX
XX 14-FEB-2002.
XX
XX 09-AUG-2001; 2001WO-US025059.
XX
XX 09-AUG-2000; 2000US-00635501.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Acton S, Robison KE, Hsieh FY;
XX
XX WPI; 2002-257481/30.
XX
XX Isolated human polypeptide, known as angiotensin converting enzyme-2,
XX useful for treating or preventing the development of an abnormal blood
XX pressure or related diseases, e.g. hypertension, heart failure or
XX myocardial infarction.
XX
XX Example 10; Page 115; 218pp; English.
XX
CC The invention relates to human angiotensin converting enzyme-2 (ACE-2)
CC polypeptides and polynucleotides. ACE-2 is also known as peptidyl
CC dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
CC treating or preventing the development of abnormal blood pressure and
CC diseases or disorders associated with the protein in a subject. The
CC diseases include hypertension, hypotension, congestive heart failure,
CC chronic heart failure, acute heart failure, myocardial infarction,
CC atherosclerosis, arrhythmia and renal failure. They are also useful for
CC treating inflammatory conditions and diseases relating to fertility. The
CC present sequence is a PCR primer used in single strand conformation
CC polymorphism (SSCP) analysis of human ACE-2 DNA
XX
SQ Sequence 25 BP; 2 A; 6 C; 5 G; 12 T; 0 U; 0 Other;
Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2712 CTGTCCTCGATTGACTTCTGTTTC 2736
Db 1 CTGTCCTCGATTGACTTCTGTTTC 25
```

```

XX
KW Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
KW myocardial infarction; heart failure; arrhythmia; renal failure;
XX inflammation; fertility; enzyme; polymorphism; ds.
XX Homo sapiens.
XX
XX FH Location/Qualifiers
XX FT variation
XX FT replace(13, A)
XX FT /*tag= a
XX
XX PN WO200212471-A2.
XX
XX PD 14-FEB-2002.
XX
XX PF 09-AUG-2001; 2001WO-US025059.
XX
XX PR 09-AUG-2000; 2000US-00635501.
XX
XX PA (MILL-) MILLENNIUM PHARM INC.
XX
XX PI Acton S, Robison KE, Hsieh FY;
XX
XX DR WPI; 2002-257481/30.
XX
XX PT Isolated human polypeptide, known as angiotensin converting enzyme-2,
XX useful for treating or preventing the development of an abnormal blood
XX pressure or related diseases, e.g. hypertension, heart failure or
XX myocardial infarction.
XX
XX PS Example 10; Page 117; 218pp; English.
XX
XX CC The invention relates to human angiotensin converting enzyme-2 (ACE-2)
XX polypeptides and polynucleotides. ACE-2 is also known as peptidyl
XX dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
XX treating or preventing the development of abnormal blood pressure and
XX diseases or disorders associated with the protein in a subject. The
XX diseases include hypertension, hypotension, congestive heart failure,
XX chronic heart failure, acute heart failure, myocardial infarction,
XX atherosclerosis, arrhythmia and renal failure. They are also useful for
XX treating inflammatory conditions and diseases relating to fertility. The
XX present sequence is human ACE-2 DNA fragment polymorphic variant
XX
XX SQ Sequence 26 BP; 6 A; 3 C; 10 G; 7 T; 0 U; 0 Other;

Query Match      0.7%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 44;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 58 CTAGGGAAGTCATTCAGTGGATGTG 83
DB 1 CTAGGGAAGTCGTTTCAGTGGATGTG 26

RESULT 36
AAD32653
ID AAD32653 standard; DNA; 26 BP.
XX
XX AC AAD32653;
XX
XX DT 18-JUN-2002 (first entry)
XX
XX DE Human ACE-2 exon 18 DNA fragment polymorphic variant.
XX
XX KW Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
XX peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
XX myocardial infarction; heart failure; arrhythmia; renal failure;
XX inflammation; fertility; enzyme; exon 18; polymorphism; ds.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers

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XX
KW Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang.(1-9);
KW blood pressure; hypertension; congestive heart failure; atherosclerosis;
KW chronic heart failure; acute heart failure; myocardial infarction;
KW renal failure; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200018899-A2.
XX
XX PD 06-APR-2000.
XX
XX PF 29-SEP-1999; 99WO-US022976.
XX
XX PR 30-SEP-1998; 98US-00163648.
XX
XX PA (MILL-) MILLENNIUM PHARM INC.
XX
XX PI Acton LS, Robison KE, Hsieh FY;
XX
XX DR WPI; 2000-293140/25.
XX
XX PT Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
XX polypeptide useful for detecting an ACE-2 therapeutic for treating
XX hypertension, congestive heart failure, myocardial infarction,
XX atherosclerosis and renal failure.
XX
XX PS Example; Page 107; 138pp; English.
XX
XX CC AAA12740-41 represent nucleotide sequences containing a G to T
XX polymorphism in 3' UTR of human angiotensin converting enzyme-2 (ACE-2).
XX CC AAA12741 represents the variant sequence, with position 13 representing
XX the polymorphism. ACE-2 is expressed predominantly in kidneys and testis.
XX CC The sequence of the full length ACE-2 cDNA was determined from a clone
XX obtained from a cDNA library prepared from mRNA of a human heart of a
XX subject who had congestive heart failure. ACE-2 has significant sequence
XX homologies with ACE enzymes, and has also been shown to hydrolyse
XX angiotensin I into Ang.(1-9). The ACE-2 therapeutics are used to treat
XX blood pressure related diseases and conditions, such as hypertension,
XX congestive heart failure, chronic heart failure, acute heart failure,
XX myocardial infarction, atherosclerosis and renal failure
XX
XX SQ Sequence 26 BP; 11 A; 2 C; 5 G; 8 T; 0 U; 0 Other;

Query Match      0.7%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 44;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2844 AGTTGAAAACAAGGATATATCATTTGG 2869
DB 1 AGTTGAAAACAATGATATATCATTTGG 26

RESULT 35
AAD32655
ID AAD32655 standard; DNA; 26 BP.
XX
XX AC AAD32655;
XX
XX DT 18-JUN-2002 (first entry)
XX
XX DE Human ACE-2 DNA fragment polymorphic variant.

```


CC polymorphism (SSCP) analysis of human angiotensin converting enzyme-2
 CC (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
 CC sequence of the full length ACE-2 cDNA was determined from a clone
 CC obtained from a cDNA library prepared from mRNA of a human heart of a
 CC subject who had congestive heart failure. ACE-2 has significant sequence
 CC homologies with ACE enzymes, and has also been shown to hydrolyse
 CC angiotensin I into Ang.(1-9). The ACE-2 therapeutics are used to treat
 CC blood pressure related diseases and conditions, such as hypertension,
 CC congestive heart failure, chronic heart failure, acute heart failure,
 CC myocardial infarction, atherosclerosis and renal failure
 XX
 SQ Sequence 24 BP; 3 A; 6 C; 6 G; 9 T; 0 U; 0 Other;
 Query Match 0.7%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 420 CAGTGCTCTCAGAAGACAGAGCA 443
 Db 24 CAGTGCTCTCAGAAGACAGAGCA 1
 RESULT 39
 AAA12788/c
 ID AAA12788 standard; DNA; 24 BP.
 AC AAA12788;
 XX
 DT 25-JUL-2000 (first entry)
 DE PCR primer ace2e8c used in SSCP analysis of human ACE-2.
 XX
 KW Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang.(1-9);
 KW blood pressure; hypertension; congestive heart failure; atherosclerosis;
 KW chronic heart failure; acute heart failure; myocardial infarction;
 KW renal failure; PCR primer; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200018899-A2.
 XX
 PD 06-APR-2000.
 PF 29-SEP-1999; 99WO-US022976.
 XX
 PR 30-SEP-1998; 98US-00163648.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Acton LS, Robison KE, Hsieh FY;
 XX
 DR WPI; 2000-293140/25.
 XX
 PT Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
 PT polypeptide useful for detecting an ACE-2 therapeutic for treating
 PT hypertension, congestive heart failure, myocardial infarction,
 PT atherosclerosis and renal failure.
 XX
 PS Example; Page 105; 138pp; English.
 XX
 CC PCR primers AAA12766-A12821 were used for single strand conformation
 CC polymorphism (SSCP) analysis of human angiotensin converting enzyme-2
 CC (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
 CC sequence of the full length ACE-2 cDNA was determined from a clone
 CC obtained from a cDNA library prepared from mRNA of a human heart of a
 CC subject who had congestive heart failure. ACE-2 has significant sequence
 CC homologies with ACE enzymes, and has also been shown to hydrolyse
 CC angiotensin I into Ang.(1-9). The ACE-2 therapeutics are used to treat
 CC blood pressure related diseases and conditions, such as hypertension,
 CC congestive heart failure, chronic heart failure, acute heart failure,
 CC myocardial infarction, atherosclerosis and renal failure
 XX
 SQ Sequence 24 BP; 5 A; 4 C; 8 G; 7 T; 0 U; 0 Other;
 Query Match 0.7%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 420 CAGTGCTCTCAGAAGACAGAGCA 443
 Db 24 CAGTGCTCTCAGAAGACAGAGCA 1
 RESULT 41
 AAA12738

Query Match 0.7%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1119 TTCAAGAAAGCAGCTGCGCATCCCA 1142
 Db 24 TTCAAGAAAGCAGCTGCGCATCCCA 1
 RESULT 40
 AAA12784/c
 ID AAA12784 standard; DNA; 24 BP.
 XX
 AC AAA12784;
 XX
 DT 25-JUL-2000 (first entry)
 DE PCR primer ace2e7c used in SSCP analysis of human ACE-2.
 XX
 KW Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang.(1-9);
 KW blood pressure; hypertension; congestive heart failure; atherosclerosis;
 KW chronic heart failure; acute heart failure; myocardial infarction;
 KW renal failure; PCR primer; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200018899-A2.
 XX
 PD 06-APR-2000.
 PF 29-SEP-1999; 99WO-US022976.
 XX
 PR 30-SEP-1998; 98US-00163648.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Acton LS, Robison KE, Hsieh FY;
 XX
 DR WPI; 2000-293140/25.
 XX
 PT Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
 PT polypeptide useful for detecting an ACE-2 therapeutic for treating
 PT hypertension, congestive heart failure, myocardial infarction,
 PT atherosclerosis and renal failure.
 XX
 PS Example; Page 105; 138pp; English.
 XX
 CC PCR primers AAA12766-A12821 were used for single strand conformation
 CC polymorphism (SSCP) analysis of human angiotensin converting enzyme-2
 CC (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
 CC sequence of the full length ACE-2 cDNA was determined from a clone
 CC obtained from a cDNA library prepared from mRNA of a human heart of a
 CC subject who had congestive heart failure. ACE-2 has significant sequence
 CC homologies with ACE enzymes, and has also been shown to hydrolyse
 CC angiotensin I into Ang.(1-9). The ACE-2 therapeutics are used to treat
 CC blood pressure related diseases and conditions, such as hypertension,
 CC congestive heart failure, chronic heart failure, acute heart failure,
 CC myocardial infarction, atherosclerosis and renal failure
 XX
 SQ Sequence 24 BP; 7 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 0.7%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 978 ATGTTACTGATGCAATGTGGACC 1001
 Db 24 ATGTTACTGATGCAATGTGGACC 1
 RESULT 41
 AAA12738


```

PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Acton LS, Robison KE, Hsieh FY;
XX
DR WPI; 2000-293140/25.
XX
PT Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
PT polypeptide useful for detecting an ACE-2 therapeutic for treating
PT hypertension, congestive heart failure, myocardial infarction,
PT atherosclerosis and renal failure.
XX
PS Example; Page 105; 138pp; English.
XX
CC PCR primers AAA12766-Al2821 were used for single strand conformation
CC polymorphism (SSCP) analysis of human angiotensin converting enzyme-2
CC (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
CC sequence of the full length ACE-2 cDNA was determined from a clone
CC subject who had congestive heart failure. ACE-2 has significant sequence
CC homologies with ACE enzymes, and has also been shown to hydrolyse
CC angiotensin I into Ang. (1-9). The ACE-2 therapeutics are used to treat
CC blood pressure related diseases and conditions, such as hypertension,
CC congestive heart failure, chronic heart failure, acute heart failure,
CC myocardial infarction, atherosclerosis and renal failure
XX
SQ Sequence 24 BP; 6 A; 8 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 0.7%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 ATCTCAGCTCAAGCTTCAGCTGC 395
Db 1 ATCTCAGCTCAAGCTTCAGCTGC 24

RESULT 44
AAD32610/c
ID AAD32610 standard; DNA; 24 BP.
XX
AC AAD32610;
XX
XX 18-JUN-2002 (first entry)
XX
DE ace2e8c PCR primer for SSCP analysis of human ACE-2 DNA.
XX
KW Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
KW myocardial infarction; heart failure; arrhythmia; renal failure;
KW inflammation; fertility; enzyme; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200212471-A2.
XX
PD 14-FEB-2002.
XX
PF 09-AUG-2001; 2001WO-US025059.
XX
PR 09-AUG-2000; 2000US-00635501.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Acton S, Robison KE, Hsieh FY;
XX
DR WPI; 2002-257481/30.
XX
PT Isolated human polypeptide, known as angiotensin converting enzyme-2,
PT useful for treating or preventing the development of an abnormal blood
PT pressure or related diseases, e.g. hypertension, heart failure or
PT myocardial infarction.
XX
PS Example 10; Page 115; 218pp; English.

The invention relates to human angiotensin converting enzyme-2 (ACE-2)
polypeptides and polynucleotides. ACE-2 is also known as peptidyl
dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
treating or preventing the development of abnormal blood pressure and
diseases or disorders associated with the protein in a subject. The
diseases include hypertension, hypotension, congestive heart failure,
chronic heart failure, acute heart failure, myocardial infarction,
atherosclerosis, arrhythmia and renal failure. They are also useful for
treating inflammatory conditions and diseases relating to fertility. The
present sequence is a PCR primer used in single strand conformation
polymorphism (SSCP) analysis of human ACE-2 DNA

Sequence 24 BP; 5 A; 4 C; 8 G; 7 T; 0 U; 0 Other;
Query Match 0.7%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1119 TTCAGAAAGCAGCTGCCATCCCA 1142
Db 24 TTCAGAAAGCAGCTGCCATCCCA 1

RESULT 45
AAD32642/c
ID AAD32642 standard; DNA; 24 BP.
XX
AC AAD32642;
XX
XX 18-JUN-2002 (first entry)
XX
DE ace2e18i PCR primer for SSCP analysis of human ACE-2 DNA.
XX
KW Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
KW myocardial infarction; heart failure; arrhythmia; renal failure;
KW inflammation; fertility; enzyme; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200212471-A2.
XX
PD 14-FEB-2002.
XX
PF 09-AUG-2001; 2001WO-US025059.
XX
PR 09-AUG-2000; 2000US-00635501.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Acton S, Robison KE, Hsieh FY;
XX
DR WPI; 2002-257481/30.
XX
PT Isolated human polypeptide, known as angiotensin converting enzyme-2,
PT useful for treating or preventing the development of an abnormal blood
PT pressure or related diseases, e.g. hypertension, heart failure or
PT myocardial infarction.
XX
PS Example 10; Page 116; 218pp; English.

The invention relates to human angiotensin converting enzyme-2 (ACE-2)
polypeptides and polynucleotides. ACE-2 is also known as peptidyl
dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
treating or preventing the development of abnormal blood pressure and
diseases or disorders associated with the protein in a subject. The
diseases include hypertension, hypotension, congestive heart failure,
chronic heart failure, acute heart failure, myocardial infarction,
atherosclerosis, arrhythmia and renal failure. They are also useful for
treating inflammatory conditions and diseases relating to fertility. The
present sequence is a PCR primer used in single strand conformation
polymorphism (SSCP) analysis of human ACE-2 DNA

```

```
XX SQ Sequence 24 BP; 4 A; 5 C; 6 G; 9 T; 0 U; 0 Other;
Query Match 0.7%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2648 TTGTCCCAAGACACATGCGCAAG 2671
Db 24 TTGTCCCAAGACACATGCGCAAG 1

RESULT 46
AAD32635
ID AAD32635 standard; DNA; 24 BP.
XX AC AAD32635;
XX DT 18-JUN-2002 (first entry)
XX DE ace2e18b PCR primer for SSCP analysis of human ACE-2 DNA.
XX Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
XX peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
XX myocardial infarction; heart failure; arrhythmia; renal failure;
XX inflammation; fertility; enzyme; PCR; primer; ss.
XX OS Homo sapiens.
XX PN WO200212471-A2.
XX PD 14-FEB-2002.
XX PF 09-AUG-2001; 2001WO-US025059.
XX PR 09-AUG-2000; 2000US-00635501.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Acton S, Robison KE, Hsieh FY;
XX WPI; 2002-257481/30.
XX Isolated human polypeptide, known as angiotensin converting enzyme-2,
XX useful for treating or preventing the development of an abnormal blood
XX pressure or related diseases, e.g. hypertension, heart failure or
XX myocardial infarction.
XX Example 10; Page 115; 218pp; English.
XX The invention relates to human angiotensin converting enzyme-2 (ACE-2)
XX polypeptides and polynucleotides. ACE-2 is also known as peptidyl
XX dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
XX treating or preventing the development of abnormal blood pressure and
XX diseases or disorders associated with the protein in a subject. The
XX diseases include hypertension, hypotension, congestive heart failure,
XX chronic heart failure, acute heart failure, myocardial infarction,
XX atherosclerosis, arrhythmia and renal failure. They are also useful for
XX treating inflammatory conditions and diseases relating to fertility. The
XX present sequence is a PCR primer used in single strand conformation
XX polymorphism (SSCP) analysis of human ACE-2 DNA
XX SQ Sequence 24 BP; 9 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 0.7%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3210 CAGAGCATGCGCTGATAGAACTCA 3233
Db 1 CAGAGCATGCGCTGATAGAACTCA 24

RESULT 47
AAD32593
ID AAD32593 standard; DNA; 24 BP.
XX AC AAD32593;
XX DT 18-JUN-2002 (first entry)
XX DE ace2e2b PCR primer for SSCP analysis of human ACE-2 DNA.
XX Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
XX peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
XX myocardial infarction; heart failure; arrhythmia; renal failure;
XX inflammation; fertility; enzyme; PCR; primer; ss.
XX OS Homo sapiens.
XX PN WO200212471-A2.
XX PD 14-FEB-2002.
XX PF 09-AUG-2001; 2001WO-US025059.
XX PR 09-AUG-2000; 2000US-00635501.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Acton S, Robison KE, Hsieh FY;
XX WPI; 2002-257481/30.
XX Isolated human polypeptide, known as angiotensin converting enzyme-2,
XX useful for treating or preventing the development of an abnormal blood
XX pressure or related diseases, e.g. hypertension, heart failure or
XX myocardial infarction.
XX Example 10; Page 114; 218pp; English.
XX The invention relates to human angiotensin converting enzyme-2 (ACE-2)
XX polypeptides and polynucleotides. ACE-2 is also known as peptidyl
XX dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
XX treating or preventing the development of abnormal blood pressure and
XX diseases or disorders associated with the protein in a subject. The
XX diseases include hypertension, hypotension, congestive heart failure,
XX chronic heart failure, acute heart failure, myocardial infarction,
XX atherosclerosis, arrhythmia and renal failure. They are also useful for
XX treating inflammatory conditions and diseases relating to fertility. The
XX present sequence is a PCR primer used in single strand conformation
XX polymorphism (SSCP) analysis of human ACE-2 DNA
XX SQ Sequence 24 BP; 6 A; 8 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 0.7%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 372 ATCTCAGAGTCAGGCTTCAGTGC 395
Db 1 ATCTCAGAGTCAGGCTTCAGTGC 24

RESULT 48
AAD32594/c
ID AAD32594 standard; DNA; 24 BP.
XX AC AAD32594;
XX DT 18-JUN-2002 (first entry)
XX DE ace2e2c PCR primer for SSCP analysis of human ACE-2 DNA.
XX Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
XX peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
```


KW myocardial infarction; heart failure; arrhythmia; renal failure;
 KW inflammation; fertility; enzyme; PCR; primer; ss.
 XX

OS Homo sapiens.

PN WO200212471-A2.

XX 14-FEB-2002.

PD 09-AUG-2001; 2001WO-US025059.

PF 09-AUG-2000; 2000US-00635501.

PR (MILL-) MILLENNIUM PHARM INC.

XX Acton S, Robison KE, Hsieh FY;

XX WPI; 2002-257481/30.

XX Isolated human polypeptide, known as angiotensin converting enzyme-2,
 PT useful for treating or preventing the development of an abnormal blood
 PT pressure or related diseases, e.g. hypertension, heart failure or
 PT myocardial infarction.
 PT

PS Example 10; Page 114; 218pp; English.

XX The invention relates to human angiotensin converting enzyme-2 (ACE-2)
 CC polypeptides and polynucleotides. ACE-2 is also known as peptidyl
 CC dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
 CC treating or preventing the development of abnormal blood pressure and
 CC diseases or disorders associated with the protein in a subject. The
 CC diseases include hypertension, hypotension, congestive heart failure,
 CC chronic heart failure, acute heart failure, myocardial infarction,
 CC atherosclerosis, arrhythmia and renal failure. They are also useful for
 CC treating inflammatory conditions and diseases relating to fertility. The
 CC present sequence is a PCR primer used in single strand conformation
 CC polymorphism (SSCP) analysis of human ACE-2 DNA
 XX

SQ Sequence 24 BP; 3 A; 6 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 0.7%; Score 24; DB 1; Length 24;

Best Local Similarity 100.0%; Pred. No. 42;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 CAGTGCTCTCAGAGACAGACGA 443

DB 24 CAGTGCTCTCAGAGACAGACGA 1

RESULT 49

AAD32606/c

ID AAD32606 standard; DNA; 24 BP.

XX AAD32606;

XX 18-JUN-2002 (first entry)

DE ace2e7c PCR primer for SSCP analysis of human ACE-2 DNA.

XX Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
 KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
 KW myocardial infarction; heart failure; arrhythmia; renal failure;
 KW inflammation; fertility; enzyme; PCR; primer; ss.
 XX

OS Homo sapiens.

PN WO200212471-A2.

XX 14-FEB-2002.

PD 09-AUG-2001; 2001WO-US025059.

PF 09-AUG-2000; 2000US-00635501.

PR (BRIM) BRISTOL-MYERS SQUIBB CO.

XX (MILL-) MILLENNIUM PHARM INC.

XX Acton S, Robison KE, Hsieh FY;

XX WPI; 2002-257481/30.

XX Isolated human polypeptide, known as angiotensin converting enzyme-2,
 PT useful for treating or preventing the development of an abnormal blood
 PT pressure or related diseases, e.g. hypertension, heart failure or
 PT myocardial infarction.
 PT

PS Example 10; Page 114; 218pp; English.

XX The invention relates to human angiotensin converting enzyme-2 (ACE-2)
 CC polypeptides and polynucleotides. ACE-2 is also known as peptidyl
 CC dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
 CC treating or preventing the development of abnormal blood pressure and
 CC diseases or disorders associated with the protein in a subject. The
 CC diseases include hypertension, hypotension, congestive heart failure,
 CC chronic heart failure, acute heart failure, myocardial infarction,
 CC atherosclerosis, arrhythmia and renal failure. They are also useful for
 CC treating inflammatory conditions and diseases relating to fertility. The
 CC present sequence is a PCR primer used in single strand conformation
 CC polymorphism (SSCP) analysis of human ACE-2 DNA
 XX

SQ Sequence 24 BP; 7 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.7%; Score 24; DB 1; Length 24;

Best Local Similarity 100.0%; Pred. No. 42;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 978 AGTTACTGATGCAATGGTGACC 1001

DB 24 ATGTTACTGATGCAATGGTGACC 1

RESULT 50

ABS61009

ID ABS61009 standard; DNA; 24 BP.

XX ABS61009;

XX 05-NOV-2002 (first entry)

XX Human genotyping PCR primer #162.

XX Human; ss; aminopeptidase P; XPNEP2; bradykinin receptor B1; primer;
 KW BDKRB1; tachykinin receptor B1; TACR1; Cl esterase inhibitor; C1NH;
 KW kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
 KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
 KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
 KW cardiovascular disease; angina pectoris; hypertension; heart failure;
 KW myocardial infarction; ventricular hypertrophy; vascular disease;
 KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
 KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis; PCR;
 KW autoimmune disease; inflammatory arthritis; cancer; wound; genotyping;
 KW viral infection; bacterial infection; fungal infection; COPD;
 KW Chronic obstructive pulmonary disease; enterocolitis.
 XX

OS Homo sapiens.

XX WO200261131-A2.

XX 08-AUG-2002.

XX 03-DEC-2001; 2001WO-US047235.

XX 04-DEC-2000; 2000US-0251015P.

XX 23-JAN-2001; 2001US-0263678P.

XX 02-WAR-2001; 2001US-0273037P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

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PA (TSUC/) TSUCHIHASHI Z.
PA (HUIL/) HUI L.
PI Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
PI Swanson EN, Powell JR;
XX WPI; 2002-619265/66.
XX
XX New isolated nucleic acid with at least one polymorphic position, useful
XX for detecting, diagnosing and treating disorders such as angiodema,
XX cancer, viral, bacterial or fungal infection, cardiovascular and
XX autoimmune diseases.
XX
XX Example 3; Page 914; 977pp; English.
XX
XX The invention relates to an isolated nucleic acid from a human gene
XX encoding aminopeptidase P (XNPEP2), bradykinin receptor B1 (BDRKB1),
XX tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
XX 1 (KLK1), bradykinin receptor B2 (BDRB2), angiotensin converting enzyme
XX 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
XX polymorphic position. Also included are (1) a probe that hybridises to a
XX nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
XX sequence; (2) analysing (M1) at least one nucleic acid sample comprising
XX obtaining the sample from one or more individuals and determining the
XX nucleic acid sequence at one or more polymorphic positions in a gene
XX encoding a protein selected from the group above; (3) constructing (M2)
XX haplotypes using the genes comprising grouping at least two nucleic acids
XX; (4) identifying (M3) an individual at risk of developing a disorder
XX upon administration of an ACE inhibitor and/or vasopeptidase inhibitor
XX using the polymorphic data; (5) a library of nucleic acids, each of which
XX comprises one or more polymorphic positions within a gene encoding a
XX human protein selected from the group above; and (6) genotyping (M4) an
XX individual comprising obtaining a nucleic acid sample, determining the
XX nucleotide present in at least one polymorphic position, and comparing at
XX least one position with a known data set. The genes, (M1, M2, M3 and M4)
XX preventing various disorders such as angiodema and diseases which
XX involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
XX disease, trachomas, and cardiovascular diseases like angina pectoris,
XX hypertension, heart failure, myocardial infarction, ventricular
XX hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
XX artery disease, arteriosclerosis and/or atherosclerosis, and
XX hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
XX arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
XX obstructive pulmonary disease (COPD) and enterocolitis (many other
XX diseases and disorders are listed in the specification). The
XX polynucleotides are also useful for chromosome identification. Antibodies
XX against the proteins may be utilised for immunophenotyping of cell lines
XX and biological samples. The present sequence is a genotyping PCR primer
XX for the gene encoding one of the proteins listed above
XX
XX Sequence 24 BP; 11 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.7%; Score 24; DB 1; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 42;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1885 GCTGAAGACCAAGACCAAGATTC 1908
XX Db 1 GCTGAAGACCAAGACCAAGATTC 24
XX
XX RESULT 51
XX AAA12809
XX ID AAA12809 standard; DNA; 23 BP.
XX AC AAA12809;
XX
XX 25-JUL-2000 (first entry)
XX
XX PCR primer ace2e17b1 used in SSCP analysis of human ACE-2.
XX
XX Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang. (1-9);
XX blood pressure; hypertension; congestive heart failure; atherosclerosis;
XX chronic heart failure; acute heart failure; myocardial infarction;
XX renal failure; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200018899-A2.
XX
XX 06-APR-2000.
XX
XX 29-SEP-1999; 99WO-US022976.
XX
XX 30-SEP-1998; 98US-00163648.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Acton LS, Robison KE, Hsieh FY;
XX WPI; 2000-293140/25.
XX
XX Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
XX polypeptide useful for detecting an ACE-2 therapeutic for treating
XX hypertension, congestive heart failure, myocardial infarction,
XX atherosclerosis and renal failure.
XX
XX Example; Page 106; 138pp; English.
XX
XX PCR primers AAA12766-AL2821 were used for single strand conformation
XX polymorphism (SSCP) analysis of human angiotensin converting enzyme-2
XX (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
XX sequence of the full length ACE-2 cDNA was determined from a clone
XX obtained from a cDNA library prepared from mRNA of a human heart of a
XX subject who had congestive heart failure. ACE-2 has significant sequence
XX homologies with ACE enzymes, and has also been shown to hydrolyse
XX angiotensin I into Ang. (1-9). The ACE-2 therapeutics are used to treat
XX blood pressure related diseases and conditions, such as hypertension,
XX congestive heart failure, chronic heart failure, acute heart failure,
XX myocardial infarction, atherosclerosis and renal failure
XX
XX Sequence 23 BP; 7 A; 9 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.7%; Score 23; DB 1; Length 23;
XX Best Local Similarity 100.0%; Pred. No. 49;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2286 AGCCACACTTGGACCTCTTAC 2308
XX Db 1 AGCCACACTTGGACCTCTTAC 23
XX
XX RESULT 52
XX AAA12791
XX ID AAA12791 standard; DNA; 23 BP.
XX AC AAA12791;
XX
XX 25-JUL-2000 (first entry)
XX
XX PCR primer ace2e9b used in SSCP analysis of human ACE-2.
XX
XX Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang. (1-9);
XX blood pressure; hypertension; congestive heart failure; atherosclerosis;
XX chronic heart failure; acute heart failure; myocardial infarction;
XX renal failure; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200018899-A2.
XX
XX 06-APR-2000.
XX
XX 29-SEP-1999; 99WO-US022976.
XX

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XX 30-SEP-1998; 98US-00163648.
XX (MILL-) MILLENNIUM PHARM INC.
XX Acton LS, Robison KE, Hsieh FY;
XX WPI; 2000-293140/25.
XX Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
XX polypeptide useful for detecting an ACE-2 therapeutic for treating
XX hypertension, congestive heart failure, myocardial infarction,
XX atherosclerosis and renal failure.
XX Example; Page 105; 138pp; English.
XX PCR primers AAA12766-A12821 were used for single strand conformation
XX polymorphism (SSCP) analysis of human angiotensin converting enzyme-2
XX (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
XX sequence of the full length ACE-2 cDNA was determined from a clone
XX obtained from a cDNA library prepared from mRNA of a human heart of a
XX subject who had congestive heart failure. ACE-2 has significant sequence
XX homologies with ACE enzymes, and has also been shown to hydrolyse
XX angiotensin I into Ang.(1-9). The ACE-2 therapeutics are used to treat
XX blood pressure related diseases and conditions, such as hypertension,
XX congestive heart failure, chronic heart failure, acute heart failure,
XX myocardial infarction, atherosclerosis and renal failure
XX
XX Sequence 23 BP; 5 A; 7 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 0.7%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1252 GGCATATGCTGCACACCTTTTC 1274
DB 1 GGCATATGCTGCACACCTTTTC 23
RESULT 53
AAA12768/c
ID AAA12768 standard; DNA; 23 BP.
AC AAA12768;
XX
XX 25-JUL-2000 (first entry)
XX PCR primer ace2elc used in SSCP analysis of human ACE-2.
XX Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang.(1-9);
XX blood pressure; hypertension; congestive heart failure; atherosclerosis;
XX chronic heart failure; acute heart failure; myocardial infarction;
XX renal failure; PCR primer; ss.
XX Homo sapiens.
XX
XX WO200018899-A2.
XX
XX 06-APR-2000.
XX 29-SEP-1999; 99WO-US022976.
XX 30-SEP-1998; 98US-00163648.
XX (MILL-) MILLENNIUM PHARM INC.
XX Acton LS, Robison KE, Hsieh FY;
XX WPI; 2000-293140/25.
XX Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
XX polypeptide useful for detecting an ACE-2 therapeutic for treating
XX hypertension, congestive heart failure, myocardial infarction,
XX atherosclerosis and renal failure.
XX Example; Page 111; 138pp; English.
XX PCR primers AAA12742-43 were used for chromosome localisation of human
XX angiotensin converting enzyme-2 (ACE-2). ACE-2 is expressed predominantly
XX in kidneys and testis. The sequence of the full length ACE-2 cDNA was
XX determined from a clone obtained from a cDNA library prepared from mRNA
XX of a human heart of a subject who had congestive heart failure. ACE-2 has
XX significant sequence homologies with ACE enzymes, and has also been shown
XX to hydrolyse angiotensin I into Ang.(1-9). The ACE-2 therapeutics are
XX used to treat blood pressure related diseases and conditions, such as
XX
XX Sequence 23 BP; 2 A; 6 C; 6 G; 9 T; 0 U; 0 Other;
Query Match 0.7%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 160 CACCATTGAGGAAACAGGCCAAGA 182
DB 23 CACCATTGAGGAAACAGGCCAAGA 1
RESULT 54
AAA12742
ID AAA12742 standard; DNA; 23 BP.
XX
XX AAA12742;
XX
XX 25-JUL-2000 (first entry)
XX PCR primer used for chromosome localisation of human ACE-2.
XX Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang.(1-9);
XX blood pressure; hypertension; congestive heart failure; atherosclerosis;
XX chronic heart failure; acute heart failure; myocardial infarction;
XX renal failure; PCR primer; ss.
XX Homo sapiens.
XX
XX WO200018899-A2.
XX
XX 06-APR-2000.
XX 29-SEP-1999; 99WO-US022976.
XX 30-SEP-1998; 98US-00163648.
XX (MILL-) MILLENNIUM PHARM INC.
XX Acton LS, Robison KE, Hsieh FY;
XX WPI; 2000-293140/25.
XX Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
XX polypeptide useful for detecting an ACE-2 therapeutic for treating
XX hypertension, congestive heart failure, myocardial infarction,
XX atherosclerosis and renal failure.
XX Example; Page 105; 138pp; English.
XX PCR primers AAA12766-A12821 were used for single strand conformation
XX polymorphism (SSCP) analysis of human angiotensin converting enzyme-2
XX (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
XX sequence of the full length ACE-2 cDNA was determined from a clone
XX obtained from a cDNA library prepared from mRNA of a human heart of a
XX subject who had congestive heart failure. ACE-2 has significant sequence
XX homologies with ACE enzymes, and has also been shown to hydrolyse
XX angiotensin I into Ang.(1-9). The ACE-2 therapeutics are used to treat
XX blood pressure related diseases and conditions, such as hypertension,
XX congestive heart failure, chronic heart failure, acute heart failure,
XX myocardial infarction, atherosclerosis and renal failure
XX
XX Sequence 23 BP; 2 A; 6 C; 6 G; 9 T; 0 U; 0 Other;
Query Match 0.7%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 160 CACCATTGAGGAAACAGGCCAAGA 182
DB 23 CACCATTGAGGAAACAGGCCAAGA 1

```

CC hypertension, congestive heart failure, chronic heart failure, acute
 CC heart failure, myocardial infarction, atherosclerosis and renal failure
 XX
 SQ Sequence 23 BP; 6 A; 5 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.7%; Score 23; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2902 GGATCACTTCTGAAGGACAGTGCC 2924
 |||||
 Db 1 GGATCACTTCTGAAGGACAGTGCC 23

RESULT 55

AAA12814/c

ID AAA12814 standard; DNA; 23 BP.

XX AAA12814;

XX 25-JUL-2000 (first entry)

DE PCR primer ace2el8c used in SSCP analysis of human ACE-2.

XX Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang. (1-9);
 KW blood pressure; hypertension; congestive heart failure; atherosclerosis;
 KW chronic heart failure; acute heart failure; myocardial infarction;
 KW renal failure; PCR primer; ss.

XX Homo sapiens.

XX WO200018899-A2.

XX 06-APR-2000.

XX 29-SEP-1999; 99WO-US022976.

XX 30-SEP-1998; 98US-00163648.

XX (MILL-) MILLENNIUM PHARM INC.

XX Acton LS, Robison KE, Hsieh FY;

XX WPI; 2000-293140/25.

XX Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
 PT polypeptide useful for detecting an ACE-2 therapeutic for treating
 PT hypertension, congestive heart failure, myocardial infarction,
 PT atherosclerosis and renal failure.

XX Example; Page 106; 138pp; English.

XX PCR primers AAA12766-A12821 were used for single strand conformation
 CC polymorphism (SSCP) analysis of human angiotensin converting enzyme-2
 CC (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
 CC sequence of the full length ACE-2 cDNA was determined from a clone
 CC obtained from a cDNA library prepared from mRNA of a human heart of a
 CC subject who had congestive heart failure. ACE-2 has significant sequence
 CC homologies with ACE enzymes, and has also been shown to hydrolyse
 CC angiotensin I into Ang. (1-9). The ACE-2 therapeutics are used to treat
 CC blood pressure related diseases and conditions, such as hypertension,
 CC congestive heart failure, chronic heart failure, acute heart failure,
 CC myocardial infarction, atherosclerosis and renal failure

XX Sequence 23 BP; 7 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.7%; Score 23; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3279 ATGTTACCCCTCTGAAGTGGTA 3301
 |||||
 Db 23 ATGTTACCCCTCTGAAGTGGTA 1

RESULT 56

AAA12810/c

ID AAA12810 standard; DNA; 23 BP.

XX AAA12810;

XX 25-JUL-2000 (first entry)

DE PCR primer ace2el7c used in SSCP analysis of human ACE-2.

XX Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang. (1-9);
 KW blood pressure; hypertension; congestive heart failure; atherosclerosis;
 KW chronic heart failure; acute heart failure; myocardial infarction;
 KW renal failure; PCR primer; ss.

XX Homo sapiens.

XX WO200018899-A2.

XX 06-APR-2000.

XX 29-SEP-1999; 99WO-US022976.

XX 30-SEP-1998; 98US-00163648.

XX (MILL-) MILLENNIUM PHARM INC.

XX Acton LS, Robison KE, Hsieh FY;

XX WPI; 2000-293140/25.

XX Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
 PT polypeptide useful for detecting an ACE-2 therapeutic for treating
 PT hypertension, congestive heart failure, myocardial infarction,
 PT atherosclerosis and renal failure.

XX Example; Page 106; 138pp; English.

XX PCR primers AAA12766-A12821 were used for single strand conformation
 CC polymorphism (SSCP) analysis of human angiotensin converting enzyme-2
 CC (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
 CC sequence of the full length ACE-2 cDNA was determined from a clone
 CC obtained from a cDNA library prepared from mRNA of a human heart of a
 CC subject who had congestive heart failure. ACE-2 has significant sequence
 CC homologies with ACE enzymes, and has also been shown to hydrolyse
 CC angiotensin I into Ang. (1-9). The ACE-2 therapeutics are used to treat
 CC blood pressure related diseases and conditions, such as hypertension,
 CC congestive heart failure, chronic heart failure, acute heart failure,
 CC myocardial infarction, atherosclerosis and renal failure

XX Sequence 23 BP; 8 A; 4 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 23; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2369 GGCATTGTCATCTGATCTTCAC 2391
 |||||
 Db 23 GGCATTGTCATCTGATCTTCAC 1

RESULT 57

AAD32636/c

ID AAD32636 standard; DNA; 23 BP.

XX AAD32636;

XX 18-JUN-2002 (first entry)

DE ace2el8c PCR primer for SSCP analysis of human ACE-2 DNA.

XX

KW Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
 KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
 KW myocardial infarction; heart failure; arrhythmia; renal failure;
 XX inflammation; fertility; enzyme; PCR; primer; ss.
 OS Homo sapiens.
 XX WO200212471-A2.
 XX 14-FEB-2002.
 XX 09-AUG-2001; 2001WO-US025059.
 XX 09-AUG-2000; 2000US-00635501.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Acton S, Robison KE, Hsieh FY;
 XX WPI; 2002-257481/30.
 XX Isolated human polypeptide, known as angiotensin converting enzyme-2,
 PT useful for treating or preventing the development of an abnormal blood
 PT pressure or related diseases, e.g. hypertension, heart failure or
 PT myocardial infarction.
 XX Example 10; Page 115; 218pp; English.
 XX The invention relates to human angiotensin converting enzyme-2 (ACE-2)
 CC polypeptides and polynucleotides. ACE-2 is also known as peptidyl
 CC dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
 CC treating or preventing the development of abnormal blood pressure and
 CC diseases or disorders associated with the protein in a subject. The
 CC diseases include hypertension, hypotension, congestive heart failure,
 CC chronic heart failure, acute heart failure, myocardial infarction,
 CC atherosclerosis, arrhythmia and renal failure. They are also useful for
 CC treating inflammatory conditions and diseases relating to fertility. The
 CC present sequence is a PCR primer used in single strand conformation
 CC polymorphism (SSCP) analysis of human ACE-2 DNA
 XX Sequence 23 BP; 7 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 0.7%; Score 23; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3279 ATGTTACCCCTCTGAAGTGGGTA 3301
 Db 23 ATGTTACCCCTCTGAAGTGGGTA 1
 RESULT 58
 AAD32650
 ID AAD32650 standard; DNA; 23 BP.
 AC AAD32650;
 XX 18-JUN-2002 (first entry)
 DT Human ACE-2 exon 17 fragment.
 DE Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
 KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
 KW myocardial infarction; heart failure; arrhythmia; renal failure;
 KW inflammation; fertility; enzyme; exon 17; ds.
 XX Homo sapiens.
 OS Key Location/Qualifiers
 XX variation replace(13, G)
 FT /*tag= a
 XX WO200212471-A2.
 PN

XX 14-FEB-2002.
 PD 09-AUG-2001; 2001WO-US025059.
 XX 09-AUG-2000; 2000US-00635501.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Acton S, Robison KE, Hsieh FY;
 XX WPI; 2002-257481/30.
 XX Isolated human polypeptide, known as angiotensin converting enzyme-2,
 PT useful for treating or preventing the development of an abnormal blood
 PT pressure or related diseases, e.g. hypertension, heart failure or
 PT myocardial infarction.
 XX Example 10; Page 116; 218pp; English.
 XX The invention relates to human angiotensin converting enzyme-2 (ACE-2)
 CC polypeptides and polynucleotides. ACE-2 is also known as peptidyl
 CC dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
 CC treating or preventing the development of abnormal blood pressure and
 CC diseases or disorders associated with the protein in a subject. The
 CC diseases include hypertension, hypotension, congestive heart failure,
 CC chronic heart failure, acute heart failure, myocardial infarction,
 CC atherosclerosis, arrhythmia and renal failure. They are also useful for
 CC treating inflammatory conditions and diseases relating to fertility. The
 CC present sequence is human ACE-2 exon 17 fragment
 XX Sequence 23 BP; 8 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 0.7%; Score 23; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2249 CGTCTGAATGACACACGCGCTAGA 2271
 Db 1 CGTCTGAATGACACACGCGCTAGA 23
 RESULT 59
 AAD32613
 ID AAD32613 standard; DNA; 23 BP.
 XX AAD32613;
 XX 18-JUN-2002 (first entry)
 DT ace2e9b PCR primer for SSCP analysis of human ACE-2 DNA.
 DE Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
 KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
 KW myocardial infarction; heart failure; arrhythmia; renal failure;
 KW inflammation; fertility; enzyme; PCR; primer; ss.
 XX Homo sapiens.
 OS WO200212471-A2.
 XX 14-FEB-2002.
 XX 09-AUG-2001; 2001WO-US025059.
 XX 09-AUG-2000; 2000US-00635501.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Acton S, Robison KE, Hsieh FY;
 XX WPI; 2002-257481/30.
 XX

PT Isolated human polypeptide, known as angiotensin converting enzyme-2,
 PT useful for treating or preventing the development of an abnormal blood
 PT pressure or related diseases, e.g. hypertension, heart failure or
 PT myocardial infarction.
 XX Example 10; Page 115; 218pp; English.
 CC The invention relates to human angiotensin converting enzyme-2 (ACE-2)
 CC polypeptides and polynucleotides. ACE-2 is also known as peptidyl
 CC dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
 CC treating or preventing the development of abnormal blood pressure and
 CC diseases or disorders associated with the protein in a subject. The
 CC diseases include hypertension, hypotension, congestive heart failure,
 CC chronic heart failure, acute heart failure, myocardial infarction,
 CC atherosclerosis, arrhythmia and renal failure. They are also useful for
 CC treating inflammatory conditions and diseases relating to fertility. The
 CC present sequence is a PCR primer used in single strand conformation
 CC polymorphism (SSCP) analysis of human ACE-2 DNA
 XX Sequence 23 BP; 5 A; 7 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 0.7%; Score 23; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1252 GGCATATGCTGCACACCTTTTC 1274
 Db 1 GGCATATGCTGCACACCTTTTC 23
 RESULT 60
 AAD32660
 ID AAD32660 standard; DNA; 23 BP.
 XX AAD32660;
 AC AAD32660;
 XX 18-JUN-2002 (first entry)
 DE Human ACE-2 gene amplifying forward PCR primer.
 KW Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
 KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
 KW myocardial infarction; heart failure; arrhythmia; renal failure;
 KW inflammation; fertility; enzyme; PCR; primer; ss.
 OS Homo sapiens.
 XX WO200212471-A2.
 PD 14-FEB-2002.
 PF 09-AUG-2001; 2001WO-US025059.
 PR 09-AUG-2000; 2000US-00635501.
 XX (MILL-) MILLENNIUM PHARM INC.
 PI Acton S, Robison KE, Hsieh FY;
 DR WPI; 2002-257481/30.
 Isolated human polypeptide, known as angiotensin converting enzyme-2,
 useful for treating or preventing the development of an abnormal blood
 pressure or related diseases, e.g. hypertension, heart failure or
 myocardial infarction.
 XX Example 13; Page 123; 218pp; English.
 CC The invention relates to human angiotensin converting enzyme-2 (ACE-2)
 CC polypeptides and polynucleotides. ACE-2 is also known as peptidyl
 CC dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
 CC treating or preventing the development of abnormal blood pressure and
 CC diseases or disorders associated with the protein in a subject. The

CC diseases include hypertension, hypotension, congestive heart failure,
 CC chronic heart failure, acute heart failure, myocardial infarction,
 CC atherosclerosis, arrhythmia and renal failure. They are also useful for
 CC treating inflammatory conditions and diseases relating to fertility. The
 CC present sequence is a PCR primer used to amplify human ACE-2 gene
 XX Sequence 23 BP; 6 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 0.7%; Score 23; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2902 GGATCATTGTGAAGCAGTGCC 2924
 Db 1 GGATCATTGTGAAGCAGTGCC 23
 RESULT 61
 AAD32590/c
 ID AAD32590 standard; DNA; 23 BP.
 XX AAD32590;
 AC AAD32590;
 XX 18-JUN-2002 (first entry)
 DE ace2elc PCR primer for SSCP analysis of human ACE-2 DNA.
 KW Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
 KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
 KW myocardial infarction; heart failure; arrhythmia; renal failure;
 KW inflammation; fertility; enzyme; PCR; primer; ss.
 OS Homo sapiens.
 XX WO200212471-A2.
 PD 14-FEB-2002.
 PF 09-AUG-2001; 2001WO-US025059.
 PR 09-AUG-2000; 2000US-00635501.
 XX (MILL-) MILLENNIUM PHARM INC.
 PI Acton S, Robison KE, Hsieh FY;
 DR WPI; 2002-257481/30.
 Isolated human polypeptide, known as angiotensin converting enzyme-2,
 useful for treating or preventing the development of an abnormal blood
 pressure or related diseases, e.g. hypertension, heart failure or
 myocardial infarction.
 XX Example 10; Page 114; 218pp; English.
 CC The invention relates to human angiotensin converting enzyme-2 (ACE-2)
 CC polypeptides and polynucleotides. ACE-2 is also known as peptidyl
 CC dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
 CC treating or preventing the development of abnormal blood pressure and
 CC diseases or disorders associated with the protein in a subject. The
 CC diseases include hypertension, hypotension, congestive heart failure,
 CC chronic heart failure, acute heart failure, myocardial infarction,
 CC atherosclerosis, arrhythmia and renal failure. They are also useful for
 CC treating inflammatory conditions and diseases relating to fertility. The
 CC present sequence is a PCR primer used in single strand conformation
 CC polymorphism (SSCP) analysis of human ACE-2 DNA
 XX Sequence 23 BP; 2 A; 6 C; 6 G; 9 T; 0 U; 0 Other;
 Query Match 0.7%; Score 23; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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PD 06-APR-2000.
XX
XX PF 29-SEP-1999; 99WO-US022976.
XX
XX PR 30-SEP-1998; 98US-00163648.
XX
XX PA (MILL-) MILLENNIUM PHARM INC.
XX
XX PI Acton LS, Robison KE, Hsieh FY;
XX
XX PS WPI; 2000-293140/25.
XX
XX PT Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
XX PT polypeptide useful for detecting an ACE-2 therapeutic for treating
XX PT hypertension, congestive heart failure, myocardial infarction,
XX PT atherosclerosis and renal failure.
XX
XX PS Example; Page 107; 138pp; English.
XX
XX CC AAA12738-39 represent nucleotide sequences containing a A to G
XX CC polymorphism in intron 17 of human angiotensin converting enzyme-2 (ACE-
XX CC 2). AAA12739 represents the variant sequence, with position 13
XX CC representing the polymorphism. ACE-2 is expressed predominantly in
XX CC kidneys and testis. The sequence of the full length ACE-2 cDNA was
XX CC determined from a clone obtained from a cDNA library prepared from mRNA
XX CC of a human heart of a subject who had congestive heart failure. ACE-2 has
XX CC significant sequence homologies with ACE enzymes, and has also been shown
XX CC to hydrolyse angiotensin I into Ang. (1-9). The ACE-2 therapeutics are
XX CC used to treat blood pressure related diseases and conditions, such as
XX CC hypertension, congestive heart failure, chronic heart failure, acute
XX CC heart failure, myocardial infarction, atherosclerosis and renal failure
XX
XX SQ Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
      Query Match      0.7%; Score 22.4; DB 1; Length 24;
      Best Local Similarity 95.8%; Pred. No. 60;
      Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2249 CGTCTGAATGACACAGCCTAGAG 2272
Db 1 CGTCTGAATGACGACGCTAGAG 24

RESULT 65
AAD32651
ID AAD32651 standard; DNA; 24 BP.
XX
XX AC AAD32651;
XX
XX DT 18-JUN-2002 (first entry)
XX
XX DE Human ACE-2 exon 17 DNA fragment polymorphic variant.
XX
XX KW Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
XX KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
XX KW myocardial infarction; heart failure; arrhythmia; renal failure;
XX KW inflammation; fertility; enzyme; exon 17; polymorphism; ds.
XX
XX OS Homo sapiens.
XX
XX PH Key Location/Qualifiers
XX FT variation replace(13, A)
XX FT /*tag= a
XX
XX PN WO200212471-A2.
XX
XX PD 14-FEB-2002.
XX
XX PF 09-AUG-2001; 2001WO-US025059.
XX
XX PR 09-AUG-2000; 2000US-00635501.
XX
XX PA (MILL-) MILLENNIUM PHARM INC.

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XX
XX PI Acton S, Robison KE, Hsieh FY;
XX
XX DR WPI; 2002-257481/30.
XX
XX PT Isolated human polypeptide, known as angiotensin converting enzyme-2,
XX PT useful for treating or preventing the development of an abnormal blood
XX PT pressure or related diseases, e.g. hypertension, heart failure or
XX PT myocardial infarction.
XX
XX PS Example 10; Page 116; 218pp; English.
XX
XX CC The invention relates to human angiotensin converting enzyme-2 (ACE-2)
XX CC polypeptides and polynucleotides. ACE-2 is also known as peptidyl
XX CC dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
XX CC treating or preventing the development of abnormal blood pressure and
XX CC diseases or disorders associated with the protein in a subject. The
XX CC diseases include hypertension, hypotension, congestive heart failure,
XX CC chronic heart failure, acute heart failure, myocardial infarction,
XX CC atherosclerosis, arrhythmia and renal failure. They are also useful for
XX CC treating inflammatory conditions and diseases relating to fertility. The
XX CC present sequence is human ACE-2 exon 17 fragment polymorphic variant
XX
XX SQ Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
      Query Match      0.7%; Score 22.4; DB 1; Length 24;
      Best Local Similarity 95.8%; Pred. No. 60;
      Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2249 CGTCTGAATGACACAGCCTAGAG 2272
Db 1 CGTCTGAATGACGACGCTAGAG 24

RESULT 66
AAA12767
ID AAA12767 standard; DNA; 21 BP.
XX
XX AC AAA12767;
XX
XX DT 25-JUL-2000 (first entry)
XX
XX DE PCR primer ace2elb used in SSCP analysis of human ACE-2.
XX
XX KW Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang. (1-9);
XX KW blood pressure; hypertension; congestive heart failure; atherosclerosis;
XX KW chronic heart failure; acute heart failure; myocardial infarction;
XX KW renal failure; PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO2000018899-A2.
XX
XX PD 06-APR-2000.
XX
XX PF 29-SEP-1999; 99WO-US022976.
XX
XX PR 30-SEP-1998; 98US-00163648.
XX
XX PA (MILL-) MILLENNIUM PHARM INC.
XX
XX PI Acton LS, Robison KE, Hsieh FY;
XX
XX DR WPI; 2000-293140/25.
XX
XX PT Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
XX PT polypeptide useful for detecting an ACE-2 therapeutic for treating
XX PT hypertension, congestive heart failure, myocardial infarction,
XX PT atherosclerosis and renal failure.
XX
XX PS Example; Page 105; 138pp; English.
XX
XX CC PCR primers AAA12766-A12821 were used for single strand conformation

```


CC polymorphism (SSCP) analysis of human angiotensin converting enzyme-2
 CC (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
 CC sequence of the full length ACE-2 cDNA was determined from a clone
 CC obtained from a cDNA library prepared from mRNA of a human heart of a
 CC subject who had congestive heart failure. ACE-2 has significant sequence
 CC homologies with ACE enzymes, and has also been shown to hydrolyse
 CC angiotensin I into Ang (1-9). The ACE-2 therapeutics are used to treat
 CC blood pressure related diseases and conditions, such as hypertension,
 CC congestive heart failure, chronic heart failure, acute heart failure,
 CC myocardial infarction, atherosclerosis and renal failure
 XX
 SQ Sequence 21 BP; 1 A; 9 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 TCTTCTGGCTCCTTCTCAGC 133
 |||||
 DB 1 TCTTCTGGCTCCTTCTCAGC 21

RESULT 67
 AAD32589
 ID AAD32589 standard; DNA; 21 BP.
 XX
 AC AAD32589;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE ace2elb PCR primer for SSCP analysis of human ACE-2 DNA.
 XX
 KW Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
 KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
 KW myocardial infarction; heart failure; arrhythmia; renal failure;
 KW inflammation; fertility; enzyme; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200212471-A2.
 XX
 PD 14-FEB-2002.
 XX
 PF 09-AUG-2001; 2001WO-US025059.
 XX
 XX 09-AUG-2000; 2000US-00635501.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 XX
 XX Acton S, Robison KE, Hsieh FY;
 XX WPI; 2002-257481/30.
 DR
 PT Isolated human polypeptide, known as angiotensin converting enzyme-2,
 PT useful for treating or preventing the development of an abnormal blood
 PT pressure or related diseases, e.g. hypertension, heart failure or
 PT myocardial infarction.
 XX
 PS Example 10; Page 114; 218pp; English.
 XX
 CC The invention relates to human angiotensin converting enzyme-2 (ACE-2)
 CC polypeptides and polynucleotides. ACE-2 is also known as peptidyl
 CC dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
 CC treating or preventing the development of abnormal blood pressure and
 CC diseases or disorders associated with the protein in a subject. The
 CC diseases include hypertension, hypotension, congestive heart failure,
 CC chronic heart failure, acute heart failure, myocardial infarction,
 CC atherosclerosis, arrhythmia and renal failure. They are also useful for
 CC treating inflammatory conditions and diseases relating to fertility. The
 CC present sequence is a PCR primer used in single strand conformation
 CC polymorphism (SSCP) analysis of human ACE-2 DNA
 XX
 SQ Sequence 21 BP; 1 A; 9 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 TCTTCTGGCTCCTTCTCAGC 133
 |||||
 DB 1 TCTTCTGGCTCCTTCTCAGC 21

RESULT 68
 ABN13755/c
 ID ABN13755 standard; DNA; 25 BP.
 XX
 AC ABN13755;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13747.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 XX (AEOM-) AEOMICA INC.
 XX
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon MB;
 XX WPI; 2002-179446/23.
 DR
 PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
 XX
 PS Disclosure; SEQ ID NO 13747; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
 CC nucleic acids can be used as probes to detect, characterize and quantify
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1

CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMIP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMIP-1, in particular heart
 CC and skeletal muscle disorders. hGDMIP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMIP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 25 BP; 4 A; 7 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 20.2; DB 1; Length 25;
 Best Local Similarity 88.0%; Pred. No. 1.1e+02;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2213 ATCAGGATGTCGGAGCCGGATCA 2237
 DB 25 ATCAGGCTGTCCGAGCCGGATCA 1
 ||||| ||||| ||||| ||||| |||||

RESULT 69
 AA12769
 ID AA12769 standard; DNA; 22 BP.

XX
 AC AA12769;
 DT 25-JUL-2000 (first entry)

DE PCR primer ace2eld used in SSCP analysis of human ACE-2.

XX Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang. (1-9);
 KW blood pressure; hypertension; congestive heart failure; atherosclerosis;
 KW chronic heart failure; acute heart failure; myocardial infarction;
 KW renal failure; PCR primer; ss.

XX Homo sapiens.

XX WO200018899-A2.

XX 06-APR-2000.

XX 29-SEP-1999; 99WO-US022976.

XX 30-SEP-1998; 98US-00163648.

XX (MILL-) MILLENNIUM PHARM INC.

XX Acton LS, Robison KE, Haieh FY;

XX WPI; 2000-293140/25.

XX Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)
 PT polypeptide useful for detecting an ACE-2 therapeutic for treating
 PT hypertension, congestive heart failure, myocardial infarction,
 PT atherosclerosis and renal failure.

XX Example; Page 105; 138pp; English.

XX PCR primers AA12766-A12821 were used for single strand conformation
 CC polymorphism (SSCP) analysis of human angiotensin converting enzyme-2
 CC (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The
 CC sequence of the full length ACE-2 cDNA was determined from a clone
 CC obtained from a cDNA library prepared from mRNA of a human heart of a
 CC subject who had congestive heart failure. ACE-2 has significant sequence
 CC homologies with ACE enzymes, and has also been shown to hydrolyse
 CC angiotensin I into Ang. (1-9). The ACE-2 therapeutics are used to treat
 CC blood pressure related diseases and conditions, such as hypertension,
 CC congestive heart failure, chronic heart failure, acute heart failure,
 CC myocardial infarction, atherosclerosis and renal failure

XX Sequence 22 BP; 8 A; 8 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 20; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCCAACCCAGTTCAAAG 20
 DB 3 CGCCCAACCCAGTTCAAAG 22
 ||||| ||||| ||||| |||||

RESULT 70

AA32591

ID AAD32591 standard; DNA; 22 BP.

XX
 AC AAD32591;

DT 18-JUN-2002 (first entry)

DE ace2eld PCR primer for SSCP analysis of human ACE-2 DNA.

XX Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension;
 KW peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis;
 KW myocardial infarction; heart failure; arrhythmia; renal failure;
 KW inflammation; fertility; enzyme; PCR; primer; ss.

XX Homo sapiens.

XX WO200212471-A2.

XX 14-FEB-2002.

XX 09-AUG-2001; 2001WO-US025059.

XX 09-AUG-2000; 2000US-00635501.

XX (MILL-) MILLENNIUM PHARM INC.

XX Acton S, Robison KE, Haieh FY;

XX WPI; 2002-257481/30.

XX Isolated human polypeptide, known as angiotensin converting enzyme-2,
 PT useful for treating or preventing the development of an abnormal blood
 PT pressure or related diseases, e.g. hypertension, heart failure or
 PT myocardial infarction.

XX Example 10; Page 114; 218pp; English.

XX The invention relates to human angiotensin converting enzyme-2 (ACE-2)
 CC polypeptides and polynucleotides. ACE-2 is also known as peptidyl
 CC dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for
 CC treating or preventing the development of abnormal blood pressure and
 CC diseases or disorders associated with the protein in a subject. The
 CC diseases include hypertension, hypotension, congestive heart failure,
 CC chronic heart failure, acute heart failure, myocardial infarction,
 CC atherosclerosis, arrhythmia and renal failure. They are also useful for
 CC treating inflammatory conditions and diseases relating to fertility. The
 CC present sequence is a PCR primer used in single strand conformation
 CC polymorphism (SSCP) analysis of human ACE-2 DNA

XX Sequence 22 BP; 8 A; 8 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 20; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCCCAACCCAGTTCAAAG 20
 DB 3 CGCCCAACCCAGTTCAAAG 22
 ||||| ||||| ||||| |||||

RESULT 71

AAQ57377

ID AAQ57377 standard; mRNA; 23 BP.

```

XX AC AAQ57377;
XX DT 25-MAR-2003 (revised)
XX DT 26-JUL-1994 (first entry)
XX DE Enzymatic RNA molecule ACE mRNA target sequence.
XX DE Specific; cleavage; target RNA; protein; prophylaxis; expression;
XX KW inhibitor; inhibition; ribozyme; treatment; prevention; psoriasis;
XX KW asthma; inflammatory diseases; cardiovascular condition; hypertension;
XX KW arthritis; restenosis; angiotensin converting enzyme; ss.
XX OS Synthetic.
XX PN WO9402595-A1.
XX PD 03-FEB-1994.
XX PF 02-JUL-1993; 93WO-US006316.
XX PR 17-JUL-1992; 92US-00916763.
XX PR 07-DEC-1992; 92US-00987132.
XX PR 07-DEC-1992; 92US-00989848.
XX PR 07-DEC-1992; 92US-00989849.
XX PR 19-JAN-1993; 93US-00008895.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Sullivan SM, Draper KG;
XX DR WPI; 1994-048853/06.
XX PT Enzymatic RNA molecules which cleave mRNA - used to treat or prevent
XX PT inflammatory, arthritic, stenotic or cardiovascular diseases or
XX PT conditions.
XX PS Claim 3; Page 23; 65pp; English.
XX CC This is a ACE mRNA target sequence (nucleotide no. 1749) of an enzymatic
XX CC RNA molecule (ribozyme) which cleaves mRNA associated with the
XX CC development or maintenance of a cardiovascular condition. The concn. of
XX CC the ribozyme necessary to effect a therapeutic treatment is lower than
XX CC that of an antisense oligonucleotide and the specificity of action is
XX CC higher. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 23 BP; 5 A; 9 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 1e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1713 GCCTCTGCACAAATGTGACATC 1735
DB 1 GCCCCTGCACAAATGTGACATC 23

RESULT 72
ABK52626/c
ID ABK52626 standard; DNA; 28 BP.
XX AC ABK52626;
XX DT 27-AUG-2002 (first entry)
XX DE Minority genome method VIH-MUT-12 DNA sequence.
XX KW Minority genome method; viral quasi-species; majority genome;
XX KW genetic diagnosis; viral infection; human immune deficiency virus;
XX KW hepatitis B; hepatitis C; antiviral therapy; ss.
XX OS Unidentified.
XX

key Location/Qualifiers
misc_difference 1
FT FT /*tag= a
FT FT /label= unknown
FT FT /note= "C6 aminolinker sequence"
XX WO200183815-A1.
XX PN PN
XX PD 08-NOV-2001.
XX PF 27-APR-2001; 2001WO-ES000165.
XX PR 27-APR-2000; 2000ES-00001068.
XX PA (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
XX PI Arias Eteban A, Baranowski E, Briones Llorente C;
XX PI Domingo Solans E, Escarmis Homs C, Gomez Castilla J;
XX PI Martin Ruiz- Jarabo C, Parro Garcia V;
XX DR WPI; 2002-147445/19.
XX PT Detecting minority genomes in viral quasi-species, useful for identifying
XX PT mutants responsible for drug resistance and to individualize therapy.
XX PS Example 2; Page 55; 107pp; Spanish.
XX CC The present invention relates to a new method for detecting minority
XX CC genomes, present at less than 50%, in a population of nucleic acids of a
XX CC viral quasi-species and having at least one mutation with respect to the
XX CC majority genome. The invention can be used for genetic diagnosis of viral
XX CC infections, especially human immune deficiency virus and hepatitis B or
XX CC C, particularly to detect memory minority genomes that are implicated in
XX CC failure of antiviral therapy, so the method may make possible design of
XX CC therapies customised for individual patients. The present nucleic acid
XX CC sequence represents the VIH-MUT-12 DNA sequence that was used in the
XX CC methods of the invention
XX SQ Sequence 28 BP; 3 A; 1 C; 4 G; 19 T; 0 U; 1 Other;

Query Match 0.6%; Score 19.8; DB 1; Length 28;
Best Local Similarity 91.3%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3383 TTTCACACTCTCAAAAAAAAAA 3405
DB 25 TTTCACACAAAAAAAAAAAAA 3

RESULT 73
ABN13756/c
ID ABN13756 standard; DNA; 25 BP.
XX AC ABN13756;
XX DT 29-MAY-2002 (first entry)
XX DE Human GDMPL-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13748.
XX KW Human; genome-derived myosin-like protein 1; GDMPL-1; hGDMPL-1; heart;
XX KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX KW skeletal muscle disorder; amplicon; screening; ss.
XX OS Homo sapiens.
XX PN WO200192524-A2.
XX PD 06-DEC-2001.
XX PF 25-MAY-2001; 2001WO-US016981.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 21-SEP-2000; 2000US-0234687P.

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Query Match 0.5%; Score 18.4; DB 1; Length 25;
Best Local Similarity 95.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3386 ACACACTCAAAAAAAAAA 3405
DB 20 ACGCACTCAAAAAAAAAA 1

RESULT 77
ABN13757/c
ID ABN13757 standard; DNA; 25 BP.
XX
AC ABN13757;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13749.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
FN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 13749; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1

polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
disorder associated with the expression of hGDMLP-1, in particular heart
and skeletal muscle disorders. hGDMLP-1 is localized to chromosome 22.
The present sequence represents an oligomer used in the screening of the
hGDMLP-1 sequence in the exemplification of the present invention. N.B.
The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequence

Sequence 25 BP; 5 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
Query Match 0.5%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2213 ATCAGGATGTCGGAGCGGAT 2235
DB 23 ATCAGGCTGTCGGAGCGGAT 1

RESULT 78
ABN13753/c
ID ABN13753 standard; DNA; 25 BP.
XX
AC ABN13753;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13745.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
FN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 13745; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1


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XX 12-NOV-2002.
XX
XX 26-FEB-2002; 2002JP-00049656.
XX
XX 27-FEB-2001; 2001JP-00052647.
XX
XX (TOHO ) UNIV TOHOKU.
XX
XX WPI; 2003-367143/35.
XX
XX New polypeptide having transporter activity and a gene encoding the
XX polypeptide which is useful as a probe for finding other homologous
XX genes.
XX
XX Example 1; Page 5; 18pp; Japanese.
XX
XX The present invention describes a protein (I) having transporter
XX activity. A gene encoding (I) can be used as a probe for finding a
XX homologous gene encoding another transporter protein. The present
XX sequence represents a PCR primer for mouse MGT transporter protein, which
XX is used in an example from the present invention
XX
XX Sequence 24 BP; 3 A; 6 C; 3 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 0.5%; Score 17.8; DB 1; Length 24;
XX Best Local Similarity 90.5%; Pred. No. 1.6e+02;
XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 664 AAATGAGATGGCAGAGCAAA 684
XX ||||| ||||| ||||| |||||
XX Db 21 AAATAAGATGTCAAGAGCAAA 1
XX
XX RESULT 81
XX AAC96708/c
XX ID AAC96708 standard; DNA; 25 BP.
XX
XX AC AAC96708;
XX
XX DT 26-FEB-2001 (first entry)
XX
XX DE HLA HLA-A gene PCR primer #85.
XX
XX DNA sequence analysis; sequencing; protein sequence; protein structure;
XX gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
XX human leukocyte antigen; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200065088-A2.
XX
XX 02-NOV-2000.
XX
XX 20-APR-2000; 2000WO-EP003636.
XX
XX 26-APR-1999; 99EP-00303215.
XX
XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
XX Ulfendahl P, Wong K;
XX
XX Identifying extendible primers for use in identification, or
XX classification of a nucleic acid of an organism, allele or gene such as
XX gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
XX human leukocyte antigen; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200065088-A2.
XX
XX 02-NOV-2000.
XX
XX 20-APR-2000; 2000WO-EP003636.
XX
XX 26-APR-1999; 99EP-00303215.
XX
XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
XX Ulfendahl P, Wong K;
XX
XX WPI; 2000-679677/66.
XX
XX Identifying extendible primers for use in identification, or
XX classification of a nucleic acid of an organism, allele or gene such as
XX class 1/2 HLA comprises identifying all possible nucleotide sequences of
XX specific length.
XX
XX Claim 14; Page 56; 66pp; English.
XX
XX The present invention provides a method for identifying a set of
XX extendible primers which can be used in the identification, typing and
XX

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CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
XX Sequence 25 BP; 3 A; 1 C; 6 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.5%; Score 17.8; DB 1; Length 25;
XX Best Local Similarity 90.5%; Pred. No. 1.7e+02;
XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 3385 TACACACTCAAAAAAAAAAAAA 3405
XX ||||| ||||| ||||| |||||
XX Db 21 TACATCTCTCAAAAAAAAAAAAA 1
XX
XX RESULT 82
XX AAC96023/c
XX ID AAC96023 standard; DNA; 25 BP.
XX
XX AC AAC96023;
XX
XX DT 26-FEB-2001 (first entry)
XX
XX DE HLA HLA-C gene PCR primer #35.
XX
XX DNA sequence analysis; sequencing; protein sequence; protein structure;
XX gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
XX human leukocyte antigen; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200065088-A2.
XX
XX 02-NOV-2000.
XX
XX 20-APR-2000; 2000WO-EP003636.
XX
XX 26-APR-1999; 99EP-00303215.
XX
XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
XX Ulfendahl P, Wong K;
XX
XX WPI; 2000-679677/66.
XX
XX Identifying extendible primers for use in identification, or
XX classification of a nucleic acid of an organism, allele or gene such as
XX class 1/2 HLA comprises identifying all possible nucleotide sequences of
XX specific length.
XX
XX Claim 14; Page 44; 66pp; English.
XX
XX The present invention provides a method for identifying a set of
XX extendible primers which can be used in the identification, typing and
XX classification of genes. This can then be used to predict protein
XX sequence and structure, in organ donation to match the organ with the
XX receiver, and to identify bacteria in a sample. The method can be used to
XX type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
XX particular
XX
XX Sequence 25 BP; 4 A; 1 C; 4 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 0.5%; Score 17.8; DB 1; Length 25;
XX Best Local Similarity 90.5%; Pred. No. 1.7e+02;
XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 3385 TACACACTCAAAAAAAAAAAAA 3405
XX ||||| ||||| ||||| |||||
XX Db 21 TACATATTCAAAAAAAAAAAAA 1
XX
XX RESULT 83
XX AAC96023/c
XX ID AAC96023 standard; DNA; 25 BP.
XX
XX AC AAC96023;
XX
XX DT 26-FEB-2001 (first entry)
XX
XX DE HLA HLA-C gene PCR primer #35.
XX
XX DNA sequence analysis; sequencing; protein sequence; protein structure;
XX gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
XX human leukocyte antigen; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200065088-A2.
XX
XX 02-NOV-2000.
XX
XX 20-APR-2000; 2000WO-EP003636.
XX
XX 26-APR-1999; 99EP-00303215.
XX
XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
XX Ulfendahl P, Wong K;
XX
XX WPI; 2000-679677/66.
XX
XX Identifying extendible primers for use in identification, or
XX classification of a nucleic acid of an organism, allele or gene such as
XX class 1/2 HLA comprises identifying all possible nucleotide sequences of
XX specific length.
XX
XX Claim 14; Page 44; 66pp; English.
XX
XX The present invention provides a method for identifying a set of
XX extendible primers which can be used in the identification, typing and

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RESULT 83
ACIO2723/C
ID ACIO2723 standard; DNA; 25 BP.
XX AC
XX ACIO2723;
XX AC
XX DT 13-OCT-2003 (first entry)
XX DT
XX DE Human microarray DNA oligonucleotide SEQ ID NO 2714.
XX DE
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX KW genetic variation; biallelic marker; polymorphism; human;
XX KW cross-species comparison.
XX OS
XX Homo sapiens.
XX PN
XX US2003104410-A1.
XX PD
XX 05-JUN-2003.
XX PF
XX 15-MAR-2002; 2002US-00098263.
XX PR
XX 16-MAR-2001; 2001US-0276759P.
XX PA (AFFY-) AFFYMETRIX INC.
XX PI
XX Mittmann MP;
XX DR
XX WPI; 2003-567953/53.
XX PT
XX New array of nucleic acid probes, useful for in situ hybridization, in
XX Southern, Northern or dot-blot hybridization to identify or detect the
XX sequence or specific mutations of any gene.
XX Claim 1; SEQ ID NO 2714; 9pp; English.
XX CC
XX The invention discloses a microarray comprising a plurality of nucleic
XX acid probes including one of 2,018,500 fully defined sequences, or its
XX perfect match, perfect mismatch, antisense match or antisense mismatch.
XX Also disclosed is a method of gene expression analysis. The array is used
XX in monitoring gene expression levels by hybridisation to a DNA library,
XX in analysis of genetic variation or in hybridisation of tag-labelled
XX compounds. The nucleic acid probes are specifically designed for analysis
XX of at least one target sequence. The method of analysis comprises
XX hybridising at least one or more nucleic acids to at least two or more
XX nucleic acid probes and detecting the hybridisation. The nucleic acid
XX probes are attached to a solid support. The analysis comprises monitoring
XX gene expression levels, identifying biallelic markers or polymorphisms,
XX or family members of a gene and a cross-species comparison. Each of the
XX nucleic acids further comprises a tag sequence. The array of nucleic acid
XX probes is useful in situ hybridisation, in Southern, Northern or dot-
XX blot hybridisation to identify or detect the sequence or specific
XX mutations of any gene, in mapping the 5' termini of mRNA molecules by
XX primer extensions or in screening cDNA or genomic libraries or subclones
XX for additional subclones containing segments of DNA that have been
XX isolated and previously sequenced. The sequence presented is one of the
XX nucleic acid probes incorporated in the microarray. Note: The sequence
XX data for this patent can also be obtained in electronic format directly
XX from USPTO at seqdata.uspto.gov/sequence.html
XX SQ
XX Sequence 25 BP; 10 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
XX Query Match 0.5%; Score 17.8; DB 1; Length 25;
XX Best Local Similarity 90.5%; Pred. No. 1.7e+02;
XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX QY 2018 GAAATGTACCTCTTCGATCA 2038
XX DB
XX 25 GAAATGTTCTCTTCGATCA 5
XX
XX RESULT 84
XX AAC83056
XX
XX AAC83056 standard; DNA; 24 BP.
XX AC
XX AAC83056;
XX DT 22-FEB-2001 (first entry)
XX DE
XX 5' primer for RANBP2.
XX KW
XX Primer; reverse transcription; RANBP2; ss.
XX OS
XX Synthetic.
XX PN
XX EP1050587-A2.
XX PD
XX 08-NOV-2000.
XX PF
XX 02-MAY-2000; 2000EP-00109078.
XX PR
XX 03-MAY-1999; 99US-00304452.
XX PA (QIAG-) QIAGEN GMBH.
XX PI
XX Missel A, Loeffert D, Kang J, Korfhaage C;
XX DR
XX WPI; 2001-018016/03.
XX PT
XX Composition for reverse transcription for use in medicine and forensics,
XX comprises a homopolymeric nucleic acid to prevent interference between
XX polymerases.
XX Example 1; Page 14; 24pp; English.
XX CC
XX The present invention relates to reverse transcription of RNA using a
XX homopolymeric nucleic acid and at least one of reverse transcriptase, DNA
XX polymerase, oligonucleotide primer/s, one or more nucleotides. The method
XX is used to generate cDNA from RNA templates, specifically in RT-
XX polymerase chain reaction (PCR), for various industrial, medical or
XX forensic purposes. The method is sensitive and efficient
XX SQ
XX Sequence 24 BP; 9 A; 0 C; 10 G; 5 T; 0 U; 0 Other;
XX Query Match 0.5%; Score 17.6; DB 1; Length 24;
XX Best Local Similarity 83.3%; Pred. No. 1.7e+02;
XX Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX QY 1466 ATGTTAGAGAACTGGAGGTGGATG 1489
XX DB
XX 1 ATGTTAGTGAAGAGAGAGGATG 24
XX
XX RESULT 85
XX ABI88435
XX ID ABI88435 standard; DNA; 24 BP.
XX AC
XX ABI88435;
XX DT 15-FEB-2002 (first entry)
XX DE
XX Capture oligonucleotide Zip ID#3019 oligo #2.
XX KW
XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
XX ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
XX infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
XX oncogene; tumour suppressor; human papillomavirus; forensic;
XX environmental monitoring; food industry; feed industry; ss.
XX OS
XX Synthetic.
XX PN
XX WO200179548-A2.
XX PD
XX 25-OCT-2001.
XX PR
XX 04-APR-2001; 2001WO-US010958.

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XX PR 14-APR-2000; 2000US-0197271P.
XX PA (CORR ) CORNELL RES FOUND INC.
XX PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX PT WPI; 2002-034366/04.
XX DR
XX PT Designing capture oligonucleotide probes for use on a support to which
XX PT complementary oligonucleotides hybridize with little mismatch.
XX PS Example 5; Fig 25; 300pp; English.
XX CC The present invention describes a method (M1) for designing capture
XX CC oligonucleotide probes (I) for use on a support to which complementary
XX CC oligonucleotide probes (II) will hybridise with little mismatch, where
XX CC (I) have melting temperatures within a narrow range. The method is useful
XX CC for detecting infectious diseases caused by bacterial infectious agents
XX CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
XX CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
XX CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
XX CC Epstein-Barr virus and polio virus, and parasitic infectious agents
XX CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
XX CC medinensis. The method is also useful for detecting genetic diseases such
XX CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
XX CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
XX CC involved in DNA amplification, replication, recombination or repair, the
XX CC cancer is specifically associated with a gene selected from BRCA1 gene,
XX CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
XX CC method is also used for environmental monitoring, forensics and the food
XX CC and feed industry, detecting comprises scanning (using e.g. a scanning
XX CC electron microscope and infrared microscope) the support at the
XX CC particular sites and identifying (using a computer) identified ligation to a
XX CC sets occurred and correlating (using a computer) identified ligation to a
XX CC presence or absence of the target nucleotide sequences. AB182074 to
XX CC AB197546 represent oligonucleotide sequences used in the exemplification
XX CC of the present invention
XX SQ Sequence 24 BP; 5 A; 5 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2939 GCTGCAAGGATTGAGATGGCATG 2962
DB 1 GCTGCAAGGATTGAGATGGCATG 24

RESULT 86
AB188434/c
ID AB188434 standard; DNA; 24 BP.
XX AC AB188434;
XX DT 15-FEB-2002 (first entry)
XX DE Capture oligonucleotide Zip ID#3019 oligo #1.
XX KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
XX KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
XX KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
XX KW oncogene; tumour suppressor; human papillomavirus; forensic;
XX KW environmental monitoring; food industry; feed industry; ss.
XX OS Synthetic.
XX PN WO200179548-A2.
XX PD 25-OCT-2001.
XX PF 04-APR-2001; 2001WO-US010958.
XX PR

Query Match 0.5%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2939 GCTGCAAGGATTGAGATGGCATG 2962
DB 1 GCTGCAAGGATTGAGATGGCATG 24

RESULT 87
AAC96624/c
ID AAC96624 standard; DNA; 25 BP.
XX AC AAC96624;
XX DT 26-FEB-2001 (first entry)
XX DE HLA HLA-A gene PCR primer #1.
XX KW DNA sequence analysis; sequencing; protein sequence; protein structure;
XX KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
XX KW human leukocyte antigen; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200065088-A2.
XX PD 02-NOV-2000.
XX PF 20-APR-2000; 2000WO-EP003636.
XX PR 26-APR-1999; 99EP-00303215.

```

XX PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
 XX PI Ulfendahl P, Wong K;
 XX DR WPI; 2000-679677/66.
 XX
 PT Identifying extendible primers for use in identification, or
 PT classification of a nucleic acid of an organism, allele or gene such as
 PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
 PT specific length.
 XX
 PS Claim 14; Page 54; 66pp; English.
 XX
 CC The present invention provides a method for identifying a set of
 CC extendible primers which can be used in the identification, typing and
 CC classification of genes. This can then be used to predict protein
 CC sequence and structure, in organ donation to match the organ with the
 CC receiver, and to identify bacteria in a sample. The method can be used to
 CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
 CC particular
 XX
 SQ Sequence 25 BP; 2 A; 2 C; 4 G; 17 T; 0 U; 0 Other;
 XX
 XX Query Match 0.5%; Score 17.6; DB 1; Length 25;
 XX Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 XX Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 XX
 QY 3382 ATTACACACTCAAAAAAAAAA 3405
 DB 25 ACTCAGACTGAAAAAAAAA 2
 XX
 RESULT 89
 AAC95821/c
 ID AAC95821 standard; DNA; 25 BP.
 AC AAC95821;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE HLA HLA-A gene PCR primer #1.
 XX
 KW DNA sequence analysis; sequencing; protein sequence; protein structure;
 KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
 KW human leukocyte antigen; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200065088-A2.
 XX
 PD 02-NOV-2000.
 XX
 PF 20-APR-2000; 2000WO-EP003636.
 XX
 PR 26-APR-1999; 99EP-00303215.
 XX
 PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
 XX
 PI Ulfendahl P, Wong K;
 XX
 DR WPI; 2000-679677/66.
 XX
 PT Identifying extendible primers for use in identification, or
 PT classification of a nucleic acid of an organism, allele or gene such as
 PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
 PT specific length.
 XX
 PS Claim 14; Page 40; 66pp; English.
 XX
 CC The present invention provides a method for identifying a set of
 CC extendible primers which can be used in the identification, typing and
 CC classification of genes. This can then be used to predict protein

CC sequence and structure, in organ donation to match the organ with the
 CC receiver, and to identify bacteria in a sample. The method can be used to
 CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
 CC particular
 XX
 SQ Sequence 25 BP; 2 A; 2 C; 4 G; 17 T; 0 U; 0 Other;
 XX
 XX Query Match 0.5%; Score 17.6; DB 1; Length 25;
 XX Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 XX Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 XX
 QY 3382 ATTACACACTCAAAAAAAAAA 3405
 DB 25 ACTCAGACTGAAAAAAAAA 2
 XX
 RESULT 89
 ABN15246/c
 ID ABN15246 standard; DNA; 25 BP.
 XX
 AC ABN15246;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:15238.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX
 DR WPI; 2002-179446/23.
 XX
 PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX
 PS Disclosure; SEQ ID NO 15238; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for

CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence

XX Sequence 25 BP; 7 A; 7 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 17.6; DB 1; Length 25;

Best Local Similarity 83.3%; Pred. No. 1.8e+02; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 391 GCTGCAGGCTCTTCAGCAAAATGG 414

DB 24 GCTCCGGGCTCTTCTTCAAAATGG 1

RESULT 90

ABN15245/c

ID ABN15245 standard; DNA; 25 BP.

XX

AC ABN15245;

XX

29-MAY-2002 (first entry)

XX

Human GDMPLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:15237.

XX

Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;

KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;

KW skeletal muscle disorder; amplicon; screening; BS.

XX

OS Homo sapiens.

XX

WO200192524-A2.

XX

06-DEC-2001.

XX

25-MAY-2001; 2001WO-US016981.

XX

26-MAY-2000; 2000US-0207456P.

XX

21-SEP-2000; 2000US-0234687P.

XX

27-SEP-2000; 2000US-0236359P.

XX

04-OCT-2000; 2000GB-00024263.

XX

30-JAN-2001; 2001WO-US000661.

XX

30-JAN-2001; 2001WO-US000662.

XX

30-JAN-2001; 2001WO-US000663.

XX

30-JAN-2001; 2001WO-US000664.

XX

30-JAN-2001; 2001WO-US000665.

XX

30-JAN-2001; 2001WO-US000666.

XX

30-JAN-2001; 2001WO-US000667.

XX

30-JAN-2001; 2001WO-US000668.

XX

30-JAN-2001; 2001WO-US000669.

XX

30-JAN-2001; 2001WO-US000670.

XX

05-FEB-2001; 2001US-0266860P.

XX

XX

PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.

XX

PS Disclosure; SEQ ID NO 15237; 214pp; English.

XX

CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence

XX Sequence 25 BP; 8 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 17.6; DB 1; Length 25;

Best Local Similarity 83.3%; Pred. No. 1.8e+02;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 391 GCTGCAGGCTCTTCAGCAAAATGG 414

DB 25 GCTCCGGGCTCTTCTTCAAAATGG 2

RESULT 91

ACK22080/c

ID ACK22080 standard; DNA; 25 BP.

XX

ACK22080;

XX

14-OCT-2003 (first entry)

XX

Human microarray DNA oligonucleotide SEQ ID NO 122061.

XX

EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.

XX

OS Homo sapiens.

XX

US2003104410-A1.

XX

05-JUN-2003.

XX

15-MAR-2002; 2002US-00098263.

XX

16-MAR-2001; 2001US-0276759P.

XX

(AFFY-) AFFYMETRIX INC.

XX

Mittmann MP;

XX

WPI; 2003-567953/53.

XX

New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.

XX

Claim 1; SEQ ID NO 122061; 9pp; English.

PS

New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 or as specific biomolecule capture probes for surface-enhanced laser

XX The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying allelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USFTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 10 A; 4 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 17.6; DB 1; Length 25;

Best Local Similarity 83.3%; Pred. No. 1.8e-02;

Matches 20; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 531 TACTTGAACACCGTTTGAATGAAA 554

Db 24 TACTTGAACCTGTTTACTTAAA 1

RESULT 92

ABS60430/c

ID ABS60430 standard; DNA; 19 BP.

AC ABS60430;

DT 05-NOV-2002 (first entry)

XX Human DNA representing a single nucleotide polymorphism #181.

XX Aminopeptidase P; XNPEP2; bradykinin receptor B1; ds; SNP; BDKRB1;
 KW tachykinin receptor B1; TACKR1; C1 esterase inhibitor; C1NH; kallikrein 1;
 KW KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
 KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; PI4;
 KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
 KW cardiovascular disease; angina pectoris; hypertension; heart failure;
 KW myocardial infarction; ventricular hypertrophy; vascular disease;
 KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
 KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;
 KW autoimmune disease; inflammatory arthritis; cancer; wound;
 KW viral infection; bacterial infection; fungal infection; COPD;
 KW Chronic obstructive pulmonary disease; enterocolitis;
 KW single-nucleotide polymorphism.

XX Homo sapiens.

XX WO200261131-A2.

XX 08-AUG-2002.

XX 03-DEC-2001; 2001WO-US047235.

XX 04-DEC-2000; 2000US-0251015P.

XX 23-JAN-2001; 2001US-0261678P.

XX 02-MAR-2001; 2001US-0273037P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

PA (TSUC/) TSUCHIHASHI Z.

PA (HUII/) HUI L.

XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Ferrone MH;

PI Swanson BN, Powell JR;

XX WPI; 2002-619265/66.

XX New isolated nucleic acid with at least one polymorphic position, useful
 PT for detecting, diagnosing and treating disorders such as angioedema,
 PT cancer, viral, bacterial or fungal infection, cardiovascular and
 PT autoimmune diseases.

PS Disclosure; Page 785; 977pp; English.

XX The invention relates to an isolated nucleic acid from a human gene
 CC encoding aminopeptidase P (XNPEP2), bradykinin receptor B1 (BDKRB1),
 CC tachykinin receptor B1 (TACKR1), C1 esterase inhibitor (C1NH), kallikrein
 CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
 CC 2 (ACE2) or protease inhibitor 4 (PI4), comprising at least one
 CC polymorphic position. Also included are (1) a probe that hybridises to a
 CC polymorphic position as provided in the detailed summary of single
 CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
 CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising
 CC obtaining the sample from one or more individuals and determining the
 CC nucleic acid sequence at one or more polymorphic positions in a gene
 CC encoding a protein selected from the group above; (3) constructing (M2)
 CC haplotypes using the genes comprising grouping at least two nucleic acids
 CC ; (4) identifying (M3) an individual at risk of developing a disorder
 CC upon administration of an ACE inhibitor and/or vasoconstrictor inhibitor
 CC using the polymorphic data; (5) a library of nucleic acids, each of which
 CC comprises one or more polymorphic positions within a gene encoding a
 CC human protein selected from the group above; and (6) genotyping (M4) an
 CC individual comprising obtaining a nucleic acid sample, determining the
 CC nucleotide present in at least one polymorphic position, and comparing at
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
 CC and compositions are useful for detecting, diagnosing, treating
 CC preventing various disorders such as angioedema and diseases which
 CC involve angiogenesis like haemangiomas, tumours, sarcomas, Crohn's
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,
 CC hypertension, heart failure, myocardial infarction, ventricular
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
 CC artery disease, arteriosclerosis and/or atherosclerosis, and
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other
 CC diseases and disorders are listed in the specification). The
 CC polynucleotides are also useful for chromosome identification. Antibodies
 CC against the proteins may be utilised for immunophenotyping of cell lines
 CC and biological samples. The present sequence represents or contains the
 CC region surrounding a single-nucleotide polymorphism in one of the genes
 CC encoding one of the proteins listed above

XX Sequence 19 BP; 5 A; 3 C; 4 G; 7 T; 0 U; 0 Other;

Query Match

Best Local Similarity 0.5%; Score 17.4; DB 1; Length 19;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2164 ACCTAAAAATGTGCTGTGAT 2182

Db 19 ACCTAAAAACGTGCTGTGAT 1

RESULT 93

AAD10927

ID AAD10927 standard; DNA; 23 BP.

XX AAD10927;

XX 24-SEP-2001 (first entry)

XX Escherichia coli SSR loci, ycgW amplifying forward PCR primer.

XX Prokaryotic classification; typing; simple sequence repeat; SSR;
 KW research; food safety; PCR primer; ss.
 XX Escherichia coli.
 OS WO200148241-A1.
 PN 05-JUL-2001.
 XX 26-DEC-2000; 2000WO-11000861.
 XX 27-DEC-1999; 99US-00472035.
 XX (TECR) TECHNION RES & DEV FOUND LTD.
 PA Kashi Y, Gur-Arie R, Cohen C, Eitan Y, Shelef L, Hallerman E;
 PI WPI; 2001-418296/44.
 DR Classification and typing of prokaryotes, e.g. Escherichia coli, by
 XX characterizing hyperpolymorphic simple sequence repeats in prokaryote
 PT genomes and classifying based on the characterization of the sequence
 PT repeat.
 XX Example; Page 33; 87pp; English.
 PS The invention relates to a method of classifying or typing a prokaryote
 XX to a class or a type. The method involves characterising at least one
 CC hyperpolymorphic mono or dinucleotide simple sequence repeat (SSR) locus
 CC in a genome of the prokaryote and based on a characterisation of the
 CC hyperpolymorphic SSR, classifying or typing the prokaryote to a class or
 CC a type. This method provides an effective, readily implementable, rapid
 CC and accurate tool for classifying or typing a prokaryote to a class or a
 CC type. The method is useful for classifying or typing prokaryotes of the
 CC genera Escherichia, Aquifex, Treponema, Bacillus, Listeria, and
 CC Mycobacterium, such as E. coli, A. aeolicus, T. pallidum, B. subtilis, L.
 CC monocytophaga and M. tuberculosis and also Haemophilus, Mycoplasma,
 CC Helicobacter, Methanococcus, Archaeoglobus and Synechocystis, such as H.
 CC influenzae, M. pneumoniae, H. pylori, M. jannaschii, A. fulgidus and
 CC Synechocystis sp. PCC6803. Classifying or typing of a prokaryote is
 CC useful in research, medical and food safety diagnostics. The present
 CC sequence is a primer used to amplify E. coli SSR loci
 XX
 SQ Sequence 23 BP; 7 A; 2 C; 4 G; 10 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17.2; DB 1; Length 23;
 Best Local Similarity 86.4%; Pred. No. 1.7e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2751 GATTTTCATATAGATATATTA 2772
 DB 1 GATTTTCATATAGATATATTA 22
 RESULT 94
 AAH76956/c
 ID AAH76956 standard; DNA; 24 BP.
 XX AAH76956;
 AC
 XX 15-DEC-2001 (first entry)
 DT
 XX Human ATP-dependent serine hydrolase 9 RT-PCR primer, SEQ ID NO:4.
 DE Human; ATP-dependent serine hydrolase 9; recombinant production;
 XX malignant tumour; cancer; blood disease; HIV infection;
 KW human immunodeficiency virus; immune disorder; inflammatory condition;
 KW cytosstatic; anti-HIV; antiinflammatory; immunomodulator;
 KW reverse transcription-PCR; RT-PCR primer; ss.
 XX Homo sapiens.
 OS
 XX

PN WO200175038-A2.
 XX 11-OCT-2001.
 XX 26-MAR-2001; 2001WO-CN000418.
 XX 27-MAR-2000; 2000CN-00115160.
 XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
 PA Mao Y, Xie Y;
 PI WPI; 2001-639355/73.
 DR New human ATP-dependent serine hydrolase 9 for diagnosing and treating
 XX malignant tumor, hemopathy, human immunodeficiency virus infection,
 PT immunological diseases and various inflammations.
 XX Example 2; Page 18; 33pp; Chinese.
 XX The invention relates to human ATP-dependent serine hydrolase 9
 CC (AAG66793), nucleic acids encoding it (AAH76954), and a method for the
 CC recombinant production of ATP-dependent serine hydrolase 9. The protein
 CC has a molecular weight of 9 kD. The present invention additionally
 CC discloses an antagonist of ATP-dependent serine hydrolase 9 for
 CC therapeutic use, and an antibody which specifically binds to ATP-
 CC dependent serine hydrolase 9. ATP-dependent serine hydrolase 9, and
 CC nucleotides which encode it may be used for treating a variety of
 CC diseases, such as malignant tumours, blood diseases, HIV (human
 CC immunodeficiency virus) infection, immune disorders and inflammatory
 CC conditions. The protein may also be used to screen for modulators of its
 CC activity or for peptide fingerprinting identification. The polynucleotide
 CC can be used as a primer for nucleic acid amplification reactions or as a
 CC probe for hybridisation reactions, or in producing gene chips or
 CC microarrays. Sequences AAH76955-AAH76956 represent reverse transcription-
 CC PCR (RT-PCR) primers used in an exemplification of the invention to
 CC isolate human ATP-dependent serine hydrolase 9 cDNA
 XX
 SQ Sequence 24 BP; 6 A; 2 C; 3 G; 13 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17.2; DB 1; Length 24;
 Best Local Similarity 86.4%; Pred. No. 1.9e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3362 AGACACTCAATAAATGCTAGAT 3383
 DB 24 AGACATTCATAAATACTAAT 3
 RESULT 95
 ABQ08674/c
 ID ABQ08674 standard; DNA; 24 BP.
 XX ABQ08674;
 AC
 XX 11-JUN-2002 (first entry)
 DT
 XX Oligonucleotide adapter/capture probe 8665.
 DE Oligonucleotide array; adapter sequence; probe; ss.
 KW Synthetic.
 OS
 XX WO200216649-A2.
 XX 28-FEB-2002.
 XX 27-AUG-2001; 2001WO-US026519.
 XX 25-AUG-2000; 2000US-0227948P.
 XX 29-AUG-2000; 2000US-0228854P.
 XX (ILLU-) ILLUMINA INC.
 PA

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XX Gunderson K;
XX WPI; 2002-292068/33.
XX Array comprising adapter sequences useful for immobilizing or detecting a
XX target nucleic acid sequence, has different addresses comprising
XX different specific capture probes.
XX Claim 1; Page 196; 261pp; English.
XX The invention relates to an oligonucleotide array (I) comprising at least
XX 25 different addresses (adapter sequences) with each comprising a
XX different capture probe selected from a group consisting of the sequences
XX given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
XX nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
XX ABQ13409) to a target nucleic acid to form a modified target nucleic acid
XX and contacting the modified target nucleic acid with (I). The steps of
XX above method is useful for detecting a target nucleic acid, which further
XX comprises detecting the presence of the modified target nucleic acid
XX Sequence 24 BP; 5 A; 8 C; 6 G; 5 T; 0 U; 0 Other;
XX Query Match 0.5%; Score 17.2; DB 1; Length 24;
XX Best Local Similarity 86.4%; Pred. No. 1.9e+02;
XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1100 CTACGGACCCAGGAATGTTTC 1121
XX 23 CTGAGGGACCCAGGAGATGTTTC 2
XX
XX RESULT 96
XX ABQ02379/c
XX ID ABQ02379 standard; DNA; 24 BP.
XX AC ABQ02379;
XX XX
XX DT 11-JUN-2002 (first entry)
XX XX
XX DE Oligonucleotide adapter/capture probe 2370.
XX XX
XX KW Oligonucleotide array; adapter sequence; probe; ss.
XX XX
XX OS Synthetic.
XX XX
XX PN WO200216649-A2.
XX XX
XX PD 28-FEB-2002.
XX XX
XX PF 27-AUG-2001; 2001WO-US026519.
XX XX
XX PR 25-AUG-2000; 2000US-0227948P.
XX PR 29-AUG-2000; 2000US-0228854P.
XX XX
XX PA (ILLU-) ILLUMINA INC.
XX XX
XX PI Gunderson K;
XX XX
XX DR WPI; 2002-292068/33.
XX XX
XX PT Array comprising adapter sequences useful for immobilizing or detecting a
XX target nucleic acid sequence, has different addresses comprising
XX different specific capture probes.
XX Claim 1; Page 100; 261pp; English.
XX The invention relates to an oligonucleotide array (I) comprising at least
XX 25 different addresses (adapter sequences) with each comprising a
XX different capture probe selected from a group consisting of the sequences
XX given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
XX nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
XX ABQ13409) to a target nucleic acid to form a modified target nucleic acid
XX

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XX and contacting the modified target nucleic acid with (I). The steps of
XX above method is useful for detecting a target nucleic acid, which further
XX comprises detecting the presence of the modified target nucleic acid
XX Sequence 24 BP; 5 A; 8 C; 6 G; 5 T; 0 U; 0 Other;
XX Query Match 0.5%; Score 17.2; DB 1; Length 24;
XX Best Local Similarity 86.4%; Pred. No. 1.9e+02;
XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1100 CTACGGACCCAGGAATGTTTC 1121
XX 23 CTGAGGGACCCAGGAGATGTTTC 2
XX
XX RESULT 97
XX ABQ08715
XX ID ABQ08715 standard; DNA; 24 BP.
XX AC ABQ08715;
XX XX
XX DT 11-JUN-2002 (first entry)
XX XX
XX DE Oligonucleotide adapter/capture probe 8706.
XX XX
XX KW Oligonucleotide array; adapter sequence; probe; ss.
XX XX
XX OS Synthetic.
XX XX
XX PN WO200216649-A2.
XX XX
XX PD 28-FEB-2002.
XX XX
XX PF 27-AUG-2001; 2001WO-US026519.
XX XX
XX PR 25-AUG-2000; 2000US-0227948P.
XX PR 29-AUG-2000; 2000US-0228854P.
XX XX
XX PA (ILLU-) ILLUMINA INC.
XX XX
XX PI Gunderson K;
XX XX
XX DR WPI; 2002-292068/33.
XX XX
XX PT Array comprising adapter sequences useful for immobilizing or detecting a
XX target nucleic acid sequence, has different addresses comprising
XX different specific capture probes.
XX Claim 1; Page 196; 261pp; English.
XX The invention relates to an oligonucleotide array (I) comprising at least
XX 25 different addresses (adapter sequences) with each comprising a
XX different capture probe selected from a group consisting of the sequences
XX given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
XX nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
XX ABQ13409) to a target nucleic acid to form a modified target nucleic acid
XX and contacting the modified target nucleic acid with (I). The steps of
XX above method is useful for detecting a target nucleic acid, which further
XX comprises detecting the presence of the modified target nucleic acid
XX Sequence 24 BP; 5 A; 6 C; 8 G; 5 T; 0 U; 0 Other;
XX Query Match 0.5%; Score 17.2; DB 1; Length 24;
XX Best Local Similarity 86.4%; Pred. No. 1.9e+02;
XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1100 CTACGGACCCAGGAATGTTTC 1121
XX 2 CTGAGGGACCCAGGAGATGTTTC 23
XX
XX RESULT 98
XX ABS62652/c

```

ID ABS62652 standard; DNA; 24 BP.
XX
AC ABS62652;
XX
DT 05-NOV-2002 (first entry)
XX
DE Analyte sorting tag sequence #1124.
XX
KW Analyte sorting oligonucleotide tag; ss.
XX
OS Synthetic.
XX
PN WO200259355-A2.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-CA000089.
XX
PR 25-JAN-2001; 2001US-0263710P.
XX
PR 10-JUL-2001; 2001US-0303799P.
XX
PA (TM) TM BIOSCIENCE CORP.
XX
PI Kobler D, Fieldhouse D;
XX
PI WPI; 2002-619176/66.
XX
PT Polynucleotides comprising minimally cross-hybridizing nucleotide
PT sequences, useful as tags or tag complements for use in a wide variety of
PT research, medical or industrial applications, e.g. in diagnostic assays
PT or DNA sequencing.
XX
XX Example 2; Page 77; 120pp; English.
XX
XX The invention relates to a composition, which comprises molecules for use
XX as tags or tag complements. Each molecule comprises an oligonucleotide
XX selected from a set of oligonucleotides based on numeric identifiers
XX (numerals 1-3) corresponding to the pattern of nucleotide bases present
XX in 1168 nucleotide sequences fully defined in the specification. These
XX oligonucleotides were found to be non-cross hybridizing. The composition
XX is useful as a tag or tag complement, in analysing a biological sample
XX for the presence of a mutation or polymorphism at a locus in a nucleic
XX acid, and in determining the presence of a target suspected of being
XX contained in a mixture. Also for use in a wide variety of research,
XX medical, or industrial applications, e.g. identification of disease-
XX related polynucleotides in diagnostic assays, screening for clones of
XX novel target polynucleotides, identification of specific polynucleotide
XX in biots of mixtures of polynucleotides, therapeutic blocking of
XX inappropriately expressed genes or DNA sequencing. The polynucleotides of
XX the composition are particularly useful in methods involving highly
XX parallel processing of analytes. The use of the polynucleotides provides
XX minimal cross-hybridization or cross-talk during the sorting process.
XX Thus, any sequence within the family of sequences will not significantly
XX cross-hybridise with any other sequence derived from that family, making
XX it suitable for highly parallel processing of analytes. ABS61529-ABS62696
XX represent oligonucleotide tags of the invention
XX
SQ Sequence 24 BP; 12 A; 0 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3233 ATTCTACTCTCTCTAACTGT 3254
|||||
Db 23 ATTCTACATTTCTCTAACTTT 2

RESULT 99
ABL44835
ID ABL44835 standard; DNA; 20 BP.
XX
XX ABL44835;
AC

XX 11-APR-2002 (first entry)
DT
XX
DE Human chromosome 1p36-35 PCR primer SEQ ID NO:1879.
XX
XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; ss.
XX
XX Homo sapiens.
OS
XX JP2001321190-A.
FN
XX 20-NOV-2001.
PD
XX 12-MAR-2001; 2001JP-00068285.
XX
XX 10-MAR-2000; 2000JP-00066716.
XX
XX (RIKA) RIKAGAKU KENKYUSHO.
PA (GENO-) GENOTEX YG.
XX
XX WPI; 2002-144136/19.
DR
XX
XX Arraying genome clones.
PT
XX
XX Claim 4; Page 41; 528pp; Japanese.
XX
XX The present invention describes a method of arraying genome clones. The
CC method comprises: (a) clones of the genomic libraries contained in
CC multiwell plates numbered for discrimination are mixed in each of the
CC multiwell plates; (b) a primer designed based on the chromosome marker
CC sequence is added to the mixture to carry out an amplification reaction;
CC (c) a signal corresponding to the marker is detected from the resultant
CC amplified product to specify the discrimination Nos. of the multiwell
CC plates containing the clones having said marker sequence; (d) the order
CC of the markers is changed so that the same discrimination Nos. succeed to
CC the maximum in the specified discrimination Nos. to array the multiwell
CC plates; (e) the clones in the multiwell plates of the specified
CC discrimination Nos. are mixed respectively in each well of longitudinal
CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals
CC are detected from the amplified products; (h) the clones in the multiwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstituted as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention
XX
SQ Sequence 20 BP; 6 A; 1 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1533 GGTGGGAGATGAAGCGAGAG 1552
|||||
Db 1 GGTGGGAGATGCAGAGAGAG 20

RESULT 100
AAF96984/C
ID AAF96984 standard; DNA; 21 BP.
XX
XX AAF96984;
AC
XX 06-JUN-2001 (first entry)
DT
XX
XX Human gene single nucleotide polymorphism #1745.
XX
XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;

KW pulmonary embolism; paternity test; ds.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Variation replace(11,C)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX
 PN WO200118250-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 07-SEP-2000; 2000WO-US024503.
 XX
 PR 10-SEP-1999; 99US-0153357P.
 PR 26-JUL-2000; 2000US-0220947P.
 PR 16-AUG-2000; 2000US-0225724P.
 XX
 XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JU;
 XX
 DR WPI; 2001-226749/23.
 XX
 XX Nucleic acids comprising single nucleotide polymorphisms, useful in
 PT applications such as forensics, paternity testing, medicine, genetic
 PT analysis and phenotype correlations to diseases such as diabetes and
 PT atherosclerosis.
 XX
 XX Example; Page 164; 242pp; English.
 PS
 XX
 CC The present invention provides a method of diagnosing a vascular disease
 CC in an individual, involving determining the sequence at various
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
 CC genes. The sequences at a number of polymorphic sites are also provided
 CC in the specification. In particular, the method can be used in the
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
 CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
 CC useful in forensics, paternity testing, genetic analysis and phenotype
 CC correlations to diseases. The present sequence is an example of one of
 CC the human gene SNPs shown in the specification
 XX
 SQ Sequence 21 BP; 11 A; 2 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 0.5%; Score 16.8; DB 1; Length 21;
 Best Local Similarity 90.0%; Pred. NO. 1.6e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2373 TTGTCATCCTGATCTTCACT 2392
 Db |||||
 20 TTGTCCTTCTGATCTTCACT 1
 RESULT 101
 AAZ10714/C
 ID AAZ10714 standard; DNA; 22 BP.
 AC
 AC AAZ10714;
 XX
 XX 23-NOV-1999 (first entry)
 DT
 XX Forward PCR primer used to amplify exon 4A of human HKNG1.
 DE
 XX HKNG1; Hong Kong new gene 1; bipolar affective disorder; BAD;
 KW neuropsychiatric disorder; early-onset autosomal dominant myopia;
 KW schizophrenia; splice variant; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX

PN WO9947535-A1.
 XX
 PD 23-SEP-1999.
 XX
 PF 16-MAR-1999; 99WO-US005606.
 XX
 PR 16-MAR-1998; 98US-0078044P.
 PR 05-JUN-1998; 98US-0088312P.
 PR 28-OCT-1998; 98US-0106056P.
 PR 22-JAN-1999; 99US-00236134.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Chen H, Freimer NB;
 XX
 DR WPI; 1999-562047/47.
 XX
 XX New HKNG1 polynucleotides useful in diagnosis and treatment of
 PT neuropsychiatric disorders, e.g. bipolar affective disorders and
 PT schizophrenia.
 XX
 PS Disclosure; Page 56; 205pp; English.
 XX
 CC PCR primers AAZ10708-33 were used to amplify exons 1 to 11 of human HKNG1
 CC (Hong Kong new gene 1). HKNG1 is a gene associated with bipolar affective
 CC disorder (BAD). HKNG1 polynucleotides are useful to identify compounds
 CC modulating HKNG1 gene expression or HKNG1 polypeptide expression/
 CC activity. Compounds inhibiting or enhancing HKNG1 gene expression or
 CC activity in individuals can then be administered therapeutically to treat
 CC HKNG1-mediated disorders, especially neuropsychiatric disorders e.g. BAD,
 CC schizophrenia, or HKNG1-mediated myopia disorders, such as early-onset
 CC autosomal dominant myopia. The polynucleotides can be used in gene
 CC therapy techniques to treat such disorders. They are also useful in
 CC diagnosis to identify individuals having, or at risk of developing, HKNG1
 CC mediated disorders due to mutations in the HKNG1 gene. Such mutations
 CC especially result in the production of a protein with a different
 CC sequence to the human full-length HKNG1 polypeptide or splice variant
 CC sequences, especially the substitution of a lysine for a glutamic acid at
 CC residue 202 or 184. The polynucleotides are also useful in gene mapping,
 CC to produce probes or primers to identify similar sequences (e.g. mutants
 CC or sequences from different species) and to produce transgenic animals
 XX
 SQ Sequence 22 BP; 1 A; 2 C; 7 G; 12 T; 0 U; 0 Other;
 Query Match 0.5%; Score 16.8; DB 1; Length 22;
 Best Local Similarity 90.0%; Pred. NO. 1.8e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3356 CAAGCGACACTCAATAAA 3375
 Db |||||
 22 CACAGCAGACACACAATAAA 3
 RESULT 102
 ABK43238/C
 ID ABK43238 standard; DNA; 22 BP.
 XX
 AC ABK43238;
 XX
 XX 05-JUN-2002 (first entry)
 DT
 XX Human HKNG1 exon 4A PCR primer #1.
 DE
 XX HKNG1; ss; chromosome 18p; bipolar affective disorder; BAD; PCR; primer;
 KW severe bipolar affective (mood) disorder; BP-I; schizophrenia;
 KW Hong Kong new gene 1; antimanic; antidepressant; neuroleptic.
 XX
 OS Homo sapiens.
 OS
 XX WO200210366-A2.
 XX
 PD 07-FEB-2002.

XX 02-AUG-2001; 2001WO-US024417.
 XX PF
 XX PR 02-AUG-2000; 2000US-00631275.
 XX PR 28-NOV-2000; 2000US-00722544.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI Chen H, Freimer NB, Novak T;
 XX WPI; 2002-195962/25.
 XX DR
 XX PT New nucleic acid molecule Hong Kong New Gene 1 (HKNG1), useful for
 XX screening for molecules which modulate HKNG1 expression for the treatment
 XX of bipolar disorder and schizophrenia.
 XX PT
 XX PS Disclosure; Page 73; 367pp; English.
 XX PI
 XX CC The invention relates to an isolated nucleic acid molecule comprising a
 CC nucleotide sequence that encodes a Hong Kong New Gene (HKNG) 1 gene
 CC product. The human gene for HKNG1 is located on chromosome 18p in an area
 CC associated with bipolar affective disorder, BAD. Also included are an
 CC expression vector comprising the nucleic acid, a host cell expressing the
 CC nucleic acid, an anti-HKNG1 antibody, a method of identifying modulators
 CC of HKNG1, and identifying an individual (at risk of) having HKNG1-
 CC mediated disorder comprising detecting the presence or absence of a
 CC polymorphism that correlates with an HKNG1 allele associated with the
 CC disorder, where the presence of the polymorphism indicates that the
 CC individual (is at risk of) having HKNG1-mediated disorder. A (small
 CC molecule) compound which modulates (inhibits or potentiates) expression
 CC of a HKNG1 gene or gene product in a human individual is useful for the
 CC treatment of a HKNG1-mediated disorder such as bipolar affective disorder
 CC (BAD), severe bipolar affective (mood) disorder (BP-I) and schizophrenia.
 CC The present sequence is PCR primer which amplifies a HKNG1 exonic
 CC sequence
 XX
 XX SQ Sequence 22 BP; 1 A; 2 C; 7 G; 12 T; 0 U; 0 Other;
 Query Match 0.5%; Score 16.8; DB 1; Length 22;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3356 CAAAGCAGACACTCAATAAA 3375
 |||||
 DB 22 CACAGCAGACACACATAAA 3
 RESULT 103
 AAH18816/c
 ID AAH18816 standard; DNA; 24 BP.
 XX
 XX AC AAH18816;
 XX
 XX DT 25-JUN-2001 (first entry)
 XX
 XX DE Human IL4 gene PCR primer SEQ ID NO: 75.
 XX KW Human; interleukin-4; IL4; single nucleotide polymorphism; SNP; atopy;
 KW inflammatory disorder; immune disorder; population diversity;
 KW paternity test; forensic test; cytokine; chromosome 5q31.1; probe;
 KW PCR primer; ss.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO200123404-A1.
 XX
 XX PD 05-APR-2001.
 XX
 XX PF 28-SEP-2000; 2000WO-US026608.
 XX PR 30-SEP-1999; 99US-0156825P.
 XX

PA (GENA-) GENAISSANCE PHARM INC.
 XX Chew A, Choi JY, Denton RR, Nandabalan K, Stephens JC;
 XX WPI; 2001-316132/33.
 XX DR
 XX PT Polynucleotide comprising novel single nucleotide polymorphisms in human
 PT interleukin-4 gene for use in studying expression, function of
 PT interleukin-4, in developing drugs, diagnosis and treatment of immune
 PT disorders.
 XX
 XX XX Example 1A; Page 27; 71pp; English.
 XX
 XX CC The present invention provides the protein, cDNA and gene of human
 CC interleukin-4 (IL4). The coding sequences for this protein contain single
 CC nucleotide polymorphisms (SNPs) which may be associated with differences
 CC in susceptibility to atopy, inflammatory and immune diseases and
 CC different drug responses. They may also be used in applications such as
 CC forensic and paternity testing and studying population diversity and
 CC anthropological lineage. The IL4 gene is found on human chromosome 5q31.1
 XX
 XX SQ Sequence 24 BP; 4 A; 6 C; 6 G; 8 T; 0 U; 0 Other;
 Query Match 0.5%; Score 16.8; DB 1; Length 24;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3359 AGCAGACACTCAATAATGC 3378
 |||||
 DB 21 AGGAGGCACTCAATAATGC 2
 RESULT 104
 AAH48011/c
 ID AAH48011 standard; DNA; 24 BP.
 XX
 XX AC AAH48011;
 XX
 XX DT 17-SEP-2001 (first entry)
 XX
 XX DE Subtilisin 10 PCR primer #1.
 XX KW Subtilisin 10; anti-HIV; anti-inflammatory; immunostimulatory; cytostatic;
 KW malignant tumour; haemopathy; HIV infection; immunological disease;
 KW inflammation; PCR primer; ss.
 XX
 XX OS Unidentified.
 XX
 XX PN WO200146249-A1.
 XX
 XX PD 28-JUN-2001.
 XX
 XX PF 11-DEC-2000; 2000WO-CN000567.
 XX PR 21-DEC-1999; 99CN-00125655.
 XX
 XX (UYFU-) UNIV FUDAN.
 PA (SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD.
 XX Mao Y, Xie Y;
 XX WPI; 2001-418038/44.
 XX
 XX PT Subtilisin 10 and encoded polynucleotide, applicable in diagnosis and
 PT treatment of malignant tumor, hemopathy, HIV infection, immunological
 PT diseases and inflammation.
 XX
 XX PS Example 3; Page 16; 35pp; Chinese.
 XX
 XX CC The present invention relates to subtilisin 10 and coding sequence (see
 CC AAH48010 and AAG64206). The subtilisin and coding sequence are applicable
 CC in the diagnosis and treatment of malignant tumour, haemopathy, HIV
 CC infection, immunological diseases and inflammation. The present sequence

CC is a PCR primer, which was used in an example from the present invention
 XX
 SQ Sequence 24 BP; 4 A; 4 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 0.5%; Score 16.8; DB 1; Length 24;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1398 ATGAACAGAAATAAATTC 1417
 ||||| ||||| ||||| |||||
 Db 20 ATGAAGAGAAATAAATTC 1

RESULT 105
 ABX13874/C
 ID ABX13874 standard; DNA; 24 BP.
 XX
 AC ABX13874;
 XX
 DT 27-FEB-2003 (first entry)
 XX
 DE Human clathrin light chain 11.44, RT-PCR primer #1.
 XX
 KW Human; clathrin light chain 11.44; malignant tumour; haemopathy;
 KW human immunodeficiency virus; HIV; immunological disease; inflammation;
 KW reverse transcriptase PCR; RT-PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN CN1352069-A.
 XX
 PD 05-JUN-2002.
 XX
 PF 02-NOV-2000; 2000CN-00127164.
 XX
 PR 02-NOV-2000; 2000CN-00127164.
 XX
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-658697/71.
 XX
 PT New human clathrin light chain 11.44 polypeptide for treating malignant
 PT tumors, hemopathy, human immunodeficiency virus infection, immunological
 PT diseases and various inflammations.
 XX
 PS Example 2; Page 17 (Disclosure); 33pp; Chinese.
 XX
 CC The present invention discloses a new kind of polypeptide, human clathrin
 CC light chain 11.44, polynucleotides encoding the polypeptide and a DNA
 CC recombination process to produce the polypeptide. The present invention
 CC describes applying the polypeptide in treating various diseases, such as
 CC malignant tumours, haemopathy, human immunodeficiency virus (HIV)
 CC infection, immunological diseases and various inflammations. Also
 CC disclosed are the antagonist resisting the polypeptide and its treatment
 CC effect, and the application of the polynucleotides encoding human
 CC clathrin light chain 11.44. This sequence represents a reverse
 CC transcriptase PCR primer used to isolate cDNA encoding the human clathrin
 CC light chain 11.44
 XX
 SQ Sequence 24 BP; 8 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 16.8; DB 1; Length 24;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 78 GATGTGATCTGGCTCACAG 97
 ||||| ||||| ||||| |||||
 Db 20 GGTGTGATCTGGCTCACAG 1

RESULT 106

ABI90379/c
 ID ABI90379 standard; DNA; 24 BP.
 XX
 AC ABI90379;
 XX
 DT 15-FEB-2002 (first entry)
 XX
 DE Capture oligonucleotide Zip ID#3991 oligo #2.
 XX
 KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
 KW oncogene; tumour suppressor; human papillomavirus; forensic;
 KW environmental monitoring; food industry; feed industry; ss.
 XX
 OS Synthetic.
 XX
 PN WO200179548-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 04-APR-2001; 2001WO-US010958.
 XX
 PR 14-APR-2000; 2000US-0197271P.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
 XX
 DR WPI; 2002-034366/04.
 XX
 PT Designing capture oligonucleotide probes for use on a support to which
 PT complementary oligonucleotides hybridize with little mismatch.
 XX
 PS Example 5; Fig 25; 300pp; English.
 XX
 CC The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridise with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medinensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. ABI92074 to
 CC ABI97546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention
 XX
 SQ Sequence 24 BP; 3 A; 5 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 16.8; DB 1; Length 24;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1788 AATCAGACCTGGACCTTA 1807
 ||||| ||||| ||||| |||||
 Db 20 AATCGAAACCTGGACCTTA 1

RESULT 107

```

ABI90378
ID ABI90378 standard; DNA; 24 BP.
XX
AC ABI90378;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide Zip ID#3991 oligo #1.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
KW oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
XX WO200179548-A2.
XX
XX 25-OCT-2001.
XX
XX 04-APR-2001; 2001WO-US010958.
XX
XX 14-APR-2000; 2000US-0197271P.
XX
XX (CORR ) CORNELL RES FOUND INC.
XX
XX Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
XX
XX WPI; 2002-034366/04.
XX
XX Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch.
XX
XX Example 5; Fig 25; 300pp; English.
XX
XX The present invention describes a method (M1) for designing capture
XX oligonucleotide probes (I) for use on a support to which complementary
XX oligonucleotide probes (II) will hybridise with little mismatch, where
XX (I) have melting temperatures within a narrow range. The method is useful
XX for detecting infectious diseases caused by bacterial infectious agents
XX e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
XX infectious agents e.g. Cryptococcus neoformans, Candida albicans and
XX Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
XX Epstein-Barr virus and polio virus, and parasitic infectious agents
XX selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
XX medinensis. The method is also useful for detecting genetic diseases such
XX as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
XX Detecting cancer involving oncogenes, tumour suppressor genes, or genes
XX involved in DNA amplification, replication, recombination or repair, the
XX cancer is specifically associated with a gene selected from BRCA1 gene,
XX p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
XX method is also used for environmental monitoring, forensics and the food
XX and feed industry, detecting comprises scanning (using e.g. a scanning
XX electron microscope and infrared microscope) the support at the
XX particular sites and identifying if ligation of the oligonucleotide probe
XX sets occurred and correlating (using a computer) identified ligation to a
XX presence or absence of the target nucleotide sequences. ABI82074 to
XX ABI97546 represent oligonucleotide sequences used in the exemplification
XX of the present invention
XX
SQ Sequence 24 BP; 8 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1788 AATCAGAACCCCTGGACCCTA 1807
|||||
Db 5 AATCCGAACCTGGACCCTA 24
|||||

RESULT 108

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```

AAQ34279
ID AAQ34279 standard; DNA; 23 BP.
XX
AC AAQ34279;
XX
XX 25-MAR-2003 (revised)
XX 02-FEB-1993 (first entry)
XX
XX Upstream PCR primer TGLA15UP2.
XX
XX PCR; selection; microsatellite; OPTIPRIM; breeding; cattle; parentage;
XX genetic mapping; traits; amplification; ss.
XX
XX Bos taurus.
XX
XX WO9213102-A1.
XX
XX 06-AUG-1992.
XX
XX 15-JAN-1992; 92WO-US000340.
XX
XX 15-JAN-1991; 91US-00642342.
XX
XX (GENM-) GENMARK.
XX
XX Georges M, Massey JM;
XX
XX WPI; 1992-284684/34.
XX
XX Polymorphic bovine DNA markers - used in genetic identification, gene
XX mapping, and selective breeding.
XX
XX Table 8; Page 442; 517pp; English.
XX
XX The sequence shows an upstream PCR primer for in vitro amplification of
XX bovine microsatellite sequences obt'd. by screening library of bovine MboI
XX DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15
XX oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming
XX independent distribution of microsatellites and MboI sites, the frequency
XX of (76)n >9 microsatellites in the bovine genome is estimated at
XX >100,000. The sequence information for ca. 230 such bovine
XX microsatellites is summarised in the specification and indexed herein
XX (see below). For each such microsatellite sequence sufficient information
XX was obt'd. to generate the required PCR primers for in vitro amplification
XX of the corresp. microsatellite (using the program OPTIPRIM). The
XX microsatellites may be used to identify individuals, for parentage
XX testing, and in the genetic mapping of economic trait loci, or genes
XX involved the determination of economically important traits esp. in cattle,
XX to allow selective breeding. See also AAQ33501-34440. (Updated on 25-MAR-
XX 2003 to correct PN field.)
XX
XX Sequence 23 BP; 11 A; 3 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 546 TGAATGAAATAATGGCAACAGT 568
|||||
Db 1 TGAATGAACTAATGGCAACAAAT 23
|||||

RESULT 109
ACC57706/c
ID ACC57706 standard; DNA; 23 BP.
XX
XX ACC57706;
XX
XX 28-JUL-2003 (first entry)
XX
XX Coffee alpha-D-galactosidase PCR primer BETA101.
XX
XX Coffee; plant; alpha-D-galactosidase; enzyme; galactomannan; PCR; primer;

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KW ss.
 XX Coffea arabica.
 XX WO2003032713-A2.
 PN 24-APR-2003.
 PD 15-AUG-2002; 2002WO-EP009148.
 PF 10-OCT-2001; 2001EP-00124160.
 PR (NEST) SOC PROD NESTLE SA.
 PA Marraccini P, Deshayes A, Rogers J;
 PI WPI; 2003-393464/37.
 XX New coffee plants and cells producing galacto-mannans, where its
 PT galactose branching is increased, useful for producing beans that are
 PT useful for preparing soluble coffee.
 XX Disclosure; Page 18; 26pp; English.
 PS The present sequence is that of PCR primer BETA101, which was used in the
 CC PCR amplification of coffee alpha-D-galactosidase cDNA (see ACC57702).
 CC cDNA was obtained from a Coffea arabica var. Caturra T2308 cDNA library
 CC constructed from mRNA extracted at 30 weeks after flowering. The
 CC invention aims to increase the solubility of coffee galactomannans by
 CC increasing their galactose branching. The strategy adopted is to reduce
 CC the endogenous level of alpha-D-galactosidase activity, preferably by
 CC introducing an antisense copy of its cDNA under the control of the coffee
 CC cspl promoter
 XX
 SQ Sequence 23 BP; 7 A; 4 C; 1 G; 11 T; 0 U; 0 Other;
 Query Match 0.5%; Score 16.6; DB 1; Length 23;
 Best Local Similarity 82.6%; Pred. No. 2e+02;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 792 TTGAAGAGATTAAACCATATAT 814
 DB 23 TTGAAGAGATTAAAGTCAATAAT 1
 RESULT 110
 AAQ38211/c
 ID AAQ38211 standard; DNA; 20 BP.
 XX
 AC AAQ38211;
 XX 25-MAR-2003 (revised)
 DT 01-JUL-1993 (first entry)
 XX
 DE Primer #232, for NANBH virus strain HC-J8 cDNA synthesis.
 XX
 KW Non A non B hepatitis virus; HC-J1; HC-J8; plasma; antisense; ss.
 XX Synthetic.
 OS
 XX EP532167-A2.
 PN 17-MAR-1993.
 PD 30-JUL-1992; 92EP-00306952.
 XX 09-AUG-1991; 91JP-00287402.
 PR 05-DEC-1991; 91JP-00360441.
 XX (IMMO) IMMUNO JAPAN INC.
 PA Okamoto H, Nakamura T;
 PI
 XX

DR WPI; 1993-087166/11.
 XX Polynucleotide(s), polypeptide(s) and antibodies of NANBH virus - useful
 PT for detecting NANBH, as a vaccine and for screening blood samples.
 XX Example 10; Page 11; 93pp; English.
 XX RNA was isolated from the plasma of human patients positive for NANBH
 CC virus (strain HC-J8). Single stranded cDNA was synthesised using the
 CC antisense primer #232 and reverse transcriptase. A dATP tail was added to
 CC the 3' terminus by terminal deoxynucleotidyl transferase and the cDNA
 CC amplified by PCR using the sense primer #242 and the antisense primer
 CC #232. The resulting PCR prod. in clones AAC15733, AAC15734 and AAC15735
 CC corresponded to nt 6027-6889 of the NANBH virus HC-J8 strain. The PCR
 CC prod. was subcloned to nt 13 phase vector, then consensus sequence of the
 CC respective clones of each region was determined. See also AAQ38172-221.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 20 BP; 4 A; 2 C; 8 G; 6 T; 0 U; 0 Other;
 SQ Query Match 0.5%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1094 TCCATGCTAACGACCCCA 1111
 DB 20 TCCATGCTAACGACCCCA 3
 RESULT 111
 ADE14426/c
 ID ADE14426 standard; DNA; 20 BP.
 XX
 AC ADE14426;
 XX 29-JAN-2004 (first entry)
 DT HSD11B1 antisense oligonucleotide seq id 28.
 DE osteopathic; antidepressant; anorectic; antidiabetic;
 XX antiarteriosclerotic; antilipemic; antisense-therapy;
 KW hydroxysteroid 11-beta dehydrogenase 1; osteoporosis; depression;
 KW metabolic disorder; obesity; HSD11B1; diabetes; atherosclerosis;
 KW hyperlipidaemia; antisense technology; human; ss.
 XX Homo sapiens.
 OS US2003198965-A1.
 PN 23-OCT-2003.
 PD 19-APR-2002; 2002US-00126355.
 PF 19-APR-2002; 2002US-00126355.
 PR (ISIS-) ISIS PHARM INC.
 PA Freier SM;
 XX WPI; 2003-852782/79.
 DR New antisense compounds useful for treating disorders associated with
 PT hydroxysteroid 11-beta dehydrogenase 1 expression, such as osteoporosis,
 PT depression and metabolic disorders like obesity, diabetes and
 PT atherosclerosis.
 XX Claim 3; SEQ ID NO 28; 53pp; English.
 PS The invention describes a compound (I) 8-80 nucleobases in length
 CC targeted to a nucleic acid molecule encoding hydroxysteroid 11-beta
 CC dehydrogenase 1, inhibiting expression of hydroxysteroid 11-beta
 CC dehydrogenase 1. The methods and compositions of the present invention
 CC are useful for treating disorders associated with hydroxysteroid 11-beta

CC dehydrogenase 1 expression, such as osteoporosis, depression and
 CC metabolic disorders like obesity, diabetes, atherosclerosis and
 CC hyperlipidaemia. This sequence represents an antisense oligonucleotide
 CC used to control the expression of human hydroxysteroid 11-beta
 CC dehydrogenase 1.

XX Sequence 20 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 0 Other;
 SQ

Query Match 0.5%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1738 AACTCTACAGAGCTGG 1755
 |||||
 Db 20 AACTCTACAGAGTGG 3

RESULT 112
 AAT84855/C

ID AAT84855 standard; DNA; 21 BP.

XX AAT84855;

DT 14-APR-1998 (first entry)

XX Human endonuclease III encoding cDNA cloning primer P6.

XX Endonuclease III; human; DNA damage; repair modulator; screening; drug;
 KW treatment; cancer; PCR primer; ss.

XX Synthetic.

OS Homo sapiens.

PN WO9731612-A2.

XX 04-SEP-1997.

XX 27-FEB-1997; 97WO-US003242.

XX 27-FEB-1996; 96US-0012323P.

XX (UUNY) UNIV NEW YORK STATE.

XX Teebor GW, Hilbert TP;

XX WPI; 1997-448431/41.

XX Isolated mammalian endonuclease III - having DNA damage repair activity,
 PT useful to diagnose and treat conditions associated with DNA damage.

XX Example 3; Page 58; 123pp; English.

CC This primer is used for the cloning of the human endonuclease III cDNA.
 CC The endonuclease III when purified greater than 500-fold, demonstrates
 CC pyrimidine hydrate and thymine glycol DNA-glycosylase activity, and lyase
 CC activity, and reductively cross-links with a thymine glycol containing
 CC oligodeoxynucleotide. The endonuclease III is a DNA damage repair
 CC modulator and can be used to treat diseases or disorders associated with
 CC DNA damage in, e.g. UV or gamma irradiated, or chemically oxidised
 CC tissues. Susceptibility to DNA damage can be determined by measuring
 CC endonuclease III activity in tissues, while the products can be used to
 CC treat or prevent cancers or screen drugs

XX Sequence 21 BP; 8 A; 5 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 16.4; DB 1; Length 21;
 Best Local Similarity 94.4%; Pred. No. 1.8e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 385 GCTTCAGCTCAGGCTCT 402

Db 21 GCTTCGCTCAGGCTCT 4

RESULT 113

AAX30698

ID AAX30698 standard; DNA; 22 BP.

XX AAX30698;

AC (first entry)

XX Oligonucleotide primer used for PCR amplification of H. pylori DNA.

XX Vaccine; probe; diagnostic; ORF; cell envelope protein; secreted protein;
 KW cytoplasmic protein; cellular protein; ds.

XX Helicobacter pylori.

XX WO9824475-A1.

XX 11-JUN-1998.

XX 05-DEC-1997; 97WO-US022104.

XX 05-DEC-1996; 96US-00759625.

XX 25-MAR-1997; 97US-00823745.

XX 14-JUL-1997; 97US-00891928.

XX (ASTR) ASTRA AB.

XX Smith D, Alm RA, Doig PC, Kabok Z, Castriotta LM;

XX WPI; 1998-333051/29.

XX New isolated Helicobacter pylori nucleic acids - used to develop products
 PT for the diagnosis, prevention and treatment of infection by H. pylori and
 PT other Helicobacter species.

XX Disclosure; Page 94; 339pp; English.

XX Recombinant or substantially pure preparations of H. pylori polypeptides
 CC are disclosed, together with the nucleic acids encoding them. In all, 97
 CC ORFs are shown. The proteins are variously cell envelope proteins,
 CC cytoplasmic proteins, secreted proteins or other cellular proteins.
 CC Vaccines containing the nucleic acids or proteins are claimed, as are
 CC probes containing at least 8 nucleotides from the nucleic acid sequences.
 CC The vaccines are useful for treating or reducing the risk of H. pylori
 CC infections, and the probes can be used diagnostically for detecting the
 CC presence of Helicobacter in a sample. The products are also of use in
 CC screening for compounds having the ability to interfere with the H.
 CC pylori life cycle or to inhibit H. pylori infection

XX Sequence 22 BP; 10 A; 2 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 16.4; DB 1; Length 22;

Best Local Similarity 94.4%; Pred. No. 1.9e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 672 TGGCAAGAGCAATCATT 689

Db 1 TGGAAAGAGCAATCATT 18

RESULT 114

AAX30539

ID AAX30539 standard; DNA; 22 BP.

XX AAX30539;

XX 08-JUN-1999 (first entry)

XX Oligonucleotide primer used for sequencing H. pylori DNA.

XX Vaccine; probe; diagnostic; ORF; cell envelope protein; secreted protein;
 KW cellular protein; ds.

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XX OS Helicobacter pylori.
XX PN WO9818323-A1.
XX XX
XX PD 07-MAY-1998.
XX PF 28-OCT-1997; 97WO-US019575.
XX PR 28-OCT-1996; 96US-00739150.
XX PR 06-DEC-1996; 96US-00759739.
XX PR 14-JUL-1997; 97US-00891928.
XX PA (ASTR ) ASTRA AB.
XX PI Smith D, Alm RA;
XX XX
XX DR WPI; 1998-271811/24.
XX XX
XX PT Helicobacter pylori nucleic acids and proteins - used to develop products
XX PT for the detection, prevention and treatment of H. pylori infections.
XX PS Disclosure; Page 79; 279pp; English.
XX CC Recombinant or substantially pure preparations of H. pylori polypeptides
XX CC are disclosed, together with the nucleic acids encoding them. In all, 73
XX CC ORFs are shown. The proteins are variously cell envelope proteins,
XX CC secreted proteins or other cellular proteins. Vaccines containing the
XX CC nucleic acids or proteins are claimed, as are probes containing at least
XX CC 8 nucleotides from the nucleic acid sequences. The vaccines are useful
XX CC for treating or reducing the risk of H. pylori infections, and the probes
XX CC can be used diagnostically for detecting the presence of Helicobacter in
XX CC a sample. The products are also of use in screening for compounds having
XX CC the ability to interfere with the H. pylori life cycle or to inhibit H.
XX CC pylori infection
XX XX
XX SQ Sequence 22 BP; 10 A; 2 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 0.5%; Score 16.4; DB 1; Length 22;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 672 TGGCAAGAGCAAAATCATT 689
Db 1 TGGAAAGAGCAAAATCATT 18
RESULT 115
AAH19020/c
ID AAH19020 standard; DNA; 22 BP.
XX AC AAH19020;
XX DT 21-JUN-2001 (first entry)
XX DE Forward primer used to amplify UCP3 gene exon 6.
XX XX
XX KW UCP3; uncoupling protein 3; polymorphism; obesity; diabetes mellitus; ss.
XX OS Homo sapiens.
XX PN WO200118232-A2.
XX PD 15-MAR-2001.
XX PF 08-SEP-2000; 2000WO-US024784.
XX PR 08-SEP-1999; 99US-0152789P.
XX XX
XX PA (GENA-) GENAISSANCE PHARM INC.
XX PA (STEP/) STEPHENS J C.
XX PI Chew A, Choi JY, Denton RR, Nandabalan K;
XX DR WPI; 2001-218562/22.
XX XX
XX PT Nucleic acids encoding uncoupling protein 3 (mitochondrial, proton
XX PT carrier) (UCP3) proteins comprising single nucleotide polymorphisms,
XX PT useful for the design of drugs for treating obesity.
XX XX
XX PS Example 1; Page 34; 94pp; English.
XX CC The present invention relates to the human uncoupling protein 3
XX CC (mitochondrial, proton carrier) (UCP3) gene and polymorphisms. The
XX CC polymorphisms are associated with obesity, especially diabetes mellitus
XX CC associated obesity. They polymorphisms may be identified and analysed to
XX CC determine whether an individual is susceptible to obesity and may be used
XX CC as the basis for targeted design of drugs to treat obesity. The present
XX CC sequence was used in the identification and amplification of UCP3
XX CC polymorphisms
XX PA (GENO-) GENOME THERAPEUTICS CORP.

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XX PI Ellis RW, Noonan BM, Alm RA, Smith D, Guild BC;
XX DR WPI; 1999-326698/27.
XX XX
XX PT Cellular vaccine against Helicobacter pylori.
XX PS Example 5; Page 91; 352pp; English.
XX XX
XX CC The invention relates to a vaccine for preventing or treating infections
XX CC by Helicobacter pylori. The vaccine contains at least one isolated H.
XX CC pylori polypeptide, or its fragments, in a carrier, where the carrier is
XX CC a Salmonella, Vibrio cholerae or Shigella vector containing a nucleic
XX CC acid encoding the H. pylori polypeptide. The vaccines induce humoral and
XX CC cellular immune responses. The vaccines are used to treat or prevent
XX CC infections by H. pylori. The invention provides nucleic acid sequences
XX CC AAX75779 to AAX75837 encoding H. pylori outer membrane polypeptides
XX CC (OMPs) AAY17160 to AAY17218
XX SQ Sequence 22 BP; 10 A; 2 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 0.5%; Score 16.4; DB 1; Length 22;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 672 TGGCAAGAGCAAAATCATT 689
Db 1 TGGAAAGAGCAAAATCATT 18
RESULT 116
AAH19020/c
ID AAH19020 standard; DNA; 22 BP.
XX AC AAH19020;
XX DT 21-JUN-2001 (first entry)
XX DE Forward primer used to amplify UCP3 gene exon 6.
XX XX
XX KW UCP3; uncoupling protein 3; polymorphism; obesity; diabetes mellitus; ss.
XX OS Homo sapiens.
XX PN WO200118232-A2.
XX PD 15-MAR-2001.
XX PF 08-SEP-2000; 2000WO-US024784.
XX PR 08-SEP-1999; 99US-0152789P.
XX XX
XX PA (GENA-) GENAISSANCE PHARM INC.
XX PA (STEP/) STEPHENS J C.
XX PI Chew A, Choi JY, Denton RR, Nandabalan K;
XX DR WPI; 2001-218562/22.
XX XX
XX PT Nucleic acids encoding uncoupling protein 3 (mitochondrial, proton
XX PT carrier) (UCP3) proteins comprising single nucleotide polymorphisms,
XX PT useful for the design of drugs for treating obesity.
XX XX
XX PS Example 1; Page 34; 94pp; English.
XX CC The present invention relates to the human uncoupling protein 3
XX CC (mitochondrial, proton carrier) (UCP3) gene and polymorphisms. The
XX CC polymorphisms are associated with obesity, especially diabetes mellitus
XX CC associated obesity. They polymorphisms may be identified and analysed to
XX CC determine whether an individual is susceptible to obesity and may be used
XX CC as the basis for targeted design of drugs to treat obesity. The present
XX CC sequence was used in the identification and amplification of UCP3
XX CC polymorphisms

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XX SQ Sequence 22 BP; 4 A; 6 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 0.5%; Score 16.4; DB 1; Length 22;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3200 CGTGAACCTCCAGAGCAT 3217
|||||
Db 22 CGTGAACCTCCAGAGCAT 5

RESULT 117
AAT48456/c
ID AAT48456 standard; DNA; 21 BP.
XX AC AAT48456;
XX DT 12-APR-1997 (first entry)
XX DE Human beta-globin gene third-strand binding site.
XX KW Haemoglobinopathy; sickle cell anaemia; beta-thalassaemia; haemoglobin;
XX KW beta-globin; triple helix; triplex; HbS; HbA; gene therapy;
XX KW targeted DNA replacement; homologous recombination; mutagenesis; ds.
XX OS Homo sapiens.
XX PN WO9640271-A1.
XX PD 19-DEC-1996.
XX PF 06-JUN-1996; 96WO-US009430.
XX PR 07-JUN-1995; 95US-00473845.
XX PA (UYVA ) UNIV YALE.
XX PI Glazer PM;
XX WPI; 1997-099895/09.
XX PT Repairing mutation(s) in haemoglobin by targeted mutagenesis or
XX PT homologous recombination - mediated by a triplex forming
XX PT oligo:nucleotide, opt. carrying a mutagen, partic. for treatment of
XX PT sickle cell anaemia or thalassaemia.
XX PS Claim 34; Page 45; 70pp; English.
XX SQ Sequence 21 BP; 0 A; 6 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2407 GAAGAAGAAAATAAAGCAAG 2427
|||||
Db 21 CGAGAAGAAAATAAAGAAAG 1

RESULT 118
AAF97384
ID AAF97384 standard; DNA; 21 BP.
XX AC AAF97384;
XX DT 06-JUN-2001 (first entry)
XX DE Human gene single nucleotide polymorphism #2145.
XX KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
XX KW polymorphism; vascular disease; coronary artery disease; forensics;
XX KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
XX KW pulmonary embolism; paternity test; ds.
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AAK14730/c
ID AAK14730 standard; DNA; 21 BP.
XX AC AAK14730;
XX DT 24-MAR-1999 (first entry)
XX DE Triple helix forming nucleotides 917-937 of Beta-globin gene.
XX KW Triple-helix forming region; Triplex formation; DNA detection;
XX KW identification; bacteria; oncogene; virus; ds.
XX OS Homo sapiens.
XX PN US5861244-A.
XX PD 19-JAN-1999.
XX PF 22-DEC-1993; 93US-00173489.
XX PR 29-OCT-1992; 92US-00968436.
XX PA (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX PI Hepburn AG, Wang C;
XX WPI; 1999-130384/11.
XX PT Assay of genetic sequences based on triplex formation from double
XX PT stranded analyte - and hybrid of anchor and reporter sequences, with
XX PT reporter released if triplex formation occurs, used e.g. to identify
XX PT bacteria.
XX PS Disclosure; Col 17-18; 168pp; English.
XX CC The present sequence represents a potential triple-helix forming region.
XX CC It can be used to demonstrate the assay of the invention. The assay
XX CC comprises adding a sample containing double-stranded DNA test sequences,
XX CC e.g. containing the present sequence, to an aqueous medium containing at
XX CC least one complex of anchor DNA, attached to a solid support, and
XX CC reporter DNA, where either a part of the anchor DNA or reporter DNA is
XX CC designed to form a triple-strand structure with part of the test
XX CC sequence. Triplex formation results in displacement of the reporter DNA
XX CC which is detected as an indication of the presence of the DNA test
XX CC sequence. The method is used to detect DNA sequences, particularly for
XX CC identification of bacteria (by detecting genes for ribosomal RNA) in
XX CC clinical samples, but also detection of oncogenes and Hepatitis B virus
XX SQ Sequence 21 BP; 0 A; 6 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2407 GAAGAAGAAAATAAAGCAAG 2427
|||||
Db 21 CGAGAAGAAAATAAAGAAAG 1

RESULT 119
AAF97384
ID AAF97384 standard; DNA; 21 BP.
XX AC AAF97384;
XX DT 06-JUN-2001 (first entry)
XX DE Human gene single nucleotide polymorphism #2145.
XX KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
XX KW polymorphism; vascular disease; coronary artery disease; forensics;
XX KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
XX KW pulmonary embolism; paternity test; ds.
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XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Variation replace(11,A)
XX FT /*tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX PN WO200118250-A2.
XX PD 15-MAR-2001.
XX PF 07-SEP-2000; 2000WO-US024503.
XX PR 10-SEP-1999; 99US-0153357P.
XX PR 26-JUL-2000; 2000US-0220947P.
XX PR 16-AUG-2000; 2000US-0225724P.
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Lander ES, Gargill M, Ireland JS, Bolx S, Daley GO, Mccarthy JJ;
XX WI WIPI; 2001-226749/23.
XX CC Nucleic acids comprising single nucleotide polymorphisms, useful in
XX CC applications such as forensics, paternity testing, medicine, genetic
XX CC analysis and phenotype correlations to diseases such as diabetes and
XX CC atherosclerosis.
XX PS Example; Page 195; 242pp; English.
XX CC The present invention provides a method of diagnosing a vascular disease
XX CC in an individual, involving determining the sequence at various
XX CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX CC genes. The sequences at a number of polymorphic sites are also provided
XX CC in the specification. In particular, the method can be used in the
XX CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
XX CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX CC useful in forensics, paternity testing, genetic analysis and phenotype
XX CC correlations to diseases. The present sequence is an example of one of
XX CC the human gene SNPs shown in the specification
XX SQ Sequence 21 BP; 5 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1714 CCCTCTGCACAAATGTGACAT 1734
Db 1 CCCACTGCACAGTGTGACAT 21

RESULT 120
ADD19933/C
ID ADD19933 standard; DNA; 21 BP.
XX AC ADD19933;
XX DT 15-JAN-2004 (first entry)
XX DE Oreochromis niloticus microsatellite primer SEQ ID NO:568.
XX KW single nucleotide polymorphism; SNP; fish; Salmo salar;
XX KW Oreochromis niloticus; Atlantic halibut; microsatellite; cod;
XX KW polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut;
XX KW detection; primer; ss.
XX OS Synthetic.
XX OS Oreochromis niloticus.

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PN WO2003060160-A2.
XX PD 24-JUL-2003.
XX PF 17-JAN-2003; 2003WO-IB000112.
XX PR 18-JAN-2002; 2002US-0349950P.
XX PR 16-AUG-2002; 2002US-0404200P.
XX PA (GENO-) GENOMAR ASA.
XX PI Lie O, Slettan A, Hoyum M, Lingaas F;
XX WI WIPI; 2003-627388/59.
XX CC Novel isolated nucleic acid molecule comprising single nucleotide
XX CC polymorphism associated with fish, useful for forming PCR primers which
XX CC are used for detecting single nucleotide polymorphisms in fish nucleic
XX CC acids.
XX PS Claim 18; SEQ ID NO 568; 233pp; English.
XX CC The present invention describes an isolated nucleic acid (I) comprising a
XX CC single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid of
XX CC Salmo salar SNPs, Oreochromis niloticus SNPs or Atlantic halibut SNPs;
XX CC and (ii) a nucleic acid having nucleotide sequence that hybridises to
XX CC (i), or its complement under highly stringent hybridisation conditions.
XX CC Also described: (i) an isolated oligonucleotide (II) comprising at least
XX CC 17 contiguous nucleotides of a nucleotide sequence of S. salar SNPs, O.
XX CC niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
XX CC polymorphic sites and seabass polymorphic sites, or their complement; (2)
XX CC a primer pair (III) suitable for use in PCR, comprising two (II) capable
XX CC of amplifying a nucleotide sequence chosen from S. salar SNPs and O.
XX CC niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
XX CC polymorphic sites and seabass polymorphic sites; and determining (M1) the
XX CC origin of fish sample comprising providing a parentage genotype database
XX CC comprising a collection of candidate parent genotypes, where each of the
XX CC candidate parent genotype represents a distinct origin, and comparing a
XX CC sample genotype to the parentage genotype database, where a match between
XX CC the sample genotype and one of the candidate parent genotype identifies
XX CC to the origin of the sample. (M1) is useful for determining the origin of
XX CC a fish sample such as family salmonidae, S. salar, Tilapia, O. niloticus,
XX CC rainbow trout, halibut, seabass and Atlantic cod. (II) is useful for
XX CC detecting nucleic acid molecule comprising SNP in a sample, which
XX CC involves contacting the sample containing nucleic acids with one or more
XX CC (II) derived from nucleotide sequence of S. salar SNPs and O. niloticus
XX CC SNPs, and identifying nucleic acid that hybridises to (II). (II) is
XX CC useful for detecting nucleic acid molecule comprising a polymorphic
XX CC sequence in a sample, comprising contacting the sample containing nucleic
XX CC acids with one or more (II) which is derived from O. niloticus
XX CC microsatellite, O. niloticus SNPs, Atlantic halibut SNPs, cod polymorphic
XX CC sites or seabass polymorphic sites, and identifying a nucleic acid that
XX CC hybridises to (II). (III) is useful for detecting nucleic acid molecule
XX CC comprising a microsatellite sequence in sample. The present sequence is
XX CC used in the exemplification of the present invention.
XX SQ Sequence 21 BP; 8 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 850 GAATGCCTATCCTTCCTATAT 870
Db 21 GAATGCCTCCTCCTCCTAT 1

RESULT 121
AA11035/c
ID AA11035 standard; DNA; 22 BP.
XX AC AA11035;
XX AC AA11035;

```

DT 28-JUL-2000 (first entry)
 XX Mouse interleukin 18 binding protein complete coding sequence primer #2.
 DE
 XX
 KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
 KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
 KW autoimmune disease; PCR primer; ss.
 XX
 OS Mus musculus.
 XX
 XX WO200012555-A1.
 PN
 XX
 PD 09-MAR-2000.
 XX
 XX 18-NOV-1998; 98WO-JP005186.
 PF
 XX
 XX 01-SEP-1998; 98JP-00247588.
 PR
 XX 18-NOV-1998; 98JP-00327914.
 PR
 XX (HAYE) HAYASHIBARA SRIBUTSU KAGAKU.
 PA
 XX Torigoe K, Taniat M, Kurimoto M;
 PI
 XX WPI; 2000-237850/20.
 DR
 XX
 XX Interleukin 18-binding protein with activity of regulating physiological
 PT actions of interleukin 18, useful as regulator and drug for sensitivity
 PT diseases and organ rejection and in treating diseases due to excess
 PT immune reaction.
 XX
 PS Example 4; Page 31; 71pp; Japanese.
 XX
 CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
 CC from humans or mice which act as regulators and drugs for sensitivity
 CC diseases and organ rejection and in treating diseases due to excess
 CC immune reaction, e.g. in slowing down rejection after organ transplant,
 CC and in treating autoimmune diseases. This sequence represents a PCR
 CC primer used to isolate the complete coding sequence for the mouse
 CC interleukin 12 binding protein (AAA11011)
 XX
 SQ Sequence 22 BP; 4 A; 2 C; 8 G; 8 T; 0 U; 0 Other;
 Query Match 0.5%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 2e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 370 GAATCTCAGTCAAGCTTCA 390
 |||||
 DB 22 GAACCTCAAACTCAAGCTTCA 2
 RESULT 122
 AAD29030/c
 ID AAD29030 standard; DNA; 22 BP.
 XX
 AC AAD29030;
 XX
 DT 07-MAY-2002 (first entry)
 XX
 DE Human G-protein coupled-receptor 4a gene expressing forward PCR primer.
 XX
 KW G-protein coupled-receptor; GPCR; therapy; diabetes; obesity; anorexia;
 KW cancer; neurodegenerative disorders; Alzheimer's; Parkinson's; dementia;
 KW haematopoietic disorder; immune disorder; cardiac disorder; haemostatic;
 KW Crohn's disease; angina pectoris; schizophrenia; Huntington's disease;
 KW Gilles de la Tourette's syndrome; hypertension; hypertensive; neuroleptic;
 KW human immuno deficiency virus; HIV; neuroprotective; immunomodulatory;
 KW asthma; immunogen; vaccine; nootropic; anorectic; anabolic; cytostatic;
 KW depression; ulcer; cardiast; hypertensive; hypertensive; osteoporosis;
 KW anticonvulsant; anti-inflammatory; gastrointestinal; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX

PN WO200208289-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 26-JUL-2001; 2001WO-US023576.
 XX
 PR 26-JUL-2000; 2000US-0221336P.
 PR 05-OCT-2000; 2000US-0238333P.
 PR 10-JAN-2001; 2001US-0260875P.
 PR 22-FEB-2001; 2001US-0271025P.
 PR 23-MAR-2001; 2001US-0278164P.
 PR 02-APR-2001; 2001US-0280876P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 XX Padigaru M, Mezes P, Mishra V, Burgess C, Casman S, Smithson G;
 PI
 XX WPI; 2002-148464/19.
 DR
 XX
 XX New G-protein coupled-receptor polypeptides and nucleic acids encoding
 PT them are useful in therapeutics e.g. cancer.
 XX
 PS Example 1; Page 143; 168pp; English.
 XX
 CC The present invention relates to an isolated G-protein coupled-receptor
 CC (GPCR) polypeptide and its nucleic acid. GPCR is useful in treating or
 CC preventing a GPCR-associated disorder and the predisposition to a
 CC disease associated with altered expression levels of this polypeptide.
 CC GPCR is useful for treating or preventing disorders such as; diabetes,
 CC obesity, anorexia, cancer, neurodegenerative disorders, Alzheimer's,
 CC Parkinson's, haematopoietic disorders, immune disorders, asthma, cardiac
 CC disorders, Crohn's disease, angina pectoris, ulcer, schizophrenia,
 CC depression, dementia, Huntington's disease, Gilles de la Tourette's
 CC syndrome, human immuno deficiency virus (HIV), hypotension, hypertension
 CC and osteoporosis. GPCR can be used as an immunogen to produce antibodies
 CC specific for the invention, as vaccines and in screening for potential
 CC agonistic and antagonistic compounds. The present sequence is human GPCR
 CC gene expressing PCR primer
 XX
 SQ Sequence 22 BP; 4 A; 5 C; 4 G; 9 T; 0 U; 0 Other;
 Query Match 0.5%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 2e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2637 CAGAAAATAATGTCCAAAG 2657
 |||||
 DB 22 CAGAAAATAATGTCCACAG 2
 RESULT 123
 ABZ84320
 ID ABZ84320 standard; DNA; 22 BP.
 XX
 AC ABZ84320;
 XX
 DT 14-MAY-2003 (first entry)
 XX
 DE Toxicologically relevant rat PCR primer #1479.
 XX
 KW Toxicologically relevant gene; toxicological response; PCR primer; ss.
 XX
 OS Rattus sp.
 KW Synthetic.
 XX
 PN WO2003016500-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 16-AUG-2002; 2002WO-US026514.
 XX
 PR 16-AUG-2001; 2001US-0313080P.
 XX

PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
 XX Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schweiser K;
 PI Alen P;
 XX WPI; 2003-268322/26.
 XX Determining a toxicological response to an agent, useful for screening of
 PT drugs, comprises comparing the expression profile of one or more human
 PT toxic response genes to a reference gene expression profile indicative of
 PT toxicity.
 XX Claim 1; Page 341; 455pp; English.
 XX The present invention describes a method (M1) for determining a
 CC toxicological response to an agent, which comprises comparing the
 CC expression profile of one or more human toxic response genes to a
 CC reference gene expression profile indicative of toxicity, and so
 CC determining the presence of a toxic response to the agent. Also
 CC described: (1) an array comprising one or more polynucleotides selected
 CC from the genes corresponding to the partial sequences given in AS282842
 CC to AS284764, or their fragments of at least 20 nucleotides, or homologues
 CC ; and (2) determining if a gene putatively identified to be a toxic
 CC response gene plays a role on toxic response pathways by determining the
 CC expression profile of the gene after exposure of cells or a human subject
 CC to a known toxic pharmaceutical or industrial agent, comprising: (a)
 CC exposing cells to an agent or isolating cells from a human subject who
 CC was exposed to an agent; (b) obtaining the test gene expression profile
 CC for a putatively identified toxic response gene after exposure to a known
 CC toxic pharmaceutical or industrial agent; and (c) comparing the test
 CC profile to the expression profile of a gene with a similar function or
 CC comparing the test profile to the expression profile of that gene after
 CC exposure to other known toxic compounds. The methods are useful for
 CC predicting and determining toxicological responses on a cellular, organ
 CC or system level. The arrays comprising the human genes are useful for
 CC toxicological screening of drugs, pharmaceutical compounds and chemicals
 XX
 SQ Sequence 22 BP; 8 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 0.5%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 2e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1883 TGCGTGAAGACACAGAACAG 1903
 Db 1 TGCGTCAATACCAAGAG 21
 RESULT 124
 ABV72573
 ID ABV72573 standard; DNA; 22 BP.
 XX AC ABV72573;
 XX 12-FEB-2003 (first entry)
 DT PCR primer used to obtain 5' deletions of alcohol oxidase 1 promoter.
 DE Yeast; alcohol oxidase 1; AOX1; promoter; formaldehyde; methanol;
 XX protein production; peroxisome biogenesis; PCR; primer; ss.
 XX Pichia pastoris.
 OS WO200281650-A2.
 PN 17-OCT-2002.
 PD 05-APR-2002; 2002WO-US012851.
 PF 05-APR-2001; 2001US-0281861P.
 XX (UYNE-) UNIV NEBRASKA.
 PA

PI Inan M, Meagher MM, Benson AK;
 XX WPI; 2003-058528/05.
 DR Novel alcohol oxidase 1 regulatory nucleotide sequences useful for
 PT enhancing expression of genes of interest in a variety of host cells,
 PT especially yeast cells.
 XX Example; Page 37; 66pp; English.
 PS PCR primers ABV72571-75 were used to obtain 5' deletions of a yeast
 CC alcohol oxidase 1 (AOX1) promoter. AOX1 catalyses the oxidation of
 CC methanol to formaldehyde. The AOX1 promoter is an inducible promoter,
 CC primarily induced by methanol and starvation, and repressed in response
 CC to glucose and ethanol. The primers were used to identify 5' regulatory
 CC regions within the promoter. Regulatory regions within the AOX1 promoter
 CC can be used to produce expression cassettes and vectors, which are useful
 CC for protein production. The regulatory sequences are useful to increase
 CC expression of genes of interest in a variety of host cells, in a research
 CC setting to further characterize promoter function and to study peroxisome
 CC biogenesis. They are also useful as probes
 XX
 SQ Sequence 22 BP; 6 A; 4 C; 4 G; 8 T; 0 U; 0 Other;
 Query Match 0.5%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 2e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1054 TGTGCTCTTCTTAATATGAC 1074
 Db 2 TCTTGGATTCTCTTAATATGAC 22
 RESULT 125
 AAZ70487/C
 ID AAZ70487 standard; DNA; 19 BP.
 XX AC AAZ70487;
 XX 10-SEP-2001 (first entry)
 DT Human biallelic marker upstream amplification primer SEQ ID NO:4843.
 DE Human genome; biallelic marker; high density disequilibrium map;
 XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW amplification; hybridisation; identification; characterisation;
 KW diagnosis; ss.
 XX Homo sapiens.
 OS WO9954500-A2.
 PN 28-OCT-1999.
 PD 21-APR-1999; 99WO-IB000822.
 PF 21-APR-1998; 98US-0082614P.
 PR 23-NOV-1998; 98US-0109732P.
 XX (GEST) GENSET.
 XX Cohen D, Blumenfeld M, Chumakov I;
 PI WPI; 2000-013267/01.
 DR Novel biallelic markers used to construct a high density disequilibrium
 PT map of the human genome.
 XX Claim 8; Page 1263; 2745pp; English.
 PS AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 XX

CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses; they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention

SQ Sequence 19 BP; 10 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 16; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 TTCTGTCCTCTGGATT 2724

Db 17 TTCTGTCCTCTGGATT 2

RESULT 126

ACC85778/c

ID ACC85778 standard; DNA; 20 BP.

XX ACC85778;

AC ACC85778;

XX 15-OCT-2003 (first entry)

XX Human NOV3a gene expression PCR forward primer.

XX Cytostatic; immunostimulant; gene therapy; vaccine; ss; primer; NOVX;

KW LMW T kinin-like protein; cancer; PCR.

XX Homo sapiens.

XX WO2003031572-A2.

PN 17-APR-2003.

XX 02-OCT-2002; 2002WO-US031359.

XX 09-OCT-2001; 2001US-0327917P.

XX 09-OCT-2001; 2001US-0328029P.

XX 09-OCT-2001; 2001US-0328056P.

XX 29-OCT-2001; 2001US-0349575P.

XX 16-MAY-2002; 2002US-0381038P.

XX 01-OCT-2002; 2002US-00381038.

XX (CURA-) CURAGEN CORP.

XX Alabrook JP, Burgess CE, Gorman L, Guo X, Lepley DM;

XX Patturajan M, Rastelli L, Rieger DK, Spytek KA, Zhong M;

XX WPI; 2003-421273/39.

XX New NOVX polypeptide, useful for preparing a composition for treating or

XX preventing e.g., cancer.

XX Disclosure; Page 123; 135pp; English.

XX The invention relates to the isolation of novel NOVX protein and genes
 CC encoding them or sequences that are at least 95% identical to these. This
 CC sequence corresponds to a primer used to PCR amplify a fragment of NOV3a
 CC cDNA (ACC85774) for use as a probe to detect expression of the NOV3a
 CC gene. NOV3a protein has high homology to LMW T kinin-like proteins. The
 CC polypeptide is useful for preparing a composition for treating or
 CC preventing e.g., cancer

SQ Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
 Query Match 0.5%; Score 16; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3144 TCCAGGTCCTTGATC 3159

Db 20 TCCAGGTCCTTGATC 5

RESULT 127

ADB88643/c

ID ADB88643 standard; DNA; 20 BP.

XX ADB88643;

AC ADB88643;

XX 04-DEC-2003 (first entry)

XX Frizzled-4 (FZD4) modulating agent related reverse primer, SEQ ID No 90.

XX Frizzled-4; FZD4; immunomodulatory compound; ophthalmological; vasotropic;

XX antiinflammatory; vulnery; osteopathic; antimicrobial; antipsoriatic;

XX antidiabetic; modulator; neovascularisation; myocardial ischaemia;

XX coronary artery disease; wound healing; fracture; tendon repair;

XX cancer tumour growth; metastasis; ocular neovascularisation; bone;

XX cartilage destruction; inflammatory; infectious disease; psoriasis;

XX pre-eclampsia; respiratory distress; peritoneal sclerosis; diabetes;

XX FZD4; PCR; primer; ss.

XX Homo sapiens.

XX WO2003005034-A2.

XX 16-JAN-2003.

XX 04-JUL-2002; 2002WO-CA001004.

XX 05-JUL-2001; 2001US-0303285P.

XX 29-OCT-2001; 2001US-0340409P.

XX (XENO-) XENON GENETICS INC.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Macdonald ML, Zeisler JM, Samuels M, Goldberg YP, Robataille JM;

XX Hayden MR;

XX WPI; 2003-221619/21.

XX Identifying Frizzled-4 (FZD4) gene modulators for treating e.g. familial

XX exudative vitreoretinopathy or Coat's disease, comprises contacting a

XX compound with an FZD4 polypeptide or with a cell expressing FZD4

XX polypeptide.

XX Example 1; Page 109; 116pp; English.

XX The invention relates to a novel method for identifying a Frizzled-4

XX (FZD4) modulating agent. The method comprises contacting a compound with

XX an FZD4 polypeptide or with a cell expressing an FZD4 polypeptide, and

XX determining the difference in the biological activity or expression of

XX the FZD4 polypeptide compared with when the compound is not present. The

XX immunomodulatory compounds of the invention can have the following

XX activities of ophthalmological, vasotropic, antiinflammatory, vulnery,

XX osteopathic, antimicrobial, antipsoriatic, and antidiabetic. The method

XX is useful for identifying modulators of FZD4, and such modulators are

XX useful in treating diseases related to Fzd-4 expression or activity. The

XX modulators are particularly useful in treating e.g. familial exudative

XX vitreoretinopathy, retinopathy of prematurity, Coat's disease, Norrie

XX disease, retinal angiomas, ocular toxocariasis, retinoblastoma,

XX retinal dysplasia, neovascular inflammatory vitreoretinopathy or

XX retinitis pigmentosa. The modulators are also useful for treating other

XX diseases involving the physiological and pathological processes of

XX neovascularisation, such as indications that may require stimulation of

XX

CC neovascularisation (e.g. myocardial ischaemia, coronary artery disease,
 CC wound healing, or fracture and tendon repair), indications that may
 CC require inhibition of neovascularisation (e.g. cancer tumour growth and
 CC metastasis, ocular neovascularisation, bone and cartilage destruction,
 CC inflammatory and infectious diseases), indications that require vascular
 CC remodeling (e.g. psoriasis or pre-eclampsia), and indications that
 CC require inhibition of neovascularisation (e.g. respiratory distress,
 CC peritoneal sclerosis, or diabetes). This polynucleotide sequence
 CC represents a PCR primer relating to the F2D4 gene of the invention.
 XX
 SQ Sequence 20 BP; 6 A; 5 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 16; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0;

Qy 547 GAATGAATAATGGCA 562

Db 19 GAATGAATAATGGCA 4

RESULT 128

AAQ75625/c

ID AAQ75625 standard; DNA; 21 BP.

XX

AC AAQ75625;

XX

DT 04-AUG-1995 (first entry)

XX

DE Reverse transcription primer used in cDNA analysis technique.

XX

KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX

KW aggregate; restriction enzyme; ss.

XX

OS Synthetic.

XX

PN JP06303997-A.

XX

PD 01-NOV-1994.

XX

PF 16-APR-1993; 93JP-00112515.

XX

PR 16-APR-1993; 93JP-00112515.

XX

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX

DR WPI; 1995-018287/03.

XX

PT Analysis of cDNA and gene expression - by amplification of mRNA followed

XX

PT by digestion with restriction enzymes.

XX

PS Disclosure; Page 6; 11pp; Japanese.

XX

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX

SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.5%; Score 16; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3390 ACTCAAAAAAAAAAAAA 3405

Db 21 ACTCAAAAAAAAAAAAA 6

RESULT 129

ADE29835

ID ADE29835 standard; RNA; 19 BP.

XX

AC ADE29835;

XX

DT 29-JAN-2004 (first entry)

XX

DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:457.

XX

KW short interfering nucleic acid; siNA; downregulation; inhibition;
 KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
 KW cytostatic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;
 KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;
 KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
 KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;
 KW psoriasis; inflammatory bowel disease; drug screening;
 KW genetic engineering; pharmacogenomic; gene mapping; ss.

XX

OS Synthetic.

XX

PN WO2003072590-A1.

XX

PD 04-SEP-2003.

XX

PF 28-JAN-2003; 2003WO-US002510.

XX

PR 20-FEB-2002; 2002US-0358580P.

XX

PR 11-MAR-2002; 2002US-0363124P.

XX

PR 06-JUN-2002; 2002US-0386782P.

XX

PR 29-AUG-2002; 2002US-0406784P.

XX

PR 05-SEP-2002; 2002US-0408378P.

XX

PR 09-SEP-2002; 2002US-0409293P.

XX

PR 15-JAN-2003; 2003US-0440129P.

XX

(SIRN-) SIRNA THERAPEUTICS INC.

XX

PI Mcswiggen J, Beigelman L, Usman N, Haerberli P, Chowrira B;

XX

XX WPI; 2003-689980/65.

XX

PT New short interfering nucleic acid, useful e.g. for treatment and
 PT diagnosis of cancer, downregulates expression of mitogen-activated
 PT protein kinase genes.

XX

PS Example 3; SEQ ID NO 457; 164pp; English.

XX

CC The present invention describes a short interfering nucleic acid (siNA)
 CC that downregulates expression of a mitogen-activated protein kinase
 CC (MAPK) genes by RNA interference. Also described: (1) a method for
 CC modulating expression of MAPK genes in cells, tissue explants or
 CC organisms by introduction of siNA; (2) kits for in vitro or in vivo
 CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
 CC vectors that express siNA and cells containing these vectors. MAPK siNAs
 CC have cytostatic, anorectic, antidiabetic, antiinflammatory,
 CC antiasthmatic, immunosuppressive, antibacterial, antirheumatic,
 CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK
 CC siNAs can be used to modulate the expression of MAPK genes, in cells,
 CC tissue explants or organisms, e.g. for treating obesity; diabetes types I
 CC and II; a wide range of tumours, and inflammatory diseases (asthma,
 CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel
 CC disease). They can also be used for drug screening; diagnosis; target
 CC identification and validation; genetic engineering; pharmacogenomics;
 CC studying gene function and gene mapping (e.g. of single-nucleotide
 CC polymorphisms). The present sequence represents a MAPK siNA which is used
 CC in the exemplification of the present invention.

XX

SQ Sequence 19 BP; 3 A; 5 C; 5 G; 0 T; 6 U; 0 Other;

Query Match

Best Local Similarity 68.4%; Pred. No. 1.7e+02;

Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 391 GCTGCAGGCTCTTCAGCAA 409
 ||:|||||: :|||
 Db 1 GCUGCGGCUUUCAGCAA 19

RESULT 130

ADE29730/c

ID ADE29730 standard; RNA; 19 BP.

XX

AC ADE29730;

XX

DT 29-JAN-2004 (first entry)

XX

DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:352.

XX

KW short interfering nucleic acid; siNA; downregulation; inhibition;
 KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
 KW cytostatic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;
 KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;
 KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
 KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;
 KW psoriasis; inflammatory bowel disease; drug screening;
 KW genetic engineering; pharmacogenomic; gene mapping; ss.

XX

OS Synthetic.

XX

PN WO2003072590-A1.

XX

PD 04-SRP-2003.

XX

XX 28-JAN-2003; 2003WO-US002510.

XX

PR 20-FEB-2002; 2002US-0358580P.

PR

PR 11-MAR-2002; 2002US-0363124P.

PR

PR 08-JUN-2002; 2002US-0386782P.

PR

PR 29-AUG-2002; 2002US-0406784P.

PR

PR 05-SEP-2002; 2002US-0408378P.

PR

PR 09-SEP-2002; 2002US-0409293P.

PR

PR 15-JAN-2003; 2003US-0440129P.

XX

PA (SIRM-) SIRNA THERAPEUTICS INC.

XX

PI Mcswiggen J, Beigelman L, Usman N, Haerberli P, Chowrira B;

XX

XX WPI; 2003-689980/65.

DR

XX

PT New short interfering nucleic acid, useful e.g. for treatment and

PT

PT diagnosis of cancer, downregulates expression of mitogen-activated

PT

PT protein kinase genes.

XX

XX Example 3; SEQ ID NO 352; 164pp; English.

PS

CC The present invention describes a short interfering nucleic acid (siNA)
 CC that downregulates expression of a mitogen-activated protein kinase
 CC (MAPK) genes by RNA interference. Also described: (1) a method for
 CC modulating expression of MAPK genes in cells, tissue explants or
 CC organisms by introduction of siNA; (2) kits for in vitro or in vivo
 CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
 CC vectors that express siNA and cells containing these vectors. MAPK siNAs
 CC have cytostatic, anorectic, antidiabetic, antiinflammatory,
 CC antiasthmatic, immunosuppressive, antibacterial, antirheumatic,
 CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK
 CC siNAs can be used to modulate the expression of MAPK genes in cells,
 CC tissue explants or organisms, e.g. for treating obesity; diabetes types I
 CC and II; a wide range of tumours, and inflammatory diseases (asthma,
 CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel
 CC disease). They can also be used for drug screening; diagnosis; target
 CC identification and validation; genetic engineering; pharmacogenomics;
 CC studying gene function and gene mapping (e.g. of single-nucleotide
 CC polymorphisms). The present sequence represents a MAPK siNA which is used
 CC in the exemplification of the present invention.

XX

SQ Sequence 19 BP; 6 A; 5 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 0.5%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 391 GCTGCAGGCTCTTCAGCAA 409

||||| ||||| |||||

Db 19 GCTGCTGGCTTTTCAGCAA 1

RESULT 131

AAT41077

ID AAT41077 standard; DNA; 20 BP.

XX

AC AAT41077;

XX

DT 03-DEC-1996 (first entry)

XX

DE Human gene signature HUMGS01298-derived sense primer.

XX

KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
 KW human; cloning; mapping; non-biased library; diagnosis; detection;
 KW cell typing; abnormal cell function; primer; PCR; amplification;
 KW polymerase chain reaction; ss.

XX

OS Synthetic.

XX

PN WO9514772-A1.

XX

PD 01-JUN-1995.

XX

XX 11-NOV-1994; 94WO-JP001916.

XX

PR 12-NOV-1993; 93JP-00355504.

XX

PA (MATS/) MATSUBARA K.

PA

PA (OKUB/) OKUBO K.

XX

XX Matsubara K, Okubo K;

XX

XX WPI; 1995-206931/27.

XX

XX Single-stranded DNA for identifying gene signatures - isolated from 3'-
 PT directed human cDNA library that reflects relative abundance of corres.
 PT mRNA in specific human tissues.

XX

PS Example 7; Fig 7; 2245pp; Japanese.

XX

CC Primers T41001-T41382 are derived from novel human gene signature (GS)
 CC sequences which did not match with sequences deposited in Genbank release
 CC 76. The GS sequences (T19001-T26837) were obtained from 3'-directed cDNA
 CC libraries prepared from various human tissues; synthesis of cDNA was
 CC initiated from the 3'-end of mRNA by using poly(I) as the sole primer.
 CC Each library is constructed so as to reflect accurately the relative
 CC abundance of different mRNAs in the particular tissue from which it was
 CC derived. The appearance frequency of a given GS in a cDNA library can be
 CC determined (esp. using primers and probes derived from the GS sequences)
 CC as a means of diagnosing abnormal cell function or for recognising
 CC different cell types. The primers T41077-8 amplify clone pm2367 which
 CC comprises the GS HUMGS001298 (T20298), located on chromosome 4
 XX

SQ Sequence 20 BP; 7 A; 3 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.8; DB 1; Length 20;
 Best Local Similarity 89.5%; Pred. No. 1.9e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 225 ATCAAAGTTCACCTTGCTTC 243

||||| ||||| |||||

Db 1 ATCAAAGTTAATTGCTTC 19

RESULT 132

```

AAZ34920
ID  AAZ34920 standard; DNA; 20 BP.
XX
XX  AC
XX  AAZ34920;
XX
XX  DT
XX  28-JUN-1999 (first entry)
XX
XX  DE
XX  PCR primer used to amplify IGFBP3.
XX
XX  Immortalized human hair papilla cell; HPC; screening; hair growth;
KW  SV40 viral large T-antigen gene; deleted replication initiation point;
KW  hair growth stimulating agent; PCR primer; ss.
XX
XX  OS
XX  Synthetic.
XX
XX  PN
XX  JP11089565-A.
XX
XX  PD
XX  06-APR-1999.
XX
XX  PF
XX  19-SEP-1997; 97JP-00271927.
XX
XX  PR
XX  19-SEP-1997; 97JP-00271927.
XX
XX  PA
XX  (SHIS ) SHISEIDO CO LTD.
XX
XX  DR
XX  WPI; 1999-281045/24.
XX
XX  Immortalised human hair papilla cells used for evaluation of hair growth
PT  agent - are prepared by transformation of human hair papilla cells with
PT  gene with deleted replication initiation point.
XX
XX  PS
XX  Example 2; Page 8; 23pp; Japanese.
XX
XX  The specification describes the preparation of immortalized human hair
CC  papilla cells (HPC). The method comprises transformation of HPC with an
CC  SV40 viral large T-antigen gene with deleted replication initiation
CC  point. The immortalized HPC can be used in a screening method for a hair
CC  growth agent, by culture of immortalized HPC in the presence of a
CC  substance to be tested and observation of the growth of the immortalized
CC  HPC. HPC is also used in development of hair growth stimulating agents.
CC  The present sequence represents a PCR primer, which is used in the course
CC  of the invention
XX
XX  SQ
XX  Sequence 20 BP; 4 A; 2 C; 7 G; 7 T; 0 U; 0 Other;

Query Match      0.5%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. NO. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1038 AGAAGTTCCTTCTGATCTGT 1056
DB  1 AGAAGTTCGGTATCTGT 19

RESULT 133
AAZ02986
ID  AAZ02986 standard; DNA; 20 BP.
XX
XX  AC
XX  AAZ02986;
XX
XX  DT
XX  07-OCT-1999 (first entry)
XX
XX  DE
XX  PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
XX  Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW  paratrachoma; inclusion conjunctivitis; genital disease; perihhepatitis;
KW  nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
KW  bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
XX  OS
XX  Synthetic.
XX
XX  OS
XX  Chlamydia trachomatis.
XX
XX  PN
XX  WO928475-A2.

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XX  10-JUN-1999.
PD
XX  PF
XX  27-NOV-1999; 98WO-IB001939.
XX
XX  PR
XX  28-NOV-1997; 97FR-00015041.
XX  17-DEC-1997; 97FR-00016034.
XX  04-NOV-1998; 98US-0107077P.
XX
XX  PA
XX  (GEST ) GENSET.
XX
XX  PI
XX  Griffais R;
XX
XX  DR
XX  WPI; 1999-371125/31.
XX
XX  PT
XX  Genome sequence of Chlamydia trachomatis.
XX
XX  PS
XX  Disclosure; Page 1569; 1755pp; English.
XX
XX  CC
XX  PCR primers AAZ01426-Z06209 were used to amplify open reading frames
XX  (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
XX  encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
XX  against Chlamydia trachomatis. Antisense and ribozyme sequences can also
XX  be used to control growth of the microorganism. Chlamydia trachomatis is
XX  responsible for a large number of diseases, e.g. eye diseases such as
XX  conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
XX  conjunctivitis; genital diseases such as nongonococcal urethritis,
XX  epididymitis, cervicitis, salpingitis, perihhepatitis, bartholinitis;
XX  CC  pneumonia in breast feeding infants; and venereal lymphogranulomatosis.
XX  The polypeptides of the invention may be of use in treating these
XX  diseases
XX
XX  SQ
XX  Sequence 20 BP; 8 A; 2 C; 8 G; 2 T; 0 U; 0 Other;

Query Match      0.5%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. NO. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  21 GCTGATAGAGAGAGAAATC 39
DB  1 GCTGAGGAGAGAGAAATC 19

RESULT 134
AAZ36993/C
ID  AAZ36993 standard; DNA; 20 BP.
XX
XX  AC
XX  AAZ36993;
XX
XX  DT
XX  13-MAR-2000 (first entry)
XX
XX  DE
XX  Probe for peripheral benzodiazepine receptor associated protein-1 DNA.
XX
XX  Human; peripheral benzodiazepine receptor associated protein-1; PRAX-1;
KW  peripheral benzodiazepine receptor; chromosome 17;
KW  central nervous system; immune system; gene therapy;
KW  PRAX-1 deficiency condition; endocrine system; probe; PCR primer; ss.
XX
XX  OS
XX  Synthetic.
XX
XX  OS
XX  Homo sapiens.
XX
XX  PN
XX  WO9960117-A2.
XX
XX  PD
XX  25-NOV-1999.
XX
XX  PF
XX  06-MAY-1999; 99WO-FR001070.
XX
XX  PR
XX  15-MAY-1998; 98FR-00006190.
XX
XX  PA
XX  (SNFI ) SANOFI-SYNTHELABO.
XX
XX  PI
XX  Casellas P, Gallegue S, Jbilo O, Le Fur G;

```

DR WPI; 2000-062455/05.

XX New PRAX-1 polypeptide that interact with peripheral benzodiazepine

PT receptor, used to treat e.g. immune, central nervous or endocrine

PT disorders.

XX

PS Claim 14; Page 21; 44pp; French.

XX

CC AA236990-237023 represent probes for the polynucleotides encoding a human

CC peripheral benzodiazepine receptor associated protein-1, designated PRAX-

CC 1. The probes may also function as PCR primers. PRAX-1 interacts

CC specifically with the peripheral benzodiazepine receptor. The PRAX-1 gene

CC is localised on chromosome 17 in the q22-q23 region. The gene is

CC associated with markers of pathologies of the central nervous system or

CC immune system. The PRAX-1 nucleic acid is useful in gene therapy (of PRAX

CC -1 deficiency conditions, e.g. disorders of the central nervous, immune

CC or endocrine systems; as a source of diagnostic primers and probes (see

CC AA236990-237023) and of antisense therapeutics; for recombinant

CC production of the PRAX-1 protein; and for detecting allelic variants,

CC mutations, deletions, insertions, loss of heterozygosity and gene

CC rearrangements in the PRAX-1 gene. The PRAX-1 protein is used to raise

CC specific antibodies and to screen for specific modulators (potential

CC therapeutic agents). The antibodies are used as immunoassay reagents,

CC e.g. for diagnosis of abnormal expression or accumulation of PRAX-1

XX

SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.8; DB 1; Length 20;

Best Local Similarity 89.5%; Pred. No. 1.9e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1568 GAACCTGTGCCCATGATG 1586

||| ||||| ||||| |||||

DB 20 GAGCTGTGCCCATGATG 2

RESULT 135

AA236990-237023

ID AAC84372/c

XX AAC84372 standard; DNA; 20 BP.

AC AAC84372;

XX

DT 19-MAR-2001 (first entry)

XX

DE Mouse Zace2 gene specific probe generating primer 22997.

XX

XX Zace2; metalloenzyme; angiotensin-converting enzyme; ACE; fertility;

XX zinc metalloproteinase; blood pressure; zinc protease; hypertension;

XX ventricular systolic dysfunction; renal impairment; heart failure;

XX scleroderma renal crisis; atherosclerosis; antiinflammatory; mouse;

XX antiarthritic; bradykinin inactivator; PCR primer; ss.

XX

OS Mus sp.

XX

PN W0200070032-A1.

XX

PD 23-NOV-2000.

XX

PF 03-MAY-2000; 2000WO-US011932.

XX

PR 13-MAY-1999; 99US-00311482.

XX

PR 27-AUG-1999; 99US-00384706.

XX

PA (ZYMO) ZYMOGENETICS INC.

XX

PI Piddington CS, Petrie CR, Shoemaker KE, Bishop PD;

XX

XX WPI; 2001-025018/03.

DR

XX Angiotensin-converting enzyme, Zace2, useful for treating inflammatory

PT bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases

PT associated with inflammation such as arthritis and enterocolitis.

XX

PS Example 2; Page 88; 125pp; English.

XX

CC The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin-

CC converting enzyme is a zinc metalloproteinase that plays roles in blood

CC pressure regulation and fertility. Zace2 can be expressed by standard

CC recombinant methodology. Zace2 polypeptides are useful for treating an

CC inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis),

CC diseases associated with inflammation like arthritis and enterocolitis,

CC as targets for identifying modulators of zinc protease activity, for

CC screening or identifying new angiotensin-converting enzyme (ACE)

CC inhibitors, and as a basis for rational drug design for inhibitory

CC molecules. The nucleic acids can be used to detect the expression of a

CC Zace2 gene in a biological sample, as probes for in vivo diagnosis and

CC for detecting and localizing Zace2 gene expression in tissue samples, to

CC determine whether a subject's chromosomes contain a mutation in the Zace2

CC gene, and to detect aberrations associated with the Zace2 locus.

CC Inhibitors of ACE are used for treating hypertension of various

CC conditions, including left ventricular systolic dysfunction, progressive

CC renal impairment, scleroderma renal crisis, congestive heart failure due

CC to dysfunction, and treatment of atherosclerosis. Zace2 agonists may be

CC used to treat infertility while Zace2 antagonists are used for inducing

CC infertility. Sequences AAC84371-72 represent PCR primers for generating a

CC probe used for analysis of the murine Zace2 gene

XX

SQ Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.8; DB 1; Length 20;

Best Local Similarity 89.5%; Pred. No. 1.9e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 876 CAATTGGATGCTCCCTGTC 894

||| ||||| ||||| |||||

DB 20 CCACCTGGATGCTCCCTGTC 2

RESULT 136

ABK69446

ID ABK69446 standard; DNA; 20 BP.

XX

AC ABK69446;

XX

DT 15-JUL-2002 (first entry)

XX

DE Human phosphorylase kinase alpha-1 antisense oligonucleotide #30.

XX

XX Human; rat; antisense; phosphorylase kinase alpha 1; ss;

XX antiinflammatory; cytostatic; antimicrobial; antidiabetic;

XX metabolic disorder; diabetes; infection; inflammation; tumour; probe.

XX

OS Homo sapiens.

OS Mus sp.

OS Synthetic.

OS Chimeric.

XX

XX

Key Location/Qualifiers

modified_base 1..20

FT /tag= a

FT /mod_base= OTHER

FT /note= "OTHER = phosphorothioate backbone, all cytidine

FT residues are 5-methyl cytidine"

FT modified_base 1..5

FT /tag= b

FT /mod_base= OTHER

FT /note= "OTHER = 2'-O-methoxyethyl"

FT modified_base 5..15

FT /tag= c

FT /mod_base= OTHER

FT /note= "OTHER = 2' deoxynucleotide"

FT modified_base 15..20

FT /tag= c

FT /mod_base= OTHER

FT /note= "OTHER = 2'-O-methoxyethyl"

XX

PN WO200220546-A1.
XX 14-MAR-2002.
PD 24-AUG-2001; 2001WO-US026608.
PF 07-SEP-2000; 2000US-00657452.
XX (ISIS-) ISIS PHARM INC.
PA Monia BP, Wyatt JR;
PI WPI; 2002-351759/38.
DR
XX
XX New antisense compound which is targeted to nucleic acid encoding
PT phosphorilase kinase alpha 1 and inhibits expression of kinase protein,
PT useful for treating a condition associated with kinase, e.g. diabetes.
XX
XX Claim 3; Page 85; 140pp; English.
XX
XX This invention relates to a novel antisense nucleic acid compound
CC targeted to a nucleic acid molecule encoding phosphorilase kinase alpha-1
CC which specifically hybridizes with and inhibits expression of
CC phosphorilase kinase alpha-1. The compound of the invention is useful for
CC inhibiting the expression of phosphorilase kinase alpha-1 in cells or
CC tissues, and for treating an animal having a disease condition associated
CC with phosphorilase kinase alpha-1, e.g. a metabolic disorder such as
CC diabetes. The compounds are also useful prophylactically, e.g. to prevent
CC or delay infection, inflammation or tumour formation. The antisense
CC compounds are also useful as therapeutic, diagnostic and research
CC reagent, for distinguishing functions of various members of a biological
CC pathway, and in antisense gene therapy. The present sequence represents
CC an antisense oligonucleotide probe used to create the phosphorilase
CC kinase alpha-1 inhibiting compound of the invention
XX
XX Sequence 20 BP; 9 A; 1 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 0.5%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3249 AACTGTGGAGTGAATGGAA 3267
DB 2 AACTGTGGAGTGAATGGAA 20
|||||
RESULT 137
ABZ86050
ID ABZ86050 standard; DNA; 20 BP.
XX
AC ABZ86050;
XX
XX 17-OCT-2003 (first entry)
XX Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
XX WO200285308-A2.
PN
XX
XX 31-OCT-2002.
PD
XX
XX 23-APR-2002; 2002WO-US013135.
PF
XX
XX 24-APR-2001; 2001US-0286137P.
PR
XX

PA (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shanabuddin S;
XX
XX WPI; 2003-229219/22.
DR
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Claim 15; SEQ ID NO 1292; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiasthmatic, antiasthmatic, hypotensive, a
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 5 A; 2 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 0.5%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 767 TTGATTGAAGATGTGGAC 785
DB 2 TTGATTGAAGATGTGGATC 20
|||||
RESULT 138
ABX93339/C
ID ABX93339 standard; DNA; 20 BP.
XX
AC ABX93339;
XX
XX 27-MAY-2003 (first entry)
XX
XX Oligonucleotide used to generate 3' end of mouse Zace2 DNA probe.
XX
XX Mouse; ss; Zace2; zinc metalloproteinase; ulcerative colitis;
KW inflammation; inflammatory bowel disease; arthritis; enterocolitis;
KW Crohn's disease; gene therapy; transgenic.
XX
OS Mus sp.
XX
XX US2002177211-A1.
PN
XX
XX 28-NOV-2002.
PD
XX
XX 16-OCT-2001; 2001US-00978385.
PF
XX
XX 13-MAY-1999; 99US-0133952P.
PR
XX 27-AUG-1999; 99US-0151181P.
PR
XX 03-MAY-2000; 2000US-00563516.
XX
XX (ZYMO) ZYMOGENETICS INC.
PA

XX Piddington CS, Petrie C, Shoemaker KF, Bishop PD;
 XX WPI; 2003-328489/31.
 XX
 XX Isolated human or murine Zace2 polypeptide useful for reducing
 PT inflammation in conditions such as inflammatory bowel disease, arthritis,
 PT enterocolitis, ulcerative colitis and Crohn's disease.
 XX
 XX Example 2; Page 36; 57pp; English.
 XX
 XX The invention relates to an isolated polypeptide, comprising fully
 CC defined human Zace2, murine Zace-5, or murine Zace2-10 polypeptide. An
 CC expression vector containing Zace2 polynucleotide is useful for producing
 CC Zace2 protein. The polynucleotide is useful as a diagnostic probe for
 CC detecting a product of Zace2 gene expression in a biological sample. The
 CC polypeptide is also useful for decreasing inflammation associated with a
 CC condition such as inflammatory bowel disease, arthritis or enterocolitis.
 CC The polypeptide is also useful for treating Crohn's disease and
 CC ulcerative colitis. The polypeptide is useful for producing labelled
 CC angiotensin II, for identifying modulators of zinc protease activity and
 CC for identifying angiotensin converting enzyme (ACE) inhibitors. The
 CC polynucleotide is useful in gene therapy techniques to treat the above
 CC mentioned disorders. The polynucleotide is also useful for determining
 CC whether a subject's chromosome contains a mutation in the Zace2 gene. The
 CC present sequence represents an oligonucleotide used to generate the 3',
 CC end of a DNA probe for the murine Zace2 gene
 XX
 XX Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 U; 0 Other;
 SQ

Query Match 0.5%; Score 15.8; DB 1; Length 20;
 Best Local Similarity 89.5%; Pred. No. 1.9e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 876 CAAATGGATGCTCCCTGC 894
 DB 20 CCACATGGATGCTCCCTGC 2

RESULT 139
 AAN90677/C
 ID AAN90677 standard; DNA; 21 BP.
 XX
 XX AAN90677;
 AC
 XX
 XX 24-JUN-1990 (first entry)
 DT
 XX
 XX Variant myc gene encoding variant myc protein.
 DE
 XX
 XX myc gene; variant.
 KW
 XX
 XX Unidentified.
 OS
 XX
 XX JP01039999-A.
 PN
 XX
 XX 10-FEB-1989.
 PD
 XX
 XX 06-AUG-1987; 87JP-00197197.
 PF
 XX
 XX 06-AUG-1987; 87JP-00197197.
 PR
 XX
 XX (MITK) MITSUI TOATSU CHEM INC.
 PA
 XX
 XX WPI; 1989-089714/12.
 DR
 XX
 XX N-PSDB; AAN92942.
 DR
 XX
 XX MYC protein for antibody prepn. - is stabilised by converting
 PT aminoacid(s) of MYC protein to other aminoacid to produce variant type
 PT MYC protein.
 XX
 XX Fig 1(a); page 9; 18pp; Japanese.
 PS
 XX
 XX Variant myc gene encoding variant myc protein. The myc protein is

CC produced in E. coli, B. subtilis, yeast or animal cells. It is stabilised
 CC by the variation in amino acid compsn. which does not affect the
 CC properties of the myc protein. Myc protein can be used for prepn. of poly
 CC - or monoclonal antibody
 XX
 XX Sequence 21 BP; 5 A; 5 C; 3 G; 8 T; 0 U; 0 Other;
 SQ

Query Match 0.5%; Score 15.8; DB 1; Length 21;
 Best Local Similarity 89.5%; Pred. No. 2e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 568 TTTAGACTACATGACGAGG 586
 DB 20 TTTAGACTACATGACGAGG 2

RESULT 140
 AAA48903
 ID AAA48903 standard; DNA; 21 BP.
 XX
 XX AAA48903;
 AC
 XX

DT 20-SEP-2000 (first entry)
 XX

DE Forward primer 12.253f targeted to feline IL-12.
 XX

XX PCR primer; quantitative one-tube fluorogenic real time PCR; virus;
 KW bacterium; interleukin; GAPDH; feline; equine; ss.
 XX

OS Felis sp.
 XX

PN EP1013775-A1.
 XX

PD 28-JUN-2000.
 XX

PF 21-DEC-1998; 98EP-00124317.
 XX

PR 21-DEC-1998; 98EP-00124317.
 XX

XX (LUTZ/) LUTZ H.
 XX

XX WPI; 2000-402210/35.
 XX

PT Novel PCR method useful for the detection of pathogens, genetic
 PT mutations, etc. comprises the use of very specific DNA probes.
 XX

XX Claim 17; Page 25; 68pp; English.
 XX

CC The present invention involves a new method for identification and
 CC quantification of at least one pathogen in a sample. The method uses an
 CC improved quantitative one-tube fluorogenic real time polymerase chain
 CC reaction. In this process a very specific probe labeled with a reporter
 CC dye and a quencher dye hybridises with the target sequence. PCR primers
 CC are then allowed to bind to the target nucleic acid. As the primers are
 CC extended the exonuclease activity of the polymerase causes cleavage of
 CC the probe. This separation of the reporter dye from the quencher dye
 CC leads to a detectable increase in the reporter's fluorescence. The
 CC present sequence is a PCR primer used in the method. The invention
 CC includes primer and probe sequences for the detection of viruses,
 CC bacteria and interleukins and GAPDH from feline and equine species. The
 CC method is useful for the detection of infectious agents, quantitation of
 CC mRNA expression and detection of genetic mutations
 XX

SQ Sequence 21 BP; 2 A; 4 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.8; DB 1; Length 21;
 Best Local Similarity 89.5%; Pred. No. 2e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 385 GCTTCAGTGCAGGCTCTT 403

DB 3 GCTTCAGTGCAGGCTCTT 21

```

RESULT 141
AAH27898
ID AAH27898 standard; DNA; 21 BP.
XX
XX AC AAH27898;
XX
XX 05-SEP-2001 (first entry)
XX
XX PCR primer for a minimal deletion in FRA16D oxidoreductase gene.
XX
XX Cancer associated protein; FOR gene; FRA16D; fragile site; aphidicolin;
XX chromosomal rearrangement; cancer; splice variant; DNA instability;
XX FRA16D oxidoreductase; neoplasia; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200144466-A1.
XX
XX 21-JUN-2001.
XX
XX 15-DEC-2000; 2000WO-AU001539.
XX
XX 16-DEC-1999; 99AU-00004711.
XX
XX 19-APR-2000; 2000AU-00007025.
XX
XX (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
XX
XX Richards R, Ried K, Finnis M, Hobson L, Mangelsdorf M, Dayan S;
XX Nancarrow J, Woollatt E, Baker E;
XX
XX WPI; 2001-398151/42.
XX
XX Novel isolated 16q23.2 nucleic acid molecule, FRA16D oxidoreductase (FOR)
XX gene associated with FRA16D site, useful for early diagnosis and
XX assessment of risk of cancers associated with the FRA16D region.
XX
XX Example 1; Page 46; 150pp; English.
XX
XX PCR primers AAH27888-AAH28055 represent PCR primers used to amplify and
XX identify minimal deletions in the human FRA16D oxidoreductase (FOR) gene.
XX The FOR gene encodes a cancer associated protein. The FRA16D site is a
XX fragile site induced by aphidicolin, which is located within the FOR
XX gene. The fragile site is the location of breakpoints of a variety of
XX chromosomal rearrangements, and other mutations associated with cancers.
XX The FOR protein is expressed as a number of splice variants. FOR gene
XX polynucleotide fragments are capable of acting as specific primers or
XX probes for detecting cancer associated variations of DNA sequence such as
XX a point mutation or small DNA rearrangement associated with the tumour, a
XX breakpoint of one or more chromosomal rearrangements associated with the
XX tumour and a pause site within the FRA16 gene. FOR nucleic acid molecules
XX are useful as markers to identify relationship between the fragile site
XX (FRA16D) and the DNA instability in neoplasia which allows better
XX diagnosis of cancers associated with the region
XX
XX Sequence 21 BP; 7 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.5%; Score 15.8; DB 1; Length 21;
XX Best Local Similarity 89.5%; Pred. No. 2e+02;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1588 AACATACGTGTGACCCGCA 1606
DB 1 AACATACGTGTGACCATGCA 19

RESULT 142
AAH17349/c
ID AAS17349 standard; DNA; 21 BP.
XX
XX AAS17349;
XX
XX 29-AUG-2003 (revised)
XX

DT 25-FEB-2002 (first entry)
XX
XX Sequencing primer Seq6R for HIV-1 pol gene.
XX
XX Human immunodeficiency virus; HIV-1; HIV pol gene mutation analysis;
XX AIDS; acquired immunodeficiency syndrome; sequencing primer; ss.
XX
XX Human immunodeficiency virus 1.
XX
XX WO200181624-A1.
XX
XX 01-NOV-2001.
XX
XX 20-APR-2001; 2001WO-EP004558.
XX
XX 20-APR-2000; 2000EP-00201433.
XX
XX 18-AUG-2000; 2000US-00640787.
XX
XX (VIRC-) VIRCO NV.
XX
XX Larder B, Kemp S, Bloor S, Brophy A;
XX
XX WPI; 2002-055358/07.
XX
XX Mutation analysis of pol gene of HIV-1 isolates, comprises extracting
XX virion nucleic acids, amplifying them through two cycles of nested
XX polymerase chain reaction, and sequencing useful for analyzing sequence
XX of HIV pol gene.
XX
XX Claim 8; Page 14; 40pp; English.
XX
XX The present invention relates to a method for mutation analysis (M) of
XX the pol gene of human immunodeficiency virus (HIV)-1 isolates. The method
XX comprises isolating a sample, extracting virion RNA or DNA of the
XX isolated sample material, amplifying the RNA or DNA through two cycles of
XX nested polymerase chain reaction (PCR), and sequencing the PCR product
XX using at least one sequencing primer. The primer sequences of the
XX invention (AAS17338-AAS17361) are useful for analysing the sequence of
XX HIV pol gene of HIV-1 isolates. The method is useful for mutation
XX analysis of the pol gene of HIV-1 isolates. The method is fast, reliable,
XX complete, and suitable for analysing mixed samples. The primer
XX combination used in the method reduces the analytical period since all
XX mutations can be sequenced in a single laboratory format, avoiding the
XX necessary step of additional cloning or resequencing part of the viral
XX genome to identify all mutations related to drug resistance. Using the
XX protocol of the method, the sequence of the sample is reliably determined
XX on a single day. The method and the primer combination improve the
XX monitoring of drug resistance, leading to improved management of AIDS
XX (acquired immunodeficiency syndrome) patients. The present sequence
XX represents one of the sequencing primers of the invention. (Updated on 29
XX -AUG-2003 to standardise OS field)
XX
XX Sequence 21 BP; 4 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.5%; Score 15.8; DB 1; Length 21;
XX Best Local Similarity 89.5%; Pred. No. 2e+02;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1072 GACTCAAGATTCTCGGAA 1090
DB 20 GACTCAAGACTTCTCGGAA 2

RESULT 143
AAV42577/c
ID AAV42577 standard; DNA; 22 BP.
XX
XX AAV42577;
XX
XX 06-OCT-1998 (first entry)
XX
XX PCR primer 5R2N used to find transcription start site of AtDMC1 gene.
XX

```

KW Arabidopsis thaliana meiosis-specific DMCI gene; AtDMCI; promoter;
 KW meiosis specific expression; ablation; meiotic cell; isolation;
 KW apomictic plant; increase; meiotic recombination; introgression;
 KW sterile plant; seed production; PCR primer; ss.
 XX
 OS Synthetic.
 OS Arabidopsis thaliana.
 PN WO9828431-A1.
 XX
 PD 02-JUL-1998.
 XX PF
 XX 24-DEC-1997; 97WO-GB003546.
 XX
 XX 24-DEC-1996; 96GB-00026858.
 XX
 PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.
 XX
 XX Jones JDC, Klimyuk VI, Dirks R;
 XX WPI; 1998-377661/32.
 DR
 XX New isolated Arabidopsis meiosis-specific promoter - useful for meiosis-
 PT specific transcription of genes, e.g. for isolation of apomictic plants
 PT or removing DNA from transgenic plants.
 XX
 XX Example 1; Page 27; 69pp; English.
 XX
 CC PCR primers AAV42576-78 were used to find the transcription start site of
 CC the Arabidopsis thaliana meiosis-specific DMCI gene (AtDMCI). The AtDMCI
 CC promoter and homologues can be used to confer meiosis specific expression
 CC on a sequence operably linked to the promoter. They can be used for e.g.
 CC ablation of meiotic cells and isolation of apomictic plants, designing an
 CC efficient homologous recombination system for plants, increasing meiotic
 CC recombination frequency, for introgression of alien chromosome segments
 CC into host plant, or altering normal events of cell cycle during the time
 CC of meiosis and producing male and female sterile plants. The promoters
 CC can also be used in searching for apomictic mutants or used by seed
 CC producers to produce seeds apomictically. They can also be used for
 CC removing any unwanted DNA sequences from transgenic plants
 XX
 XX Sequence 22 BP; 7 A; 6 C; 3 G; 6 T; 0 U; 0 Other;
 Query Match 0.5%; Score 15.8; DB 1; Length 22;
 Best Local Similarity 89.5%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 830 TATGTGAGGCAAGTTGA 848
 Db ||| ||||| ||||| |||||
 19 TATCTGAGGCAAGTTGA 1
 RESULT 144
 AAX91324/c
 ID AAX91324 standard; DNA; 22 BP.
 XX
 AC AAX91324;
 XX
 DT 24-SEP-1999 (first entry)
 XX
 DE Primer for RT-PCR analysis of T. gondii immunogenic protein DNA.
 XX
 KW Immunogenic protein; Toxoplasma gondii protein; oocyst shedding; cat;
 KW T. gondii infection; enteric apicomplexa oocyst; Cryptosporidium oocyst;
 KW Toxoplasma oocyst; RT-PCR primer; ss.
 XX
 OS Synthetic.
 OS Toxoplasma gondii.
 XX
 XX WO9932633-A1.
 PN
 XX 01-JUL-1999.
 PD
 XX

PF 18-DEC-1998; 98WO-US027137.
 XX
 PR 19-DEC-1997; 97US-00994825.
 XX
 PA (HESK-) HESKA CORP.
 XX
 XX Milhausen MJ, Lutz SB, Ng RK;
 XX WPI; 1999-418930/35.
 DR
 XX New isolated Toxoplasma gondii nucleic acids used, e.g. to treat
 PT infection caused by this microorganism.
 PT
 XX
 XX Example 2; Page 68; 381pp; English.
 XX
 CC The invention provides isolated Toxoplasma gondii nucleic acids that
 CC encode immunogenic polypeptides. The T. gondii nucleic acid molecules,
 CC immunogenic proteins and antibodies to the proteins can be used to
 CC inhibit T. gondii oocyst shedding in a cat due to infection with T.
 CC gondii. They can be used for preventing T. gondii infection and for
 CC preventing the spread of T. gondii infection. They can also be used for
 CC detecting T. gondii infection. The detection method can be used to detect
 CC parasite cysts or oocysts in feces, e.g. from enteric apicomplexa oocysts
 CC such as Cryptosporidium oocysts and Toxoplasma oocysts. Sequences
 CC AAX91276-395 primers used in RT-PCR analysis of nucleic acid sequences
 CC encoding immunogenic T. gondii proteins
 XX
 XX Sequence 22 BP; 6 A; 4 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 0.5%; Score 15.8; DB 1; Length 22;
 Best Local Similarity 89.5%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3132 TGCTTTTTCACCTCCAGG 3150
 Db ||| ||||| ||||| |||||
 21 TGCTTCTGCACCTCCAGG 3
 RESULT 145
 AAS42647/c
 ID AAS42647 standard; DNA; 22 BP.
 XX
 AC AAS42647;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE T. gondii immunogenic protein PCR primer ntG38 #2.
 XX
 KW Immunogenic protein; oocyst; faeces; ss; enteric apicomplexa oocyst;
 KW Cryptosporidium oocyst; Toxoplasma oocyst; Giardia cyst; vaccine;
 KW oocyte shedding; PCR primer.
 XX
 OS Toxoplasma gondii.
 XX
 PN US2001014447-A1.
 XX
 PD 16-AUG-2001.
 XX
 PF 18-DEC-1998; 98US-00216393.
 XX
 PR 19-DEC-1997; 97US-00994825.
 XX
 XX (MLH/) MILHAUSEN M J.
 PA
 XX Milhausen MJ;
 PI
 XX WPI; 2001-529100/58.
 DR
 XX Detecting parasite oocysts or cysts in feces, comprises eluting DNA from
 PT sample into aqueous solution by heating, amplifying DNA with primers
 PT specific for oocysts or cysts being detected, and detecting amplification
 PT product.
 XX
 XX

PS Example 2; Page 24; 188pp; English.

XX The invention relates to detection of parasite oocysts or cysts in a

CC faeces sample comprising contacting the sample with a solid support,

CC drying and then washing the sample with an aqueous wash solution, adding

CC an aqueous elution solution and eluting DNA from the sample by heating

CC and amplifying by PCR oocyst/cyst-specific DNA and detecting the

CC amplification products. The method is useful for detecting parasite

CC oocysts e.g., enteric apicomplexa oocysts such as *Cryptosporidium* oocysts

CC or *Toxoplasma* oocysts, or for detecting parasite cysts e.g. *Giardia*

CC cysts. The method is also useful for developing vaccines to prevent

CC oocyst shedding in cats. The present sequence is a PCR primer used to

CC isolate DNAs encoding immunogenic proteins from *Toxoplasma gondii*

XX

SQ Sequence 22 BP; 6 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.8; DB 1; Length 22;

Best Local Similarity 89.5%; Pred. No. 2.2e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3132 TGCCTTTTCACCTCCAGG 3150

DB 21 TGCCTTTCACCTCCAGG 3

RESULT 146

AAT45744/c

ID AAT45744 standard; DNA; 22 BP.

XX AC AAT45744;

XX 17-FEB-1997 (first entry)

XX Human granulocyte macrophage-colony stimulating factor gene primer.

DE Human granulocyte macrophage-colony stimulating factor gene primer.

XX Polymerase chain reaction; PCR; interleukin; IL; cytokine; growth factor;

XX animal model; stem cell; haematopoiesis; CD34; infection; HIV;

KW human immunodeficiency virus; immunomodulator; immortalise; bone marrow;

KW stromal cell; engraftment; determination; study; research; ss.

XX

OS Homo sapiens.

XX

PN WO9617627-A2.

XX

PD 13-JUN-1996.

XX

PF 08-DEC-1995; 95WO-US015986.

XX

PR 09-DEC-1994; 94US-00352957.

XX

PA (MOSC/) MOSCA J D.

PA (GART/) GARTNER S.

PA (KESS/) KESSLER S.

PA (LRUS/) LA RUSSA V.

PA (HALL/) HALL E.

PA (KAUS/) KAUSHAL S.

XX

PI Mosca JD, Gartner S, Kessler S, La Russa V, Hall E, Kaushal S;

XX

DR WPI; 1996-286928/29.

XX

PT Animal models for human haematopoiesis - have en-grafted human or primate

PT stem cells in the presence of immortalised bone marrow stromal cells.

XX

PS Example 1; Page 27; 43pp; English.

XX

CC AAT45736-T45753 are PCR primers used to determine whether or not certain

CC cytokines (IL-1, IL-6, IL-8, GM-CSF, G-CSF, M-CSF, TGF-alpha and stem

CC cell factor) are expressed by a human bone marrow stromal cell line,

CC Lof(11-10). The primers were used in a PCR to identify genes encoding the

CC cytokines. The cells were found to produce the cytokines which support

CC the growth of CD34+ stem cells. The Lof(11-10) cells were injected into

CC SCID mice (previously irradiated to provide an internal space for CD34+

CC

CC cells to populate). Five to seven days after injection the mice were

CC injected with 3 to 5 human CD34+ cells. After 3 weeks, human CD34+ cells

CC were found in the bone marrow of the mice. The immortalised bone marrow

CC stem cells create a human microenvironment supplying human cytokines in

CC the animals to provide for the engraftment, maintenance and

CC differentiation of CD34+ stem cells. Animal models created by

CC administering Lof(11-10) cells are used to study and determine the

CC effectiveness of therapies against disease such as HIV infection. They

CC can also be used to assay for haematopoietic growth factors,

CC immunomodulators and/or immune toxins

XX

SQ Sequence 22 BP; 3 A; 6 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.6; DB 1; Length 22;

Best Local Similarity 81.8%; Pred. No. 2.2e+02;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 391 GCTCAGGCTCTTCAGCAAAAT 412

DB 22 GCAGCAGGCTCTGCAGCCACAT 1

RESULT 147

AAT47004/c

ID AAT47004 standard; DNA; 22 BP.

XX AC AAT47004;

XX 01-DEC-1997 (first entry)

XX Primer A for granulocyte macrophage colony stimulating factor.

DE Primer A for granulocyte macrophage colony stimulating factor.

XX PCR; polymerase chain reaction; primer; amplify; beta-actin; IL-2; IL-4;

KW interferon-gamma; interleukin-2; peripheral blood mononuclear cell; IL-5;

KW granulocyte macrophage colony stimulating factor; GM-CSF; cytokine; PMBC;

KW CD8 cell; T-cell; cell mediated immunity; cytotoxic; CD45RA; IL-10; HIV;

KW surface marker; naive T-cell; thymus; proliferative response; antibody;

KW cognate antigen; immuno-compromised; cancer; viral infection;

KW autoimmune disease; ss.

XX

OS Synthetic.

XX

PN WO9712244-A1.

XX

PD 03-APR-1997.

XX

PF 26-SEP-1996; 96WO-US015460.

XX

PR 27-SEP-1995; 95US-0004364P.

XX

PA (STRD) UNIV LELAND STANFORD JUNIOR.

XX

PI Roederer M, Rabin R, Herzenberg LA, Herzenberg LA;

XX

DR WPI; 1997-213057/19.

XX

PT Detection of naive T cells in subjects - useful to identify production

PT stimulating drugs for immunocompromised subject treatment.

XX

PS Disclosure; Page 23; 56pp; English.

XX

CC AAT46992-T47005 represent amplification primers for DNA encoding

CC cytokines from CD8 T-cells. This sequence and AAT47005 are primers for

CC the granulocyte macrophage colony stimulating factor gene. The naive

CC subset of CD8 cells expresses the CD45RA surface marker, and make a

CC relatively poor cytokine response after T-cell receptor stimulation.

CC Naive T-cells are cells which have recently emigrated from the thymus and

CC have a predominantly proliferative response when exposed to cognate

CC antigens for the first time. These primers can be used in the method of

CC the invention. The method of the invention is for evaluating the efficacy

CC of a drug to stimulate the production of naive T-cells. The method

CC comprises obtaining a sample containing peripheral blood mononuclear

CC cells from a subject. A suitable dose of a drug is then administered

CC mouse may be used as a model for determining the allergenicity of non-
 CC donor, e.g., non-human, macromolecules; to determine the effect compounds
 CC have on a human immune system; to generate fully human polyclonal or
 CC monoclonal antibodies to specific antigens; to determine whether
 CC humanised or other monoclonal antibodies will raise a response in a human
 CC immune system; to investigate the human cell mediated response to
 CC pathogens and other immunomodulatory compounds; and to determine the
 CC factors involved in regulating the development and function of human
 CC haematopoietic cells. The transgenic mouse supports the functional
 CC properties of human haematopoietic cells, unlike previous animal models
 CC which produce functionally impaired haematopoietic cells or are
 CC immunologically dysfunctional. In addition the transgenic mouse provides
 CC a unique model system which supports T cell development in a manner which
 CC more closely resembles normal ontogeny, as they possess CD4+ T cells in
 CC the periphery that exhibit MHC-restricted antigen- specific responses.
 CC Sequences AAF76133-AAF76192 represent human cytokine PCR primers used in
 CC the development of human cytokine-expressing transgenic mice
 XX

SQ Sequence 22 BP; 3 A; 6 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.6; DB 1; Length 22;
 Best Local Similarity 81.8%; Pred. No. 2.2e+02;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 391 GCTCGAGGCTCTTCAGCAAAAT 412
 |||||
 Db 22 GCAGCAGGCTCTGCAGCCACAT 1

RESULT 150
 ABZ84117/c
 ID ABZ84117 standard; DNA; 22 BP.

XX AC ABZ84117;

XX DT 14-MAY-2003 (first entry)

XX DE Toxicologically relevant rat PCR primer #1276.

XX KW Toxicologically relevant gene; toxicological response; PCR primer; ss.

XX OS Rattus sp.

XX OS Synthetic.

XX PN WO2003016500-A2.

XX PD 27-FEB-2003.

XX PF 16-AUG-2002; 2002WO-US026514.

XX PR 16-AUG-2001; 2001US-0313080P.

XX PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

XX PI Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schmeiser K;

XX PI Alen P;

XX DR WPI; 2003-268322/26.

XX PT Determining a toxicological response to an agent, useful for screening of
 PT drugs, comprises comparing the expression profile of one or more human
 PT toxic response genes to a reference gene expression profile indicative of
 PT toxicity.

PS Claim 1; Page 332; 455pp; English.

XX The present invention describes a method (M1) for determining a
 CC toxicological response to an agent, which comprises comparing the
 CC expression profile of one or more human toxic response genes to a
 CC reference gene expression profile indicative of toxicity, and so
 CC determining the presence of a toxic response to the agent. Also
 CC described: (1) an array comprising one or more polynucleotides selected
 CC from the genes corresponding to the partial sequences given in ABZ82842

CC to ABZ84764, or their fragments of at least 20 nucleotides, or homologues
 CC ; and (2) determining if a gene putatively identified to be a toxic
 CC response gene plays a role on toxic response pathways by determining the
 CC expression profile of the gene after exposure of cells or a human subject
 CC to a known toxic pharmaceutical or industrial agent, comprising: (a)
 CC exposing cells to an agent or isolating cells from a human subject who
 CC was exposed to an agent; (b) obtaining the test gene expression profile
 CC for a putatively identified toxic response gene after exposure to a known
 CC toxic pharmaceutical or industrial agent; and (c) comparing the test
 CC profile to the expression profile of a gene with a similar function or
 CC comparing the test profile to the expression profile of that gene after
 CC exposure to other known toxic compounds. The methods are useful for
 CC predicting and determining toxicological responses on a cellular, organ
 CC or system level. The arrays comprising the human genes are useful for
 CC toxicological screening of drugs, pharmaceutical compounds and chemicals
 XX

SQ Sequence 22 BP; 4 A; 8 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.6; DB 1; Length 22;

Best Local Similarity 81.8%; Pred. No. 2.2e+02;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 156 AGTCACCATTCAGGACAGGC 177
 |||||
 Db 22 AGTACAGCATTGAGGAGCTGGC 1

RESULT 151
 ACC42617/c
 ID ACC42617 standard; DNA; 22 BP.

XX AC ACC42617;

XX DT 26-AUG-2003 (first entry)

XX DE Human GM-CSF PCR primer CT-hGMCSF-F.

XX KW Human; PCR; primer; transgenic mouse; lymphocyte maturation; IL-3; IL-7;
 KW cytokine; interleukin-3; interleukin-6; IL-6; interleukin-7; M-CSF; SCF;
 KW macrophage-colony stimulating factor; stem cell factor; oncostatin M; OM;
 KW granulocyte-colony stimulating factor; GM-CSF; LIF;
 KW leukaemia inhibitory factor; ss.

XX OS Homo sapiens.

XX PN WO2003018744-A2.

XX PD 06-MAR-2003.

XX PF 05-AUG-2002; 2002WO-US024807.

XX PR 23-AUG-2001; 2001US-00938689.

XX PA (GEMV) GENENCOR INT INC.

XX PI Harding FA, Huang M;

XX DR WPI; 2003-278650/27.

XX PT New recipient mammal, preferably a mouse, useful as a model of human
 PT disease to assess efficacy of therapeutic or prophylactic treatments, or
 PT for facilitating production of donor-specific functional immunity.

PS Example; Page 36; 70pp; English.

XX The present invention relates to a new transgenic mouse, which comprises
 CC a disruption in both alleles of a gene such that lymphocyte maturation
 CC does not occur and exogenous cytokines. The cytokines are selected from:
 CC interleukin-3 (IL-3), interleukin-6 (IL-6), interleukin-7 (IL-7),
 CC macrophage-colony stimulating factor (M-CSF), granulocyte-colony
 CC stimulating factor (GM-CSF), stem cell factor (SCF), leukaemia inhibitory
 CC factor (LIF) and oncostatin M (OM). The gene disruption is in a gene that
 CC modulated VDJ recombination e.g. a RAG gene. The gene is disrupted by

CC insertion of a transgene comprising major histocompatibility complex
 CC (MHC) Class II DR3 and DQ2 genes. The transgenic mouse is useful as a
 CC model of human disease to assess efficacy of therapeutic or prophylactic
 CC treatments, or to assess the antigenic potential of compounds. The
 CC transgenic mouse is also useful for supporting donor hematopoietic stem
 CC cells or facilitating production of donor-specific functional immunity.
 CC PCR primers ACC42571-ACC42639 were used to generate the transgenic mouse
 XX

SQ Sequence 22 BP; 3 A; 6 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.6; DB 1; Length 22;
 Best Local Similarity 81.8%; Pred. No. 2.2e+02;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 391 GCTGAGGCTCTTCAGCAAAAT 412

DB 22 GCAGCAGGCTCTTCAGCCACAT 1

RESULT 152

ABX17597/c

ID ABX17597 standard; DNA; 22 BP.

XX

AC ABX17597;

XX

DT 05-FEB-2003 (first entry)

XX

DE RTQ-PCR primer #5 for human protein NOV19.

XX

KW Human; ss; NOVX; adrenoleukodystrophy; haemophilia; stroke; VHL; PCR;
 KW congenital adrenal hyperplasia; haemophilia; hypercoagulation;
 KW idiopathic thrombocytopenic purpura; autoimmune disease; allergy;
 KW immunodeficiencies; transplantation; Von Hippel-Lindau syndrome;
 KW Alzheimer's disease; tuborous sclerosis; Parkinson's disease; epilepsy;
 KW Huntington's disease; cerebral palsy; Lesch-Nyhan syndrome; pain;
 KW multiple sclerosis; ataxia-telangiectasia; leukodystrophy; anxiety;
 KW behavioural disorder; addiction; neuroprotection; diabetes; ARDS;
 KW renal artery stenosis; interstitial nephritis; glomerulonephritis;
 KW polycystic kidney disease; systemic lupus erythematosus; IGA; primer;
 KW renal tubular acidosis; immunoglobulin A nephropathy; hypercalcaemia;
 KW cirrhosis; transplantation; asthma; emphysema; scleroderma; GVHD;
 KW adult respiratory distress syndrome; graft versus host disease;
 KW lymphedema; fertility; pancreatitis; obesity; haemophilia; ulcer;
 KW anaemia; cancer; trauma; regeneration; infection; RTQ-PCR;
 KW real-time quantitative PCR.

OS Homo sapiens.

XX

PN WO200281629-A2.

PD

XX 17-OCT-2002.

XX

PF 03-APR-2002; 2002WO-US010522.

XX

PR 03-APR-2001; 2001US-0281086P.

PR 03-APR-2001; 2001US-0281136P.

PR 05-APR-2001; 2001US-0281863P.

PR 05-APR-2001; 2001US-0281906P.

PR 06-APR-2001; 2001US-0282020P.

PR 10-APR-2001; 2001US-0282934P.

PR 12-APR-2001; 2001US-0283512P.

PR 19-APR-2001; 2001US-0285325P.

PR 23-APR-2001; 2001US-0285890P.

PR 24-APR-2001; 2001US-0286068P.

PR 25-APR-2001; 2001US-0286292P.

PR 27-APR-2001; 2001US-0287213P.

PR 02-MAY-2001; 2001US-0288257P.

PR 12-MAY-2001; 2001US-0291134P.

PR 17-MAY-2001; 2001US-0291725P.

PR 31-MAY-2001; 2001US-0294771P.

PR 08-JUN-2001; 2001US-0296965P.

PR 18-JUN-2001; 2001US-0299128P.

PR 12-JUL-2001; 2001US-0305063P.

PR 14-NOV-2001; 2001US-0332780P.

PR 04-JAN-2002; 2002US-0345221P.

PR 02-APR-2002; 2002US-00345221.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Spytek KA, Li L, Edinger SR, Ellerman K, Stone DJ, Malyankar UM;
 PI Shinkets RA, Guo X, Anderson DW, Patturajan M, Berghs C, Gerlach V;
 PI Taupier RJ, Pena CEA, Padigar M, Liu Y, Burgess CE, Miller CE;
 PI Gusev VY, Kekuda R, Gorman L, Zerhusen BD, Baumgartner JC;
 PI Tchernev VT, Vernet CAM, Smithson G, Heyes MP, Shenoy SG, Liu X;
 PI Gangolli EA;

XX

DR WPI; 2003-046863/04.

XX

PT New polypeptides, designated NOVX polypeptides, useful for treating
 PT hemophilia, idiopathic thrombocytopenic purpura, autoimmune disease,
 PT allergies, transplantation, Alzheimer's disease and stroke.

XX

PS Example C; Page 265; 320pp; English.

XX

CC The invention relates to an isolated NOVX polypeptide selected from NOV1-
 CC NOV27 polypeptides, a mature form of NOVX, a variant of NOVX or a
 CC fragment of NOVX. Also included are determining the presence or amount of
 CC NOVX in a sample (by using an antibody that immunospecifically bind to
 CC the polypeptide), determining the presence of or predisposition to
 CC disease associated with altered levels of NOVX in a first mammalian
 CC subject, identifying a potential therapeutic agent for use in the
 CC treatment of pathology related to aberrant expression of physiological
 CC interactions of NOVX, screening for a modulator of activity or of latency
 CC or predisposition to a pathology associated with NOVX, the nucleic acid
 CC encoding NOVX, vectors and host cells. NOVX is useful for identifying an
 CC agent (a cellular receptor or downstream effector) that binds to NOVX.
 CC NOVX and NOVX nucleic acids are useful for treating or preventing NOVX-
 CC associated disorders in humans, and in the manufacture of a medicament
 CC for treating a NOVX related disease human disease e.g.

CC adrenoleukodystrophy, congenital adrenal hyperplasia, haemophilia,
 CC hypercoagulation, idiopathic thrombocytopenic purpura, autoimmune
 CC disease, allergies, immunodeficiencies, transplantation, Von Hippel-
 CC Lindau (VHL) syndrome, Alzheimer's disease, stroke, tuborous sclerosis,
 CC Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy,
 CC Lesch-Nyhan syndrome, multiple sclerosis, ataxia-telangiectasia,
 CC leukodystrophies, behavioural disorders, addiction, anxiety, pain,
 CC neuroprotection, diabetes, renal artery stenosis, interstitial nephritis,
 CC glomerulonephritis, polycystic kidney disease, systemic lupus
 CC erythematosus, renal tubular acidosis, immunoglobulin (Ig) A nephropathy,
 CC hypercalcaemia, cirrhosis, transplantation, asthma, emphysema,
 CC scleroderma, adult respiratory distress syndrome (ARDS), graft versus
 CC host disease (GVHD), lymphedema, fertility, pancreatitis, obesity,
 CC haemophilia, ulcers, anaemia, cancer, trauma, regeneration, and viral,
 CC bacterial or parasitic infections. The present sequence is a real-time
 CC quantitative (RTQ)-PCR primer used to determine the tissue specific
 CC expression of a NOVX mRNA

XX

SQ Sequence 22 BP; 5 A; 5 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.6; DB 1; Length 22;

Best Local Similarity 81.8%; Pred. No. 2.2e+02;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2428 AAGTGGAGAAATCTTTATGCC 2449

DB 22 AAAAGGAGAAATCTTTATGCC 1

RESULT 153

ADC21071

ID ADC21071 standard; DNA; 22 BP.

XX

AC ADC21071;

XX

DT 18-DEC-2003 (first entry)

XX

DE XX Bovine SST gene SNP probe SEQ ID NO:24.
 KW marbling; bovine; haplotype; single nucleotide polymorphism; SNP;
 KW somatostatin; SST; breeding; characteristic; livestock; meat;
 KW chromosome 1; probe; ss.
 XX
 OS Bos taurus.
 XX synthetic construct.
 XX WO2003076573-A2.
 PN
 PD
 PD 18-SEP-2003.
 XX
 XX 04-MAR-2003; 2003WO-US006537.
 PF
 PR 04-MAR-2002; 2002US-0361589P.
 PR
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 XX Cai L, Taylor J, Smyth K, Findeisen B, Lehn C, Davis S, Davis S;
 PI WPI; 2003-748381/70.
 DR
 XX Predicting marbling in bovine, useful for determining breeding
 PT characteristics of livestock progeny comprises identifying a haplotype
 PT that is predictive of marbling, where the haplotype comprises a single
 PT nucleotide polymorphism.
 XX
 PS Claim 38; SEQ ID NO 24; 113pp; English.
 XX
 CC The present invention describes a method for predicting marbling in
 CC bovine comprising identifying a haplotype that is predictive of marbling,
 CC where the haplotype comprises a single nucleotide polymorphism (SNP) at
 CC nucleotide 244 and/or 575 of the bovine somatostatin (SST) gene. Also
 CC described is a method for predicting a trait in bovine comprising
 CC identifying a haplotype that is predictive of the trait, where the
 CC haplotype comprises a SNP at nucleotide 244 and/or 575 of the bovine SST
 CC gene, and the trait is selected from yearling weight, actual fat
 CC thickness over 10th and 11th rib, quality grade, connective tissue,
 CC flavour and juiciness. The methods can be used for identifying a
 CC haplotype comprising a SNP that is predictive of marbling is used for
 CC predicting marbling in bovine. Identifying a haplotype comprising an SNP
 CC that is predictive of a trait, is used for identifying a trait in bovine,
 CC e.g. yearling weight, actual fat thickness over 10th and 11th rib,
 CC quality grade, connective tissue, flavour and juiciness. Selecting a
 CC first parent bovine that has a haplotype predictive of increased marbling
 CC is used for selecting breeding bovines to produce offspring that exhibit
 CC increased marbling. The methods are useful for determining breeding
 CC characteristics of livestock progeny, and for optimising the management
 CC and marketing of livestock for improving feedlot performance and meat
 CC quality. The present sequence represents a bovine SST gene SNP probe, on
 CC which is used in the present invention. The bovine SST gene is located on
 CC chromosome 1, more specifically to 1q32.
 XX
 SQ Sequence 22 BP; 6 A; 8 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 0.5%; Score 15.6; DB 1; Length 22;
 Best Local Similarity 81.8%; Pred. No. 2.2e+02;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 160 CACCATTGAGGAACAGGCCAAG 181
 Db 1 CCCCATGACGAACTGGCCCAAG 22
 RESULT 154
 ABK02672
 ID ABK02672 standard; RNA; 17 BP.
 XX
 AC ABK02672;
 XX
 DT 12-MAR-2002 (first entry)
 XX

DE XX Human NOGO Amberzyme #344.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; amberyne; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 XX Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 OS Homo sapiens.
 OS Synthetic.
 XX WO200159103-A2.
 PN
 PD 16-AUG-2001.
 PD
 PF 09-FEB-2001; 2001WO-US004273.
 XX
 XX 11-FEB-2000; 2000US-0181797P.
 PR
 PR 28-FEB-2000; 2000US-0185516P.
 PR
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, Mcswiggen J, Chowrira BM;
 DR WPI; 2001-607195/69.
 XX
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 PS Claim 88; Page 138; 200pp; English.
 CC
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberyne (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease

CC	with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
CC	of CD20 in the presence of a divalent cation that is preferably Mg ²⁺ .
CC	Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC	the cell and treat a patient having a condition associated with the level
CC	of CD20. The treatment may further comprise the use of one or more
CC	therapies. In particular, the CD20 targeting nucleic acid may be used to
CC	treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC	Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC	leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC	lymphoma (MCL), immunocytoxa (IMC), small B-cell lymphocytic lymphoma,
CC	immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
CC	targeting nucleic acid is used to cleave RNA of the NOGO gene in the
CC	presence of a divalent cation that is preferably Mg ²⁺ . Furthermore, the
CC	nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC	cell and treat a patient having a condition associated with the level of
CC	NOGO. The treatment may further comprise the use of one or more
CC	therapies. In particular, the NOGO-targeting nucleic acid may be used to
CC	treat central nervous system (CNS) injury and cerebrovascular accident
CC	(CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC	chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC	Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC	disease, muscular dystrophy, and/or other neurodegenerative disease
CC	states which respond to the modulation of NOGO expression. The present
CC	sequence is an amberzyme molecule of the invention
XX	
SQ	Sequence 17 BP; 5 A; 2 C; 4 G; 0 T; 6 U; 0 Other;
	Query Match 0.5%; Score 15.4; DB 1; Length 17;
	Best Local Similarity 64.7%; Pred. No. 1.6e+02;
	Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Qy	1492 CTTTAAAGGGGAAAATTC 1508
	::: ::
Dd	1 CUUUAAGGGGAUAUC 17
RESULT 156	
ADB42476/c	
ID	ADB42476 standard; DNA; 17 BP.
XX	
AC	ADB42476;
XX	
DT	18-DEC-2003 (revised)
DT	04-DEC-2003 (first entry)
XX	
DE	Tumour suppression/reversion associated nucleotide #2799.
XX	
KW	cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW	primer; probe; tumour suppression; tumour reversion; apoptosis;
KW	virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW	diagnosis.
XX	
OS	Homo sapiens.
XX	
PN	WO2003040369-A2.
XX	
PD	15-MAY-2003.
XX	
PF	17-SEP-2002; 2002WO-IB004219.
XX	
PR	17-SEP-2001; 2001FR-00011981.
XX	
PA	(MOLE-) MOLECULAR ENGINES LAB.
XX	
PI	Telerman A, Anson R, Tuijnder M;
XX	
XX	WPI; 2003-441574/41.
XX	
PT	New nucleic acid encoding human prostate membrane-specific antigen,
PT	useful e.g. for treatment of tumors and viral infection, also related
PT	polypeptide and antibodies.
XX	
PS	Disclosure; Page 359; 771pp; French.

XX The invention relates to the isolation of 6327 nucleotide sequences.
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.
 XX Sequence 17 BP; 3 A; 3 C; 3 G; 8 T; 0 U; 0 Other;
 SQ

Query Match 0.5%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 358 ACAAGAAATTCAGATC 374
 DB 17 ACAAGAAATTCAGATC 1
 |||||

RESULT 157
 AAQ94316/c
 ID AAQ94316 standard; DNA; 18 BP.
 AC AAQ94316;
 XX 09-MAY-1996 (first entry)
 DT Human cytochrome P450IIC18 exon 2 point mutant 204 PCR primer.
 DE Human-derived; cytochrome P450IIC18 gene; point mutant; exon 2;
 KW position 204; PCR primer; polymorphism; medicine metabolism; tricyclics;
 KW benzodiazepines; beta blockers; barbiturates; ss.
 XX Synthetic.
 OS WO9526415-A1.
 XX 05-OCT-1995.
 PD 28-MAR-1995; 95WO-JP000570.
 PF 29-MAR-1994; 94JP-00059385.
 PR 29-MAR-1994; 94JP-00059386.
 XX (SUMO) SUMITOMO CHEM CO LTD.
 PA Komai K, Kaneko H, Nakatsuka I;
 XX WPI; 1995-351329/45.
 DR Oligo:nucleotide which hybridises to human cytochrome P450IIC18 gene -
 XX for detection of mutation(s) in the gene when establishing safe
 PT medication dosage in individual patients.
 PT Claim 5; Page 20; 34pp; Japanese.
 PS The oligos AAQ94315-27 which hybridise to the human-derived cytochrome
 CC P450IIC18 gene, esp. to the gene having a point mutation at position 204
 CC in exon 2, can be used as PCR amplification primers which discriminate

CC between the normal and mutated gene, allowing the degree of genetic
 CC polymorphism in a patient to be determined. As the gene prod.
 CC participates in the metabolism of medicines (e.g. tricyclics,
 CC benzodiazepines, beta blockers and barbiturates), patients with mutant
 CC genes differ in their drug metabolising ability and therefore knowledge
 CC of this allows the safe dosage of medicine to be more accurately assessed
 XX Sequence 18 BP; 4 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
 SQ

Query Match 0.5%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.7e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1516 CCAGTGGATGAAAAAGT 1532
 DB 18 CCAGTGGCTGAAAAAGT 2
 |||||

RESULT 158
 AAZ72076
 ID AAZ72076 standard; DNA; 18 BP.
 XX AAZ72076;
 AC 10-SEP-2001 (first entry)
 DT Human biallelic marker upstream amplification primer SEQ ID NO:6432.
 DE Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.
 XX Homo sapiens.
 OS WO9954500-A2.
 XX 28-OCT-1999.
 PD 21-APR-1999; 99WO-IB000822.
 PF 21-APR-1998; 98US-0082614P.
 PR 23-NOV-1998; 98US-0109732P.
 XX (GEST) GENSET.
 PA Cohen D, Blumenfeld M, Chumakov I;
 XX WPI; 2000-013267/01.
 DR Novel biallelic markers used to construct a high density disequilibrium
 PT map of the human genome.
 PT Claim 9; Page 1602; 2745pp; English.
 PS AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention
 XX Sequence 18 BP; 5 A; 2 C; 7 G; 4 T; 0 U; 0 Other;

```

Query Match      0.5%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 598 GGAAGCTGGAGATCTG 614
Db 2 GGAAGCTGGAGATCTG 18

RESULT 159
AAZ58883/c
ID AAA58883 standard; cDNA; 19 BP.
XX
AC AAA58883;
XX
DT 20-OCT-2000 (first entry)
XX
DE PCR primer for DNA encoding a BUI01 polypeptide.
XX
KW Human; BUI01; breast disease; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200041516-A2.
XX
XX 20-JUL-2000.
XX
PF 19-JAN-2000; 2000WO-US001309.
XX
PR 19-JAN-1999; 99US-00233693.
XX
PA (ABBO ) ABBOTT LAB.
XX
PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
PI Russell JC, Scheffel CP, Stroupe SD;
XX
XX WPI; 2000-475906/41.
XX
PT Detecting presence of target BUI01 polynucleotide in sample useful for
PT detection of breast cancer, comprises contacting sample with BUI01-
PT specific polynucleotide and determining binding.
XX
PS Example 9; Page 125; 127pp; English.
XX
CC PCR primer AAA58883-84 were used to amplify DNA encoding a BUI01
CC polypeptide. The BUI01 gene is transcribed from breast tissue. The
CC specification describes a method for detecting the presence of a target
CC BUI01 polynucleotide in a test sample. The method comprises contacting
CC the sample with at least one BUI01-specific polynucleotide (AAA58875-80),
CC and detecting bound polynucleotides. The method and BUI01
CC polynucleotides are useful for detecting the presence of BUI01
CC polynucleotides. The methods may be used for the diagnosis of breast
CC disease, indicated by the formation of complexes
XX
SQ Sequence 19 BP; 5 A; 2 C; 8 G; 4 T; 0 U; 0 Other;

Query Match      0.5%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2377 CATCTGATCTTCACTG 2393
Db 19 CACCTGATCTTCACTG 3

RESULT 160
AAZ37715/c
ID AAZ37715 standard; DNA; 20 BP.
XX
AC AAZ37715;
XX
XX AAZ37715;
XX

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DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #245.
XX
KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KW antisense; modulation; oligonucleotide; expression; inhibition;
KW hyperproliferation; blood cancer; brain cancer; breast cancer;
KW lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;
KW restenosis; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9949065-A1.
XX
XX 30-SEP-1999.
XX
XX 26-MAR-1999; 99WO-US006702.
XX
XX 26-MAR-1998; 98US-00048810.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsett LM;
XX
XX WPI; 1999-610754/52.
XX
PT New antisense compounds used to treat eg. hyperproliferative conditions.
XX
PS Example 9; Page 54; 157pp; English.
XX
CC AAZ37473-237738 represent human mdm2 phosphorothioate oligonucleotides.
CC AAZ37471, AAZ37472, AAZ37739, AAZ37740 and AAZ37741 are used in the
CC exemplification of the present invention. The present invention describes
CC novel nucleotide antisense compounds, targeted to the 5' untranslated,
CC translation termination codon, or 3' untranslated region of a nucleic
CC acid encoding human mdm2, that modulates expression of human mdm2. The
CC oligonucleotides mediate their effect by antisense inhibition of
CC hyperproliferative gene expression. The antisense compound is used to
CC treat an animal having a disease or condition associated with mdm2,
CC particularly a hyperproliferative condition, more particularly cancer,
CC especially of the blood, brain, breast, lung or soft tissue, or
CC psoriasis, fibrosis, atherosclerosis or restenosis
XX
SQ Sequence 20 BP; 6 A; 7 C; 5 G; 2 T; 0 U; 0 Other;

Query Match      0.5%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 81 GTGATCTTGGCTCACAG 97
Db 18 GTGATCTTGGCTCACAG 2

RESULT 161
AAZ3877
ID AAF83877 standard; DNA; 20 BP.
XX
AC AAF83877;
XX
XX 06-AUG-2001 (first entry)
XX
XX Human NOVINTRA C DNA specific forward primer of primer-probe set Ag903.
XX
XX NOVX; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;
XX gonadotropin-like protein; NOVGN; interleukin-1; NOVINTRA; human;
XX cytostatic; neuroprotective; reproductive; antiinflammatory; cancer;
XX antibacterial; cerebroprotective; antidiabetic; antiarthritic;
XX antiasthmatic; antiallergic; PCR primer; ss.
XX
OS Homo sapiens.
XX

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PN W0200140291-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 06-DEC-2000; 2000WO-US033029.
 XX
 PR 06-DEC-1999; 99US-0169056P.
 XX
 PR 09-DEC-1999; 99US-0169866P.
 XX
 PR 09-DEC-1999; 99US-0189886P.
 XX
 PR 10-DEC-1999; 99US-0170252P.
 XX
 PR 12-JAN-2000; 2000US-0175740P.
 XX
 PR 05-DEC-2000; 2000US-00170252.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 XX Burgess CB, Prayaga SK, Shinkets RA, Rastelli L, Zerhusen BD;
 PI Mezes PS;
 XX
 XX WPI; 2001-374790/39.
 DR
 XX Novel isolated human transmembrane, neuromedin peptide gonadotropin-like
 PT protein and interleukin-1 receptor antagonist proteins, useful for
 PT treating cancer, immune response disorder, metabolic function disorders.
 XX
 XX Example; Page 86; 138pp; English.
 PS
 XX The invention provides novel polypeptides (NOVX) selected from human
 CC transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR),
 CC gonadotropin-like protein (NOVGON) and two interleukin-1 receptor
 CC antagonist proteins (NOVINTRA A and B). The invention also provides
 CC methods in which a NOVX polypeptide, polynucleotide and antibody are used
 CC in the detection, prevention and treatment of a broad range of
 CC pathological states. NOVTRAN can be used to treat is a cell signaling
 CC disorder such as cancer, immune response disorder, hematopoietic
 CC disorder, neurodegenerative disorder. NOVNEUR can be used to treat
 CC endocrine disorder, muscle disorder, neurologic disorder, cancers of
 CC central nervous system, breast, colon, ovary, kidney, prostate and
 CC thyroid. NOVGON can be used to treat reproductive development disorder,
 CC metabolic function disorder and melanoma. NOVINTRA A and B can be used to
 CC treat bone metabolism or structure disorder, inflammatory response
 CC disorder, immune regulation disorder, septic shock, stroke, diabetes,
 CC arthritis and cancer. Sequences AAF83877-79 represent a primer-probe set
 CC Ag903 specific for the NOVINTRA C nucleic acid sequence
 XX
 SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
 Query Match 0.5%; Score 15.4; DB 1; Length 20;
 Best Local Similarity 94.1%; Pred. No. 2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 381 TCAGCTTCAGCTGCAG 397
 DB 1 TGAAGCTTCAGCTGCAG 17
 RESULT 162
 AAF80869/C
 ID AAF80869 standard; DNA; 20 BP.
 XX
 AC AAF80869;
 XX
 DT 02-MAY-2001 (first entry)
 XX
 DE Human mdm2 phosphorothioate oligonucleotide #243.
 XX
 XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
 KW
 XX Homo sapiens.
 OS
 XX US6184212-B1.
 PN
 XX 06-FEB-2001.
 PD

PF 26-MAR-1999; 99US-00280805.
 XX
 PR 26-MAR-1998; 98US-00048810.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowser LM;
 XX
 DR WPI; 2001-190948/19.
 XX
 PT Novel antisense compound 8-30 nucleobases in length targeted to a nucleic
 PT acid molecule encoding human mdm-2 useful for modulating the expression
 PT of human mdm-2 and reducing hyperproliferation of human cells.
 XX
 XX Example 9; Col 31; 77pp; English.
 PS
 XX The present invention relates to an antisense compound 8-30 nucleobases
 CC in length targeted to nucleobases 1-308 of the 5' untranslated region,
 CC 1776-1806 of the translation termination codon region or 1818-2370 of the
 CC 3' untranslated region of a nucleic acid molecule encoding human mdm-2.
 CC The invention is useful for reducing hyperproliferation of human cells,
 CC modulating the expression of mdm2 in human cells or tissues or in vitro.
 CC The hyperproliferative disorder includes cancer or psoriasis
 XX
 SQ Sequence 20 BP; 6 A; 7 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 0.5%; Score 15.4; DB 1; Length 20;
 Best Local Similarity 94.1%; Pred. No. 2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 81 GTGATCTTGCTGCACAG 97
 DB 18 GTGATCTTGCTGCACAG 2
 RESULT 163
 AAH42015
 ID AAH42015 standard; DNA; 20 BP.
 XX
 AC AAH42015;
 XX
 DT 24-AUG-2001 (first entry)
 XX
 DE Disease treatment related PCR primer SEQ ID NO: 6.
 XX
 KW Disease treatment; infection; chronic occlusive pulmonary disease;
 KW bronchial asthma; PCR primer; ss.
 XX
 OS Unidentified.
 XX
 PN W0200136633-A1.
 XX
 PD 25-MAY-2001.
 XX
 PF 14-NOV-2000; 2000WO-JP008015.
 XX
 PR 15-NOV-1999; 99JP-00324467.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Nakanishi A, Morita S;
 XX
 DR WPI; 2001-397791/42.
 XX
 PT New proteins, peptides and DNA for treatment of bronchial asthma, chronic
 PT occlusive lung disease and infectious disease.
 XX
 XX Example 1; Page 103; 114pp; Japanese.
 PS
 XX The present invention provides the sequence of a protein which can be
 CC used in the treatment and prevention of infectious diseases. Inhibitors
 CC of the protein can be used to treat bronchial asthma and chronic
 CC occlusive pulmonary disease. The present sequence is a PCR primer
 CC

CC described in the exemplification of the invention
 XX Sequence 20 BP; 7 A; 7 C; 4 G; 2 T; 0 U; 0 Other;
 SQ Query Match 0.5%; Score 15.4; DB 1; Length 20;
 Best Local Similarity 94.1%; Pred. No. 2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2655 AAGACACATGGCCCAAG 2671
 Db 1 AAGACACATGGCCCAAG 17

RESULT 164
 ID AAS29484/c
 XX AAS29484 standard; DNA; 20 BP.
 AC AAS29484;
 XX 21-NOV-2001 (first entry)
 XX Human mdm2 antisense oligonucleotide 31621.
 XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
 KW atherosclerosis; tumour; cytostatic; anti psoriatic;
 KW anti arteriosclerotic; vasotropic; antisense; phosphorothioate; ss.
 XX Homo sapiens.

Key Location/Qualifiers
 FH modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= All phosphorothioate linkages,
 additionally bases 1-6 and bases 15-20 are 2'-O-
 methoxyethyl bases, and bases 7-14 are deoxynucleotides"

US2001016575-A1.
 23-AUG-2001.
 02-JAN-2001; 2001US-00752983.
 26-MAR-1998; 98US-00048810.
 26-MAR-1999; 99US-00280805.
 (MIRA/) MIRAGLIA L J.
 (NERO/) NERO P.
 (GRAH/) GRAHAM M J.
 (MONI/) MONIA B P.
 (COWS/) COWSERT L M.

Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsert LM;
 WPI; 2001-535565/59.
 An antisense compound, useful for treating e.g. cancer, comprises
 nucleobases targeted a region (e.g. translation termination codon region)
 of a nucleic acid encoding human mdm2.
 Example 9; Page 18; 81pp; English.

The present invention relates to antisense compounds, 8-30 nucleobases in
 length targeted to the 5' untranslated region, translation termination
 codon region, 3' untranslated region, coding region or translation start
 site of a nucleic acid encoding human mdm2, where the antisense compound
 modulates the expression of human mdm2. The antisense oligonucleotides of
 the invention are useful for encoding human mdm2 and for inhibiting the
 expression of human mdm2. They may be used for treating an animal having
 a disease or condition associated with amplification of mdm2 gene or
 overexpression of mdm2 e.g. a hyperproliferative disorder such as cancer
 (blood, brain, breast, lung, or a soft tissue cancer) and psoriasis,
 fibrosis, atherosclerosis or restenosis, tumours, colorectal carcinoma

CC and chronic myelogenous leukemia. The antisense compound may be
 CC administered with a chemotherapeutic agent to overcome drug resistance.
 CC The antisense compound reduces hyperproliferation of human cells. The
 CC method, which involves the use of the antisense compound, is also useful
 CC for detecting the role of mdm2 expression in various cell functions and
 CC physiological processes and useful in both clinical research and
 CC diagnostic tools. AAS29242-AAS29507 represent the human mdm2 antisense
 CC oligonucleotides of the present invention
 XX Sequence 20 BP; 6 A; 7 C; 5 G; 2 T; 0 U; 0 Other;
 SQ Query Match 0.5%; Score 15.4; DB 1; Length 20;
 Best Local Similarity 94.1%; Pred. No. 2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 81 GTGATCTTGGCTCACAG 97
 Db 18 GTGATCTTGGCTCACTG 2

RESULT 165
 ID ABL44438/c
 XX ABL44438 standard; DNA; 20 BP.
 AC ABL44438;
 XX 11-APR-2002 (first entry)
 XX Human chromosome 1p36-35 PCR primer SEQ ID NO:1482.
 XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
 KW PCR primer; ss.
 XX Homo sapiens.
 XX JP2001321190-A.
 XX 20-NOV-2001.
 XX 12-MAR-2001; 2001JP-00068285.
 XX 10-MAR-2000; 2000JP-00066716.
 (RIKA) RIKAGAKU KENKYUSHO.
 (GENO-) GENOTEX YG.
 WPI; 2002-144136/19.
 Arraying genome clones.
 Claim 4; Page 34; 528pp; Japanese.

The present invention describes a method of arraying genome clones. The
 method comprises: (a) clones of the genomic libraries contained in
 multiwell plates numbered for discrimination are mixed in each of the
 multiwell plates; (b) a primer designed based on the chromosome marker
 sequence is added to the mixture to carry out an amplification reaction;
 (c) a signal corresponding to the marker is detected from the resultant
 amplified product to specify the discrimination Nos. of the multiwell
 plates containing the clones having said marker sequence; (d) the order
 of the markers is changed so that the same discrimination Nos. succeed to
 the maximum in the specified discrimination Nos. to array the multiwell
 plates; (e) the clones in the multiwell plates of the specified
 discrimination Nos. are mixed respectively in each wells of longitudinal
 and lateral directions; (f) the mixed clones are cultured and the
 resultant cultures are amplified by using the above primer; (g) signals
 are detected from the amplified products; (h) the clones in the multiwell
 plates are specified from the detected result; and (i) the clones are
 reconstituted as the positions on the chromosome and arrayed. The
 microarray is useful for gene analysis. ABL42957 to ABL45322 represent
 PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
 represent PCR primers for human chromosome 21q22.1, which are
 specifically claimed for use in the present invention

XX SQ Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 0.5%; Score 15.4; DB 1; Length 20;
 Best Local Similarity 94.1%; Pred. No. 2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 81 GTGATCTTGGCTCACAG 97
 Db 20 GTGATCTTGGCTCACTG 4
 RESULT 166
 ABQ74025
 ID ABQ74025 standard; DNA; 20 BP.
 XX AC ABQ74025;
 XX 10-OCT-2002 (first entry)
 XX Human NOVINTRA C forward PCR primer SEQ ID NO:98.
 KW Human; transmembrane protein; neuromedin protein; gonadotropin protein;
 KW interleukin-1 receptor antagonist; interleukin-1 epsilon; NOVX; probe;
 KW IL-1 epsilon; IL-1 receptor antagonist; lung disease; nontropic;
 KW cytosolic; neuroprotective; antiinflammatory; antibacterial; PCR primer;
 KW immunosuppressive; cerebroprotective; antidiabetic; antiarthritic;
 KW antiasthmatic; antiallergic; gene therapy; antibody-based therapy;
 KW cell signalling disorder; haematopoietic disorder; endocrine; muscle;
 KW neurodegenerative disorder; neurological disorder; cancer; melanoma;
 KW central nervous system cancer; reproductive development disorder; asthma;
 KW metabolic function disorder; bone metabolism; structure disorder; stroke;
 KW inflammatory response disorder; immune regulation disorder; septic shock;
 KW diabetes; arthritis; lung cancer; emphysema; allergic lung irritation;
 KW lung inflammation; ss.
 XX OS Homo sapiens.
 OS Synthetic.
 XX US2002068279-A1.
 XX 06-JUN-2002.
 XX 05-DEC-2000; 2000US-00730617.
 XX 06-DEC-1999; 99US-0169056P.
 XX 09-DEC-1999; 99US-0169866P.
 XX 09-DEC-1999; 99US-0169886P.
 XX 10-DEC-1999; 99US-0170252P.
 XX 12-JAN-2000; 2000US-0175740P.
 XX (CURA-) CURAGEN CORP.
 XX Burgess C, Prayaga SK, Shimkets RA, Rastelli L, Zerhusen B;
 PI Mezes P;
 XX WPI; 2002-582472/62.
 XX New NOVX proteins for diagnosing or treating cell signaling, immune
 PT response, hematopoietic, neurodegenerative, muscle, endocrine, bone, and
 PT reproductive development disorders.
 XX Example 1; Page 37; 110pp; English.
 XX The present invention describes an isolated NOVX polypeptide, chosen from
 CC human transmembrane (NOVTRAN), neuromedin (NOVNEUR), gonadotropin
 CC (NOVGON), interleukin-1 (IL-1) receptor antagonist (NOVINTRA A and B),
 CC and IL-1 epsilon proteins. NOVX polypeptides have nontropic, cytosolic,
 CC neuroprotective, antiinflammatory, antibacterial, immunosuppressive,
 CC cerebroprotective, antidiabetic, antiarthritic, antiasthmatic and
 CC antiallergic activities, and can be used in gene therapy and antibody-
 CC based therapy. NOVX polypeptides, nucleic acid (I) encoding them and an
 CC antibody (III) that binds the polypeptide, are useful for treating or

CC preventing a NOVX protein-associated disorder in humans, NOVTRAN can be
 CC used in the treatment of a cell signalling disorder, such as, a
 CC haematopoietic disorder or a neurodegenerative disorder. NOVNEUR can be
 CC used in the treatment of an endocrine, muscle, neurological disorder,
 CC central nervous system cancer, breast, colon, ovarian, kidney, prostate
 CC or thyroid cancer. NOVGON can be used in the treatment of a reproductive
 CC development disorder, metabolic function disorder or melanoma. NOVINTRA
 CC proteins can be used in the treatment of and a bone metabolism or
 CC structure disorder, an inflammatory response disorder, an immune
 CC regulation disorder, septic shock, stroke, diabetes, arthritis or cancer.
 CC An agent which modulates the expression or activity of a human IL-1
 CC epsilon protein is useful for treating a lung disease such as lung
 CC cancer, asthma, emphysema, allergic lung irritation and lung inflammation
 CC in a mammal. ABQ73996 to ABQ74027 and ABP51981 to ABP52048 represent
 CC sequences used in the exemplification of the present invention
 XX SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
 Query Match 0.5%; Score 15.4; DB 1; Length 20;
 Best Local Similarity 94.1%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 381 TCAAGCTTCAGCTGCAG 397
 Db 1 TGAAGCTTCAGCTGCAG 17
 RESULT 167
 ABZ91909/C
 ID ABZ91909 standard; DNA; 20 BP.
 XX AC ABZ91909;
 XX 17-OCT-2003 (first entry)
 XX Human oligonucleotide sequence.
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytosolic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX OS Homo sapiens.
 XX WO200285308-A2.
 XX 31-OCT-2002.
 XX 23-APR-2002; 2002WO-US013135.
 XX 24-APR-2001; 2001US-0286137P.
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX Disclosure; SEQ ID NO 7151; 872pp; English.
 XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or

CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive, and
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 20 BP; 6 A; 2 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 20;
 Best Local Similarity 94.1%; Pred. No. 2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2072 AAGTAAATAATCAGAT 2088
 Db 20 AAGTAAATAATCAGAT 4

RESULT 168

ADD21680/c
 ID ADD21680 standard; DNA; 20 BP.

XX AC ADD21680;

XX DT 15-JAN-2004 (first entry)

XX DE Human mdm2 antisense oligonucleotide #243.

XX KW antisense oligonucleotide; human; mdm2; hyperproliferation;
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
 KW atherosclerosis; restenosis; apoptosis modulation; p21; ss;
 KW 2'-methoxyethoxy-residue; phosphorothioate backbone.

XX OS Homo sapiens.

XX PN WO2003048315-A2.

XX PD 12-JUN-2003.

XX PF 02-DEC-2002; 2002WO-US038281.

XX PR 04-DEC-2001; 2001US-00005344.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Miraglia LJ, Nero PS, Graham MJ, Monia BP, Koller E, Chiang MY;
 PI Manoharan M;

XX PI WPI; 2003-577263/54.

XX PT Novel antisense compound targeted to 5' untranslated region, coding
 PT region, or intron:exon junction of nucleic acid molecule encoding mdm2,
 PT useful for treating e.g. cancer, psoriasis or restenosis by inhibiting
 PT mdm2 expression.

XX PS Claim 4; SEQ ID NO 245; 289pp; English.

XX CC The invention comprises antisense oligonucleotides which are targeted to
 CC the human mdm2 gene. The antisense oligonucleotides of the invention are
 CC useful for reducing hyperproliferation of human cells. The antisense
 CC oligonucleotides are also useful for treating: hyperproliferative
 CC disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or
 CC restenosis. The antisense oligonucleotides are also useful for modulating
 CC apoptosis, and for increasing expression of p21. The present DNA sequence

CC represents a human mdm2 gene antisense oligonucleotide of the invention.
 CC The present sequence contains 2'-methoxyethoxy-residues and has a
 CC phosphorothioate backbone.

XX SQ Sequence 20 BP; 6 A; 7 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 20;
 Best Local Similarity 94.1%; Pred. No. 2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 81 GTGATCTTGCTCACAG 97
 Db 18 GTGATCTTGCTCACAG 2

RESULT 169

AAQ75711/c

ID AAQ75711 standard; DNA; 21 BP.

XX AC AAQ75711;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

XX PS Disclosure; Page 7; 11pp; Japanese.

XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.5%; Score 15.4; DB 1; Length 21;

Best Local Similarity 94.1%; Pred. No. 2.2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3389 CACTCAAAAAA 3405
 Db 21 CACTAAAAA 5

RESULT 170

AAQ09565

ID AAQ09565 standard; DNA; 21 BP.

XX AC AAQ09565;

DT 24-MAR-1999 (first entry)
 DE Human biallelic polymorphic marker upstream primer #445.
 XX
 XX Polymorphism; biallelic; human; forensic; paternity testing; disease;
 KW detection; phenotypic typing; characteristic; infection; hereditary;
 KW autoimmune disease; cancer; inflammation; drug; therapy; medicament;
 KW treatment; marker; primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX WO9820165-A2.
 XX
 XX 14-MAY-1998.
 PD
 XX
 XX 05-NOV-1997; 9TWO-US020313.
 PF
 XX
 XX 06-NOV-1996; 96US-0030455P.
 PR
 XX
 XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA
 XX
 XX Lander ES, Wang D, Hudson T;
 PI
 XX
 XX WPI; 1998-286974/25.
 DR
 XX
 XX New isolated nucleic acid segments from the human genome - used for
 PT determining polymorphic forms for use in e.g. forensics, paternity
 PT testing or phenotypic typing for disease.
 XX
 XX Claim 15; Page 204; 310pp; English.
 PS
 XX
 XX AAX09121-X10268 are allele-specific oligonucleotide primers used in the
 CC isolation of various biallelic polymorphic markers found in the human
 CC genome (represented in AAX10269-X12937). These primers can be used in a
 CC method for determining polymorphic forms in an individual for use in e.g.
 CC forensics, paternity testing or for phenotypic typing for diseases such
 CC as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
 CC dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial
 CC hypercholesterolemia, polycystic kidney disease, hereditary
 CC spherocytosis, von Willebrand's disease, tuberos scleriosis, hereditary
 CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
 CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,
 CC autoimmune diseases, inflammation, cancer, diseases of the nervous
 CC system, infection by pathogenic microorganisms, and characteristics such
 CC as longevity, appearance (e.g. baldness, obesity), strength, speed,
 CC endurance, fertility, and susceptibility or receptivity to particular
 CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid
 CC segments can also be used to produce medicaments for the treatment or
 CC prophylaxis of such diseases
 XX
 XX Sequence 21 BP; 7 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 0.5%; Score 15.4; DB 1; Length 21;
 Best Local Similarity 94.1%; Pred. No. 2.2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1173 GGATCCTTATGTGCACA 1189
 DB 5 GGATCCTTATGTGCACA 21
 RESULT 171
 AAZ20494
 ID AAZ20494 standard; DNA; 21 BP.
 AC
 XX
 XX AAZ20494;
 XX
 XX 19-NOV-1999 (first entry)
 DT
 XX
 DE PCR primer for interleukin-4 gene.
 XX
 XX PCR primer; immune response; cytokine response; pathogen; neonate; IL-12;

KW interleukin-12; immunise; pathogen; infection; therapy; influenza;
 KW childhood disease; interleukin-4; IL-4; ss.
 XX
 OS Synthetic.
 OS Mus sp.
 XX
 XX WO9944634-A1.
 XX
 XX 10-SEP-1999.
 PD
 XX
 XX 04-MAR-1999; 99WO-US004677.
 PF
 XX
 XX 05-MAR-1998; 98US-00035593.
 PR
 XX
 XX (MEDI-) MEDICAL COLLEGE OHIO.
 PA
 XX
 XX Metzger DW, Arulanandam BP;
 PI
 XX
 XX WPI; 1999-550985/46.
 DR
 XX
 XX Inducing an immune, or cytokine, response in neonates by administering
 PT interleukin-12 and a pathogen-derived antigen, particularly for
 PT protection against influenza.
 PT
 XX
 XX Example 1; Page 18; 49pp; English.
 PS
 XX
 XX This sequence represents a PCR primer for the interleukin-4 (IL-4) gene.
 CC The invention relates to a method for inducing or enhancing an immune or
 CC cytokine response to a pathogen in neonates by administering IL-12 and an
 CC antigen (Ag) of the pathogen. The method is used to immunise against
 CC pathogens, bacteria, viruses, parasites, fungi and yeasts, for prevention
 CC and treatment of infection, especially against influenza but also against
 CC many common childhood diseases. IL-12 is an adjuvant that induces or
 CC enhances both cytokine response (particularly expression of interferon-
 CC gamma and IL-10) and humoral response (particularly increased expression
 CC of IgG1, G2a and G2b) and induces memory for protective responses early
 CC in life
 XX
 XX Sequence 21 BP; 1 A; 6 C; 3 G; 11 T; 0 U; 0 Other;
 SQ
 Query Match 0.5%; Score 15.4; DB 1; Length 21;
 Best Local Similarity 94.1%; Pred. No. 2.2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2373 TTGTCATCCTGCTCTTC 2389
 DB 2 TTGTCATCCTGCTCTTC 18
 RESULT 172
 AAZ43832
 ID AAZ43832 standard; DNA; 21 BP.
 AC
 XX
 XX AAZ43832;
 XX
 XX 10-MAR-2000 (first entry)
 DT
 XX
 DE Human adult skin cDNA clone vdl_1 DNA probe.
 XX
 XX Human; secreted protein; treatment; nutritional activity; cytokine;
 KW cell proliferation; cell differentiation; hematopoiesis regulation;
 KW tissue growth; activin; inhibin; chemotactic; chemokinetic; hemostatic;
 KW thrombolytic; anti-inflammatory; invasion suppressor; tumor inhibition;
 KW gene therapy; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX WO9955721-A1.
 PN
 XX
 XX 04-NOV-1999.
 PD
 XX
 XX 23-APR-1999; 99WO-US008504.

XX 24-APR-1998; 98US-0082904P.
 PR 11-JUN-1998; 98US-0088994P.
 PR 12-JUN-1998; 98US-0089278P.
 PR 02-JUL-1998; 98US-0091647P.
 PR 24-AUG-1998; 98US-0097639P.
 PR 22-APR-1999; 99US-00097639.
 XX (ALPH-) ALPHAGENE INC.
 PA Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
 XX WPI; 2000-052801/04.
 XX New polynucleotides encoding secreted human proteins, derived from human
 PT fetal brain, adult skin, adult brain, adult heart, adult thymus and adult
 PT aorta cDNA libraries.
 XX Disclosure; Page 269; 282pp; English.
 XX This invention describes novel human secreted proteins which are encoded
 CC by polynucleotides obtained from fetal brain, adult skin, adult brain,
 CC adult heart, adult thymus and adult aorta cDNA libraries. The
 CC polynucleotides and proteins are predicted to have biological activities
 CC which would make them suitable for treating, preventing or ameliorating
 CC medical conditions in humans and animals, although no supporting data is
 CC given. Suggested activities include nutritional activity, cytokine and
 CC cell proliferation/differentiation activity, immune stimulating (e.g. as
 CC vaccines) or suppressing activity, hematopoiesis regulating activity,
 CC tissue growth activity, activin/inhibin activity,
 CC chemotactic/chemokinetic activity, hemostatic and thrombolytic activity,
 CC receptor/ligand activity, anti-inflammatory activity, cadherin/tumor
 CC invasion suppressor activity, and tumor inhibition activity. The
 CC polynucleotides are also stated to be useful for gene therapy. AAZ43809-
 CC Z43840 represent DNA probes used to isolate the polynucleotides
 CC represented in AAZ43777-Z43808 which encode the secreted proteins
 CC represented in AAY50905-Y50947
 XX Sequence 21 BP; 7 A; 1 C; 10 G; 3 T; 0 U; 0 Other;
 SQ

Query Match 0.5%; Score 15.4; DB 1; Length 21;
 Best Local Similarity 94.1%; Pred. No. 2.2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1028 AAGGAGGCGAGGAGTT 1044
 Db 3 AAGGAGGCGAGGAGTT 19
 |||||

RESULT 173
 AAA63099
 ID AAA63099 standard; DNA; 21 BP.
 AC AAA63099;
 XX 09-NOV-2000 (first entry)
 DT Sense PCR primer used to amplify mouse IL-4.
 DE Mouse; IFN-gamma; interferon gamma; interleukin 10; interleukin 4; IL;
 XX immunosuppressive; PCR primer; ss.
 KW Mus sp.
 OS WO200032209-A2.
 XX 08-JUN-2000.
 PD 01-DEC-1999; 99WO-US028302.
 XX 01-DEC-1998; 98US-0110402P.
 PR (PURD) PURDUE RES FOUND.
 PA

PA (MEDI-) MEDICAL COLLEGE OHIO AT TOLEDO.
 XX Badylak SF, Mcpherson TB, Metzger D;
 XX WPI; 2000-412146/35.
 XX Suppressing cell mediated immune response and protecting immunogenic
 PT biomaterials from the host immune system using vertebrate submucosa.
 XX Example 2; Page 22; 33pp; English.
 XX The present invention relates to a method for suppressing the cell
 CC mediated immune response in vertebrate species using vertebrate
 CC submucosa. The submucosa elicits the inherently benign T helper
 CC lymphocyte-2 response and suppresses the T helper lymphocyte-1 response.
 CC RNA analysis of interferon gamma, interleukin 10 and interleukin 4 was
 CC used to determine the immune response to pig submucosa implantation in
 CC mice. The present sequence is the interleukin 4 sense primer. The method
 CC of the invention is useful for suppressing cell mediated immune response
 CC in autoimmune disorders. It is also useful for moderating immune response
 CC of vertebrate species to an implanted xenograft
 XX Sequence 21 BP; 1 A; 6 C; 3 G; 11 T; 0 U; 0 Other;
 SQ

Query Match 0.5%; Score 15.4; DB 1; Length 21;
 Best Local Similarity 94.1%; Pred. No. 2.2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2373 TTGTCATCTGCTTC 2389
 Db 2 TTGTCATCTGCTTC 18
 |||||

RESULT 174
 ABS97869/C
 ID ABS97869 standard; DNA; 21 BP.
 XX ABS97869;
 AC ABS97869;
 XX 23-DEC-2002 (first entry)
 DT Human UDP-glucuronosyl transferase 24B gene PCR primer #6.
 DE Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; PCR;
 XX cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
 KW adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
 KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
 KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
 KW epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
 KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
 KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
 KW NADPH quinone oxidoreductase 2; NQO2; sulfoltransferase thermolabile; STM;
 KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
 KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
 KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
 KW multidrug resistance associated protein 3; cancer; prostate;
 KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
 KW altered drug metabolism; cardiovascular function; colorectal tumour;
 KW central nervous system; pulmonary; immunological.
 XX Homo sapiens.
 OS WO200257410-A2.
 XX 25-JUL-2002.
 PD 28-NOV-2001; 2001WO-US044838.
 XX 28-NOV-2000; 2000US-00724389.
 PR (DNAS-) DNA SCI LAB INC.
 PA Guida M, Hall J;
 PI

PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
 XX WPI; 2002-566694/60.
 XX
 XX Constructing strains for identifying gene products as effective targets
 PT for therapeutic intervention, by inactivating in the strain one allele of
 PT a gene and placing other allele of the gene under conditional expression.
 XX
 XX Claim 36; SEQ ID NO 5294; 167pp + Sequence Listing; English.
 PS
 XX The invention relates to constructing (M1) a strain of diploid fungal
 CC cells in which both alleles of a gene are modified, comprising modifying
 CC one allele by insertion or replacement by a cassette having an
 CC expressible selectable marker and modifying other allele by
 CC recombination, of a promoter replacement fragment with a heterologous
 CC promoter, so that expression of the second allele is regulated by the
 CC promoter. (M1) is useful for constructing a strain of diploid fungal
 CC cells in which both alleles of a gene are modified. The diploid fungal
 CC cells having both alleles modified are useful for identifying a gene that
 CC is essential to the survival or growth of a fungus, a gene that
 CC contributes to the virulence and/or pathogenicity of a fungus, a gene
 CC that contributes to the resistance of a diploid fungus to an antifungal
 CC agent, an antifungal agent that inhibits the growth of a diploid fungus
 CC and for identifying a therapeutic agent for treatment of a mammalian
 CC disease. (M1) is useful for identifying a compound which modulates the
 CC activity of a gene product, preferably enzymatic activity, carbon
 CC compound catabolism, biosynthetic, transporter, transcriptional,
 CC translational, signal transduction, DNA replication and cell division
 CC activity. The method is useful for identifying a compound having the
 CC ability to inhibit growth or proliferation of C. albicans cells and for
 CC treating infection by C. albicans. The present sequence is that of a PCR
 CC primer used in the method of the invention. Note: The sequence data for
 CC this patent is not represented in the printed specification but is based
 CC on sequence information supplied to Derwent by the European Patent Office
 XX
 SQ Sequence 22 BP; 9 A; 7 C; 2 G; 4 T; 0 U; 0 Other;

 Query Match 0.5%; Score 15.4; DB 1; Length 22;
 Best Local Similarity 94.1%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 2480 CCAGGATTCCTCAAAACAC 2496
 Db | ||||| ||||| |||||
 4 CAAGGATTCCTCAAAACAC 20

 RESULT 177
 AAZ01569/C
 ID AAZ01569 standard; DNA; 20 BP.
 XX
 AC AAZ01569;
 XX
 XX 07-OCT-1999 (first entry)
 XX
 DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
 XX
 KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
 KW Bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
 XX
 OS Synthetic.
 OS Chlamydia trachomatis.
 XX
 PN WO9928475-A2.
 XX
 XX 10-JUN-1999.
 XX
 XX 27-NOV-1998; 98WO-IB001939.
 XX
 XX 28-NOV-1997; 97FR-00015041.
 PR 17-DEC-1997; 97FR-00016034.
 PR 04-NOV-1998; 98US-0107077P.
 XX
 XX
 XX (GEST) GENSET.
 XX
 XX Griffais R;
 XX
 XX WPI; 1999-371125/31.
 XX
 XX Genome sequence of Chlamydia trachomatis.
 XX
 XX Disclosure; Page 1649; 1755pp; English.

XX
 PA (GEST) GENSET.
 XX
 PI Griffais R;
 XX
 DR WPI; 1999-371125/31.
 XX
 XX Genome sequence of Chlamydia trachomatis.
 PT
 XX Disclosure; Page 1453; 1755pp; English.
 PS
 XX
 CC PCR primers AAZ01426-206209 were used to amplify open reading frames
 CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
 CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
 CC be used to control growth of the microorganism. Chlamydia trachomatis is
 CC responsible for a large number of diseases, e.g. eye diseases such as
 CC conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
 CC conjunctivitis; genital diseases such as nongonococcal urethritis,
 CC epididymitis, cervicitis, salpingitis, perihepatitis, Bartholinitis;
 CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
 CC The polypeptides of the invention may be of use in treating these
 CC diseases
 XX
 SQ Sequence 20 BP; 4 A; 1 C; 9 G; 6 T; 0 U; 0 Other;

 Query Match 0.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

 QY 3161 ACATCTCTCTGACACACAA 3180
 Db ||||| ||||| |||||
 20 ACATCTCTCTGCCACCAAA 1

 RESULT 178
 AAZ03953
 ID AAZ03953 standard; DNA; 20 BP.
 XX
 AC AAZ03953;
 XX
 XX 07-OCT-1999 (first entry)
 XX
 DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
 XX
 KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
 KW Bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
 XX
 OS Synthetic.
 OS Chlamydia trachomatis.
 XX
 PN WO9928475-A2.
 XX
 XX 10-JUN-1999.
 XX
 XX 27-NOV-1998; 98WO-IB001939.
 XX
 XX 28-NOV-1997; 97FR-00015041.
 PR 17-DEC-1997; 97FR-00016034.
 PR 04-NOV-1998; 98US-0107077P.
 XX
 XX
 XX (GEST) GENSET.
 XX
 XX Griffais R;
 XX
 XX WPI; 1999-371125/31.
 XX
 XX Genome sequence of Chlamydia trachomatis.
 XX
 XX Disclosure; Page 1649; 1755pp; English.

PCR primers AAZ01426-Z06209 were used to amplify open reading frames (ORFs) of the genome of *Chlamydia trachomatis* (see AAZ01425). These ORFs encode polypeptides (see AAY36754-Y37943) which can be used as vaccines against *Chlamydia trachomatis*. Antisense and ribozyme sequences can also be used to control growth of the microorganism. *Chlamydia trachomatis* is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal urethritis, epididymitis, cervicitis, salpingitis, perihepatitis, Bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases

XX Sequence 20 BP; 6 A; 9 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3162 CATCTCCTGACACACAAA 3181

Db 1 CATCTCTGCGCCACAAA 20

RESULT 179

AAZ93821
 ID AAZ93821 standard; DNA; 20 BP.

AC AAZ93821;

DT 13-SEP-1999 (first entry)

XX PCR primer used to amplify an ORF of *Chlamydia pneumoniae*.

Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
 neutralising epitope; PCR primer; ss.

XX Synthetic.

OS Chlamydophila pneumoniae.

XX WO9927105-A2.

PN 03-JUN-1999.

PD 20-NOV-1998; 98WO-IB001890.

PF 21-NOV-1997; 97FR-00014673.

PR 04-NOV-1998; 98US-0107078P.

XX (GEST) GENSET.

PA Griffais R;

PI WPI; 1999-357842/30.

DR Genome sequence of *Chlamydia pneumoniae*.

PT Page 1621; Disclosure; 1912pp; English.

PS AAZ91991-X97517 represent PCR primers used to amplify open reading frames

and other nucleic acid sequences from the genome of *Chlamydia pneumoniae* (see AAZ91990). *C. pneumoniae* causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the *C. pneumoniae* genome (see AAY34584-AAY35879) can be used in immunogenic compositions as vaccines. Vectors containing *C. pneumoniae* nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of *C. pneumoniae*

XX Sequence 20 BP; 7 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 475 CACCATTCTACAGTACTGGAA 494

Db 1 CACCACCTTACAGTAATGGCA 20

RESULT 180

AAZ92000

ID AAZ92000 standard; DNA; 20 BP.

XX AAZ92000;

AC AAZ92000;

DT 13-SEP-1999 (first entry)

XX PCR primer used to amplify an ORF of *Chlamydia pneumoniae*.

Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
 neutralising epitope; PCR primer; ss.

XX Synthetic.

OS Chlamydophila pneumoniae.

XX WO9927105-A2.

PN 03-JUN-1999.

PD 20-NOV-1998; 98WO-IB001890.

PF 21-NOV-1997; 97FR-00014673.

PR 04-NOV-1998; 98US-0107078P.

XX (GEST) GENSET.

PA Griffais R;

XX WPI; 1999-357842/30.

DR Genome sequence of *Chlamydia pneumoniae*.

PT Page 1477; Disclosure; 1912pp; English.

PS AAZ91991-X97517 represent PCR primers used to amplify open reading frames

and other nucleic acid sequences from the genome of *Chlamydia pneumoniae* (see AAZ91990). *C. pneumoniae* causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the *C. pneumoniae* genome (see AAY34584-AAY35879) can be used in immunogenic compositions as vaccines. Vectors containing *C. pneumoniae* nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of *C. pneumoniae*

XX Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1303 CCATGAAGCTGTGGGAAA 1322

Db 1 CCACGAATCTCTGGGAAA 20

RESULT 181

AAZ72232/c

ID AAZ72232 standard; DNA; 20 BP.

XX

```

AC AAZ72232;
XX
XX 10-SEP-2001 (first entry)
XX
DE Human biallelic marker upstream amplification primer SEQ ID NO:6588.
XX
XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
XX Homo sapiens.
XX
XX WO954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-IB000822.
XX
XX 21-APR-1998; 98US-0082614P.
XX
XX 23-NOV-1998; 98US-0109732P.
XX
XX (GEST ) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome.
XX
XX Claim 9; Page 1635; 2745pp; English.
XX
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
XX primers for the biallelic markers. The biallelic markers of the invention
XX have a variety of uses: they can be used for high density mapping of the
XX human genome, and in complex association studies and haplotyping studies
XX which are useful in determining the genetic basis for disease states.
XX Compositions and methods of the invention can also be useful for the
XX identification of the targets for the development of pharmaceutical
XX agents and diagnostic methods, as well as the characterisation of the
XX differential efficacious responses to and side effects from
XX pharmaceutical agents acting on a disease as well as other treatment.
XX N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
XX 3367, are not actually given a sequence in the Sequence Listing from the
XX present invention
XX
XX Sequence 20 BP; 10 A; 5 C; 2 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 15.2; DB 1; Length 20;
XX Best Local Similarity 85.0%; Pred. No. 2.1e+02;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1042 GTCTTTTGTATCTGTGGTC 1061
XX |||||
XX 20 GTCTATGATTTGTAGTC 1
XX
XX Db
XX
XX RESULT 182
XX AAA27540/C
XX ID AAA27540 standard; DNA; 20 BP.
XX
XX AAA27540;
XX
XX 15-AUG-2000 (first entry)
XX
XX Fas ligand promoter region homozygous at -205G.
XX
XX Fas ligand; promoter; polymorphism; systemic lupus erythematosus;
KW rheumatoid arthritis; autoimmune disease; cancer; diagnosis; haplotyping;

```

```

KW human; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX variation replace(11,C)
XX FT /*tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX
XX WO200023623-A1.
XX
XX 27-APR-2000.
XX
XX 15-OCT-1999; 99WO-US024148.
XX
XX 16-OCT-1998; 98US-0104644P.
XX
XX 17-JUN-1999; 99US-0139659P.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Kimberly RP;
XX
XX WPI; 2000-339717/29.
XX
XX Determining autoimmune disease or cancer susceptibility especially useful
XX for promoting early therapeutic intervention and for gene therapy
XX comprises haplotyping an individual in a Fas promoter and Fas ligand
XX promoter region.
XX
XX Disclosure; Fig 1D; 106pp; English.
XX
XX The present sequence is that of the Fas ligand promoter in the region by
XX nucleotide -205. A C/G single nucleotide polymorphism (SNP) has been
XX identified at -205. Donors homozygous for -205G (present sequence),
XX homozygous for -205G (see AAZ7438) and heterozygous for -205C/T (see
XX AAA27539) have been identified. The present invention is based on the
XX finding that single nucleotide allelic polymorphisms in a Fas promoter or
XX Fas ligand promoter correlate with autoimmune disease occurrence, tumour
XX resistance to the immune system through FasL expression, and infectious
XX disease susceptibility. A method for identifying the Fas or Fas ligand
XX promoter single nucleotide allelic pattern involves testing DNA from
XX individual patients for the presence of different allelic variants and
XX haplotyping the individuals for a series of SNPs suggestive of a
XX particular disease. Polymorphisms have been identified at positions -844,
XX -756, -478 and -205 of the Fas ligand promoter. TAA and TGAG haplotypes
XX at these positions are associated with individuals suffering from
XX systemic lupus erythematosus in greater than 90% of a diagnosed disease
XX group. The invention has utility as a diagnostic for identifying high
XX risk individuals that warrant early treatment. An SNP within a Fas
XX promoter or Fas ligand promoter gene of an individual can also be used
XX for determining susceptibility of the individual to a disease,
XX specifically autoimmune disease and non-lymphatic cancer
XX
XX Sequence 20 BP; 3 A; 0 C; 9 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 15.2; DB 1; Length 20;
XX Best Local Similarity 85.0%; Pred. No. 2.1e+02;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1418 CTGCTCAACAAAGCACTCAC 1437
XX |||||
XX 20 CTCTCAACAAACACCCAC 1
XX
XX Db
XX
XX RESULT 183
XX AAC59878
XX ID AAC59878 standard; DNA; 20 BP.
XX
XX AAC59878;
XX
XX 26-JAN-2001 (first entry)
XX
XX Oligonucleotide probe for human DNA clone vo16 1.

```

XX Secreted protein; human; autoimmune disorder; multiple sclerosis; ulcer;
 KW haematopoiesis regulation; rheumatoid arthritis; anaemia; stroke;
 KW systemic lupus erythematosus; tissue regrowth; wound healing; haemophilia;
 KW Alzheimer's disease; Parkinson's disease; Shy-drager syndrome; cancer;
 KW contraceptive; infection; growth inhibition; hyperproliferative disorder;
 KW psoriasis; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200055375-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 17-MAR-2000; 2000WO-US007285.
 XX
 PR 17-MAR-1999; 99US-0124808P.
 PR 17-MAR-1999; 99US-0124916P.
 PR 17-AUG-1999; 99US-0149639P.
 PR 01-OCT-1999; 99US-0157247P.
 PR 29-NOV-1999; 99US-0167824P.
 PR 15-FEB-2000; 2000US-0182711P.
 XX
 PA (ALPH-) ALPHAGENE INC.
 XX
 PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
 XX
 DR WPI; 2000-638211/61.
 XX
 XX Novel proteins and polypeptides useful for the treatment of e.g multiple
 PT sclerosis, systemic lupus erythematosus, rheumatoid arthritis, cancer,
 PT Alzheimer's disease, Parkinson's disease, stroke, anemia and ulcers.
 XX
 PS Disclosure; Page 470; 493pp; English.
 XX
 CC This invention relates to 59 human secreted proteins and the nucleotide
 CC sequences encoding them. Sequences AAC59788-C59846 and AAB34687-B34745
 CC represent the proteins and their encoding nucleotide sequences, and
 CC sequences AAB34746-B34771 represent fragments of the proteins. Probes for
 CC the DNA sequences are represented by sequences AAC59847-C59596. The
 CC proteins exhibit neuroprotective, dermatological, immunosuppressive,
 CC antiinflammatory, antianaemic, nootropic, antiparkinsonian,
 CC cerebroprotective, haemostatic, vulnetary, cytostatic, antipsoriatic,
 CC antibacterial, virucide, and fungicide activity. The proteins and
 CC nucleotide sequences are useful as nutritional sources or supplements and
 CC in research. The proteins are useful for treating immune deficiency and
 CC disorders, which may be genetic or resulting from infections, autoimmune
 CC disorders such as multiple sclerosis, systemic lupus erythematosus,
 CC rheumatoid arthritis, and for treating myeloid or lymphoid cell
 CC deficiencies such as anaemias by regulating haematopoiesis. The proteins
 CC are also useful in compositions for bone, cartilage, tendon, ligament
 CC and/or nerve tissue growth or regeneration, for wound healing, tissue
 CC repair and replacement and in the treatment of wounds, incisions and
 CC ulcers. Other uses include in the treatment of central and peripheral
 CC nervous system and neuropathies such as Alzheimer's and Parkinson's
 CC diseases and Shy-drager syndrome, and mechanical and traumatic disorders,
 CC such as spinal cord disorders, head trauma and stroke. The proteins may
 CC also be used as a contraceptive, and for treating coagulation disorders
 CC such as haemophilias. The protein and nucleotide sequences with cadherin
 CC activity are useful for treating cancer. Other uses for the protein
 CC include for inhibiting the growth, infection or function of, or killing,
 CC infectious agents such as bacteria, virus, fungi and other parasites, for
 CC effecting bodily characteristics such as height, weight, hair colour,
 CC effecting biorhythms or cardiac cycles or rhythms, effecting metabolism,
 CC catabolism, anabolism, processing, utilization, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors,
 CC effecting behavioural characteristics, providing analgesic effects and
 CC for treating hyperproliferative disorders such as psoriasis
 XX
 SQ Sequence 20 BP; 7 A; 5 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 2.1e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1248 ATATGCGATATGCTGCACAA 1267
 DB 1 ATATTGCAAAATGCTGCACCA 20
 RESULT 184
 AAC81383
 ID AAC81383 standard; DNA; 20 BP.
 XX
 AC AAC81383;
 XX
 DT 23-FEB-2001 (first entry)
 XX
 DE Human Y-box binding protein 1 antisense oligonucleotide, SEQ ID NO:67.
 KW Human Y-box binding protein 1; YB-1; DNA binding protein B; dbpB;
 KW transcription factor; nucleic acid binding; DNA repair;
 KW cell sensitisation; genotoxic stress; immune regulation; MHC expression;
 KW viral gene expression; extracellular matrix degradation regulator;
 KW redox signalling; expression inhibition; tumour formation;
 KW cancer multidrug resistance; inflammation; immune disorder; infection;
 KW phosphorothioate; antisense oligonucleotide; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6140126-A.
 XX
 PD 31-OCT-2000.
 XX
 PF 26-OCT-1999; 99US-00429323.
 XX
 PR 26-OCT-1999; 99US-00429323.
 XX
 PI (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Cowseert LM;
 XX
 DR WPI; 2001-023284/03.
 XX
 PT Antisense oligonucleotides, useful for modulating the expression of Y-box
 PT binding protein 1, as well as for treating or preventing diseases
 PT associated with Y-box binding protein 1 expression, e.g. inflammation or
 PT tumor formation.
 XX
 PS Claim 3; Col 45-46; 40pp; English.
 XX
 CC Sequences AAC81326-C81405 represent antisense oligonucleotides targeted
 CC to the human Y-box binding protein 1 gene, which inhibit its expression.
 CC The antisense oligonucleotides were designed to target different regions
 CC of the human Y-box binding protein 1 mRNA, and were analysed for their
 CC effect on Y-box binding protein 1 mRNA levels by quantitative real-time
 CC PCR. Human Y-box binding protein 1 (also known as YB-1, DNA binding
 CC protein B and dbpB) is a member of the Y-box binding protein family of
 CC transcription factors, a highly conserved family of nucleic acid binding
 CC proteins which bind to the Y-box, an inverted CCAAT sequence found in the
 CC promoters of many genes. Y box binding proteins have a broad specificity
 CC for nucleic acids, being able to bind double-stranded DNA, damaged DNA,
 CC and single-stranded DNA and RNA. Y-box binding protein 1 plays a role in
 CC DNA repair and the sensitisation of cells from a diverse array of
 CC genotoxic stresses, including DNA cross-linking agents and ultraviolet
 CC irradiation. Y-box binding protein 1 is also involved in immune
 CC regulation, being a negative regulator of MHC (major histocompatibility
 CC complex) gene expression, and additionally modulates viral gene
 CC expression. It also participates in the regulation of extracellular
 CC matrix degradation, and is thought to be involved in redox signalling.
 CC The oligonucleotides of the invention are useful for diagnosis,
 CC prevention and treatment of conditions associated with Y-box binding
 CC protein 1 expression, such as tumour formation, cancer multidrug
 CC resistance, inflammation, immune disorders and certain infections
 XX
 SQ Sequence 20 BP; 2 A; 5 C; 1 G; 12 T; 0 U; 0 Other;

XX PA (GENO-) GENOME THERAPEUTICS CORP.
 XX PI Carulli JP, Little RD, Recker RR, Johnson ML;
 XX DX WPI; 2001-657171/75.
 XX
 XX PT New high bone mass (HBM) and Zmax1 genes and proteins useful for
 XX PT modulating bone mass for the treatment of e.g. osteoporosis.
 XX PS Disclosure; Page 35; 443pp; English.
 XX
 XX CC The present invention describes the human Zmax1 gene and the high bone
 XX CC mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and HBM
 XX CC genes have osteopathic activities. The genes can be used in gene therapy,
 XX CC antisense therapy and in the production of vaccines. They can be used in
 XX CC the diagnosis and treatment of bone disorders including osteoporosis,
 XX CC Paget's disease, sclerostosis, osteomalacia and fibrous dysplasia.
 XX CC ABA82038 to ABA82700 and AAG68168 to AAG68193 represent sequences used in
 XX CC the exemplification of the present invention
 XX
 XX SQ Sequence 20 BP; 8 A; 4 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2731 CTGTTCTGTTCTTCTTAATAAG 2750
 Db 20 CTGTTCTGTTCTTCTTAATCAG 1
 RESULT 190
 AAD46615
 ID AAD46615 standard; DNA; 20 BP.
 AC AAD46615;
 XX
 XX 27-JAN-2003 (first entry)
 XX
 XX DE Human ABCC11 intron10/exon11 junction site.
 XX
 XX KW ABCC11 protein; paroxysmal kinesigenic choreoathetosis; inflammation;
 XX KW cholesterol transport; gene therapy; human; ds.
 XX OS Homo sapiens.
 XX
 XX FH Key Location/Qualifiers
 XX FT intron 1..10
 XX FT /*tag= a
 XX FT /number= 1
 XX FT /note= "partial"
 XX FT exon 11..20
 XX FT /*tag= b
 XX FT /number= 2
 XX FT /note= "partial"
 XX
 XX PN WO200272632-A2.
 XX
 XX PD 19-SEP-2002.
 XX
 XX PF 05-MAR-2002; 2002WO-EP003241.
 XX
 XX PR 05-MAR-2001; 2001US-0272757P.
 XX
 XX (AVET) AVENTIS PHARMA SA.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Rosier-Montus M, Prades C, Arnould-Reguigne I, Dean M;
 XX PI Allikmets R, Benefle P;
 XX DX WPI; 2002-723321/78.
 XX

PT New ABCC11 nucleic acids and proteins, useful in manufacturing a
 PT medicament for treating and/or preventing paroxysmal kinesigenic
 PT choreoathetosis, or pathologies linked to the transport of lipophilic
 PT substances.
 XX
 XX PS Disclosure; Page 43; 118pp; English.
 XX
 XX CC The invention relates to novel ABCC11 nucleic acids and proteins. ABCC11
 XX CC sequences are used in the manufacture of a medicament for treating and/or
 XX CC preventing subjects affected by paroxysmal kinesigenic choreoathetosis.
 XX CC They may be used for treating or preventing subjects affected by a
 XX CC dysfunction of the transport of anionic drugs such as methotrexate,
 XX CC neutral drugs conjugated to acidic ligands such as GSH, glucuronate, or
 XX CC sulphate conjugated drugs. Compositions comprising the ABCC11 polypeptide
 XX CC may also be used in the treatment and/or prevention of a deficiency in
 XX CC the transport of cholesterol or inflammatory lipid substances and
 XX CC diseases mapped on the chromosome locus 16q12. ABCC11 protein can be used
 XX CC to treat pathologies linked to the transport of lipophilic substances.
 XX CC The invention is used in gene therapy. The present sequence is human
 XX CC ABCC11 intron/exon junction site
 XX
 XX SQ Sequence 20 BP; 3 A; 2 C; 9 G; 6 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 88 TGGCTCACAGGGGACGATGT 107
 Db 1 TGGCTTGCAGGGGATGATGT 20
 RESULT 191
 AAD31423/C
 ID AAD31423 standard; DNA; 20 BP.
 XX
 XX AC AAD31423;
 XX
 XX 31-MAY-2002 (first entry)
 XX
 XX DE Human chromosome 17 92Kb gene fragment amplifying PCR primer, 12158.
 XX
 XX KW Human; Van Buchem's disease; genomic deletion; craniofacial hypertosis;
 XX KW autosomal recessive disorder; chromosome 17; chromosome 17q21;
 XX KW bone dysplasia; 92Kb gene fragment; PCR primer; ss.
 XX OS Homo sapiens.
 XX
 XX PN WO200210455-A2.
 XX
 XX PD 07-FEB-2002.
 XX
 XX PF 30-JUL-2001; 2001WO-US023968.
 XX
 XX PR 28-JUL-2000; 2000US-0221855P.
 XX PR 06-JUL-2001; 2001US-0303386P.
 XX
 XX PA (CELL-) CELLTECH R & D INC.
 XX PA (STRA/) STRAHLING HAMPTON K.
 XX
 XX PI Brunkow ME, Prohl S, Paepker B;
 XX DX WPI; 2002-227089/28.
 XX
 XX PT Methods for identifying subjects who are afflicted with or carriers of
 XX PT diseases associated with genomic deletion(s), e.g. Van Buchem's disease,
 XX PT by determining the presence of a deletion in the 92 kb region of human
 XX PT chromosome 17 at 17q21.
 XX
 XX PS Example 3; Page 25; 109pp; English.
 XX
 XX CC The present invention relates to methods for distinguishing between
 XX CC individuals homozygous for and therefore afflicted with Van Buchem's

CC disease, individuals heterozygous for and therefore carriers of Van
 CC Buchem's disease and individuals who are not afflicted with Van Buchem's
 CC disease comprise identifying a large genomic deletion in chromosome 17 at
 CC 17q21. The method is useful for identifying individuals who are afflicted
 CC with or carriers of diseases associated with one or more genomic
 CC deletion, particularly Van Buchem's disease, which is a rare autosomal
 CC recessive disorder that results in a bone dysplasia referred to a
 CC craniotubular hypertosis. The present sequence is a PCR primer used to
 CC amplify 92kb gene fragment in human chromosome 17 at 17q21
 XX
 XX Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1116 ATGTTCTGAAAGACGCTCTGC 1135
 DB 20 ATGTTCTGAAAGACGCTCTGC 1
 RESULT 192
 AEN74931
 ID AEN74931 standard; DNA; 20 BP.
 XX
 AC AEN74931;
 XX
 DT 26-JUL-2002 (first entry)
 XX
 DE Mouse caspase 2 antisense inhibitor oligonucleotide #44.
 XX
 KW Caspase 2; antisense; cytostatic; osteopathic; cerebroprotective;
 KW neuroprotective; antilipemic; antiinflammatory; antimicrobial;
 KW haematopoietic disorder; bone metabolism disorder; cholesterol disorder;
 KW hyperproliferative disorder; cancer; blood disorder; stroke;
 KW brain injury; neurodegenerative disease; infection; inflammation; tumour;
 KW ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 modified_base 1..20
 /tag= a
 /mod_base= m5C, OTHER
 /note= "Nucleotides 1-5 and 16-20 are five-nucleotide
 wings consisting 2'methoxyethyl (2'-MOE) nucleotides, 6-
 15 are 2'deoxy nucleotides, backbone linkages are
 phosphodiester, all cytosines are 5-methylcytidines"
 XX
 PN WO200224720-A1.
 XX
 PD 28-MAR-2002.
 XX
 PF 14-SEP-2001; 2001WO-US028631.
 XX
 PR 20-SEP-2000; 2000US-00667018.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Zhang H, Watt AT;
 XX
 DR WPI; 2002-351998/38.
 XX
 PT New antisense compounds targeted to nucleic acid molecule encoding
 PT caspase 2, useful for treating diseases or conditions associated with
 PT caspase 2, e.g. cancer, blood disorders, stroke, brain injury and
 PT neurodegenerative diseases.
 XX
 PS Claim 3; Page 102; 146pp; English.
 XX
 CC The invention relates to a compound 8-50 nucleobases in length targeted
 CC to a nucleic acid molecule encoding caspase 2, which specifically
 CC hybridises with and inhibits the expression of caspase 2, or specifically

CC hybridises with at least an 8-nucleobase portion of an active site on a
 CC nucleic acid molecule encoding caspase 2. The activity of antisense
 CC oligonucleotides of the invention may be described as, cytostatic,
 CC osteopathic, cerebroprotective, neuroprotective, antilipemic,
 CC antiinflammatory and antimicrobial. The antisense compounds are useful
 CC for treating an animal having a disease or condition associated with
 CC caspase 2, such as haematopoietic disorder, bone metabolism disorder,
 CC cholesterol disorder, or a hyperproliferative disorder. These compounds
 CC may further be used as research reagents and diagnostics, to distinguish
 CC between functions of various members of a biological pathway, in the
 CC treatment of a disease or disorder which can be treated by modulating the
 CC expression of caspase 2, including cancer, blood disorders, stroke, brain
 CC injury and neurodegenerative diseases. They may also be used for
 CC prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
 CC formation. Records AEN74810-AEN74952 represent caspase 2 mRNA inhibitor
 CC oligonucleotides
 XX
 XX Sequence 20 BP; 6 A; 3 C; 8 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3106 GAATCCAGCGGACACAGGTAGA 3125
 DB 1 GTAGCCTGGGACACAGGTAGA 20
 RESULT 193
 ABK23143/c
 ID ABK23143 standard; DNA; 20 BP.
 XX
 AC ABK23143;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Human Zmax1 cDNA forward PCR primer #153.
 XX
 KW Human; mouse; Zmax1; HBM; high bone mass gene; lipid regulation; stroke;
 KW lipid-associated condition; arteriosclerosis; cardiovascular disease; ss;
 KW osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up;
 KW neurovascular condition; wound healing; gene therapy; PCR primer; probe;
 KW bone development disorder; antiarteriosclerotic; cardiovascular;
 KW osteopathic; cerebroprotective.
 XX
 OS Homo sapiens.
 XX
 PN WO200192891-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016946.
 XX
 PR 26-MAY-2000; 2000US-00578900.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 PA (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
 XX
 PI Carulli JP, Little RD, Recker RR, Johnson ML;
 XX
 DR WPI; 2002-097784/13.
 XX
 PT Identifying molecules involved in lipid regulation, useful for
 PT diagnosing, treating or preventing e.g., arteriosclerosis, comprises
 PT identifying a molecule that binds to high bone mass gene or its
 PT corresponding wild type gene.
 XX
 PS Disclosure; Page 40; 409pp; English.
 XX
 CC The invention relates to a method for identifying a molecule involved in
 CC lipid regulation comprising identifying a molecule that binds to or
 CC inhibits binding of a molecule to high bone mass (HBM) or its wild type
 CC gene, Zmax1. Compounds identified by the method are useful for treating,

CC diagnosing, preventing or screening for normal and abnormal lipid-
 CC associated conditions, including arteriosclerosis, cardiovascular
 CC disease, stroke, and osteoporosis. The compounds may also be used in
 CC treatment or prevention of diabetic atherosclerosis, neurovascular
 CC conditions caused by plaque build-up, poor circulation due to plaque
 CC build-up and associated poor wound healing. The methods may be used in
 CC gene therapy, pharmaceutical development, and diagnostic assays for bone
 CC development disorders. Molecules identified by comparison of Zmax1 and
 CC HBM systems can be used as surrogate markers in pharmaceutical
 CC development, in diagnosis of human or animal bone disease, and in the
 CC treatment of bone diseases. Sequences ABK2776-ABK23411 represent cDNA
 CC molecules encoding human Zmax1 and HBM, and PCR primers, probes, linkers
 CC and adapters of the invention
 CC
 XX
 SQ Sequence 20 BP; 8 A; 4 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 CTGTCCTGTTCTTCTTAATAAG 2750
 |||||
 Db 20 CTGTCCTGTTCTTCTTAATAAG 1

RESULT 194

ABT06120
 ID ABT06120 standard; DNA; 20 BP.

XX
 AC ABT06120;

XX 28-OCT-2002 (first entry)

XX Human light chain kappa gene related oligo SEQ ID No 134.

XX Single Primer Amplification; nested oligonucleotide extension reaction;
 XX hairpin; SPA; library; ds.

XX Homo sapiens.

XX WO200248401-A2.

XX 20-JUN-2002.

XX 10-DEC-2001; 2001WO-US047727.

XX 11-DEC-2000; 2000US-0254669P.

PR 19-SEP-2001; 2001US-0323400P.

XX (ALEX-) ALEXION PHARM INC.

XX Bowdish KS, Barbas-Frederickson S, Lin Y, McWhirter J, Maruyama T;

PI WPI; 2002-500537/53.

XX Amplifying nucleic acid by synthesizing template nucleic acid containing
 PT a predetermined sequence and hairpin structure and using the template for
 PT target amplification by Single Primer Amplification.

PS Example 5; Page 32; 54pp; English.

XX The invention relates to a method for amplifying a nucleic acid using
 CC Single Primer Amplification (SPA). The method comprises synthesising a
 CC template nucleic acid containing a predetermined sequence and hairpin
 CC structure with the nested oligonucleotide extension reaction. The method
 CC is useful for amplifying a nucleic acid, preferably for amplifying a
 CC family of related nucleic acid sequences to build a complex library of
 CC polypeptides encoded by the sequences. The engineered nucleic acid strand
 CC is useful for amplifying a nucleic acid strand by providing a nucleic
 CC acid with a predetermined sequence engineered onto its first end, a
 CC sequence complementary to the predetermined sequence and a hairpin
 CC structure between them and contacting the engineered nucleic acid strand
 CC with a primer containing at least a portion of the predetermined

CC sequence. This process is done in the presence of a polymerase and
 CC nucleotides under conditions suitable for polymerisation to produce a
 CC complementary nucleic acid strand. The method of the invention is useful
 CC for producing large amounts of a target nucleic acid sequence and for
 CC amplifying simultaneously more than one different target nucleic acid
 CC sequence located on the same or different nucleic acid molecules. This
 CC polynucleotide sequence represents an oligonucleotide relating to the
 CC invention

XX
 SQ Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2385 TCTTCACTGGGATCAGAGAT 2404

|||||
 Db 1 TCTGCCCTGGTATCAGAGAT 20

RESULT 195

ABI93955

ID ABI93955 standard; DNA; 20 BP.

XX
 AC ABI93955;

XX 16-FEB-2002 (first entry)

XX Capture oligonucleotide Zip ID#1042 oligo #9.

XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 KW ligase detection reaction; LDR; p53; BRCA2; infectious disease;
 KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
 KW oncogene; tumour suppressor; human papillomavirus; forensic;
 KW environmental monitoring; food industry; feed industry; ss.

XX Synthetic.

XX WO200179548-A2.

XX 25-OCT-2001.

XX 04-APR-2001; 2001WO-US010958.

XX 14-APR-2000; 2000US-0197271P.

XX (CORR) CORNELL RES FOUND INC.

XX Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;

XX WPI; 2002-034366/04.

XX Designing capture oligonucleotide probes for use on a support to which
 PT complementary oligonucleotides hybridize with little mismatch.

PS Example 5; Fig 29; 300pp; English.

XX The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridise with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC melioides. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The

CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. ABI92074 to
 CC ABI97546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention
 XX
 SQ Sequence 20 BP; 3 A; 4 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2231 CGTATCAATGATGCTTTCG 2250
 ||| ||||| ||||| ||||| ||
 Db 1 CGTTGCAATGATGCTTTCG 20

RESULT 196
 ABI94540
 ID ABI94540 standard; DNA; 20 BP.
 XX
 AC ABI94540;
 XX
 DT 16-FEB-2002 (first entry)
 XX
 DE Capture oligonucleotide Zip ID#1627 oligo #9.
 XX
 KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
 KW oncogene; tumour suppressor; human papillomavirus; forensic;
 KW environmental monitoring; food industry; feed industry; ss.

OS Synthetic.
 XX
 XX WO200179548-A2.
 PN
 XX 25-OCT-2001.
 PD
 XX 04-APR-2001; 2001WO-US010958.
 PP
 XX 14-APR-2000; 2000US-0197271P.
 PR
 XX (CORR) CORNELL RES FOUND INC.
 PA
 XX Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
 PI
 XX WPI; 2002-034366/04.
 DR

XX Designing capture oligonucleotide probes for use on a support to which
 PT complementary oligonucleotides hybridize with little mismatch.
 PT

PS Example 5; Fig 29; 300pp; English.

XX The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridize with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medinis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The

CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. ABI82074 to
 CC ABI97546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention
 XX

SQ Sequence 20 BP; 5 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1095 CCATGCTAACGCCACGGA 1114
 ||||| ||||| ||||| ||||| ||
 Db 1 CCATGATGACGTCGCCAGGA 20

RESULT 197
 ABK98200
 ID ABK98200 standard; DNA; 20 BP.
 XX
 AC ABK98200;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Triple helix forming associated oligonucleotide #58.

XX Triple-helix formation; purine-rich target sequence; double-helix DNA;
 KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
 KW pathogenic bacteria; virus; replication; virulence; cancer;
 KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

OS Synthetic.
 XX
 XX US6403302-B1.
 PN
 XX 11-JUN-2002.
 PD
 XX 16-DEC-1993; 93US-00168920.
 PP
 XX 17-SEP-1992; 92US-00946976.
 PR
 XX (CALY) CALIFORNIA INST OF TECHNOLOGY.
 PA
 XX Dervan PB, Beal PA;
 PI
 XX WPI; 2002-536030/57.
 DR

XX A triple-helix comprising a double helical nucleic acid (DHNA) and an
 PT oligonucleotide which binds in parallel and antiparallel orientation,
 PT respectively, for targeting sequences on alternate strands of DHNA to
 PT control gene expression.
 PT

PS Example 8; Fig 27; 108pp; English.

XX The present invention relates to methods and oligonucleotides for forming
 CC a triple-helix comprising a double helical nucleic acid comprising first
 CC and second substantially complementary strands, and an oligonucleotide
 CC bound to a purine-rich target sequence within the double helical nucleic
 CC acid, where the oligonucleotide binds in a parallel and antiparallel
 CC orientation, respectively, to target sequences on alternate strands of
 CC the double helical nucleic acid. The method has therapeutic applications,
 CC where gene expression is controlled by selective triple-helix formation,
 CC within expression regulatory sequences of a target gene. The
 CC oligonucleotides can be used to form triple-helices, and are useful to
 CC detect the presence or absence of specific sequences within genomic DNA
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be
 CC selected to specifically bind to pathogenic double-stranded DNA including
 CC specific sequences required by pathogenic bacteria or viruses for
 CC replication or virulence, reducing their pathogenicity. Alternatively,

CC the oligonucleotide can be chosen to target a unique sequence of the
 CC pathogen which is not found in the genome of pathogen's host. The
 CC oligonucleotides can be used in cancer treatment by way of triple-helix
 CC suppression of specific oncogenes including those of endogenous or viral
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-
 CC helices with such sequences in cancerous cells containing the activated
 CC oncogene, so preferentially killing or repressing the cancer causing
 CC cell. The present sequence represents an oligonucleotide used in the
 CC methods of the present invention

XX Sequence 20 BP; 2 A; 3 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 2.1e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2091 TTCTTTTGGGAGGAGAT 2110

Db 1 TTCTTTTGGGAGGAGGT 20

RESULT 198

ABK98203

ID ABK98203 standard; DNA; 20 BP.

AC ABK98203;

DT 07-OCT-2002 (first entry)

DE Triple helix forming associated oligonucleotide #59.

XX Triple-helix formation; purine-rich target sequence; double-helix DNA;
 KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
 KW pathogenic bacteria; virus; replication; virulence; cancer;
 KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

XX Synthetic.

XX US6403302-B1.

XX 11-JUN-2002.

XX 16-DEC-1993; 93US-00168920.

XX 17-SEP-1992; 92US-00946976.

XX (CALY) CALIFORNIA INST OF TECHNOLOGY.

XX Dervan PB, Beal PA;

XX WPI; 2002-536030/57.

XX A triple-helix comprising a double helical nucleic acid (DHNA) and an
 PT oligonucleotide which binds in parallel and antiparallel orientation,
 PT respectively, for targeting sequences on alternate strands of DHNA to
 PT control gene expression.

XX Example 8; Fig 27; 108pp; English.

XX The present invention relates to methods and oligonucleotides for forming
 CC a triple-helix comprising a double helical nucleic acid comprising first
 CC and second substantially complementary strands, and an oligonucleotide
 CC bound to a purine-rich target sequence within the double helical nucleic
 CC acid, where the oligonucleotide binds in a parallel and antiparallel
 CC orientation, respectively, to target sequences on alternate strands of
 CC the double helical nucleic acid. The method has therapeutic applications,
 CC where gene expression is controlled by selective triple-helix formation
 CC within expression regulatory sequences of a target gene. The
 CC oligonucleotides can be used to form triple-helices, and are useful to
 CC detect the presence or absence of specific sequences within genomic DNA
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be
 CC selected to specifically bind to pathogenic double-stranded DNA including
 CC specific sequences required by pathogenic bacteria or viruses for

CC replication or virulence, reducing their pathogenicity. Alternatively,
 CC the oligonucleotide can be chosen to target a unique sequence of the
 CC pathogen which is not found in the genome of pathogen's host. The
 CC oligonucleotides can be used in cancer treatment by way of triple-helix
 CC suppression of specific oncogenes including those of endogenous or viral
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-
 CC helices with such sequences in cancerous cells containing the activated
 CC oncogene, so preferentially killing or repressing the cancer causing
 CC cell. The present sequence represents an oligonucleotide used in the
 CC methods of the present invention

XX Sequence 20 BP; 2 A; 3 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 2.1e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2091 TTCTTTTGGGAGGAGAT 2110

Db 1 TTCTTTTGGGAGGAGGT 20

RESULT 199

ABZ86330/c

ID ABZ86330 standard; DNA; 20 BP.

AC ABZ86330;

XX 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX Claim 15; SEQ ID NO 1572; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or

CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1333 TTCTGCAGGCACACTAAGC 1352
 ||||| ||||| |||||
 Db 1 TTCTGCAGGCACACTCAGC 20

RESULT 202

ABZ90063
 ID ABZ90063 standard; DNA; 20 BP.

XX AC ABZ90063;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX Disclosure; SEQ ID NO 5305; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or

CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 20 BP; 10 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2426 AGAAGTGGAGAAATCCTTA 2445
 ||||| ||||| |||||
 Db 1 AGAAGAGAGAGACATCCTTA 20

RESULT 203

ABQ84467/C

ID ABQ84467 standard; DNA; 20 BP.

XX AC ABQ84467;

DT 20-FEB-2003 (first entry)

DE DPP10 PCR primer #98.

XX DPP10; dipeptidyl peptidase; prolyl oligopeptidase; enzyme; asthma;
 KW antiinflammatory; antiasthmatic; antipsoriatic; antiarthritic;
 KW antirheumatic; vaccine; gene therapy; inflammatory disease;
 KW inflammatory bowel disease; atopy; rheumatoid arthritis; psoriasis;
 KW chromosome 2q14; PCR primer; ss.

XX Homo sapiens.

XX Synthetic.

XX WO200286113-A2.

XX 31-OCT-2002.

XX 24-APR-2002; 2002WO-GB001887.

XX 24-APR-2001; 2001GB-00010044.

XX 24-APR-2001; 2001GB-00010046.

XX 12-OCT-2001; 2001GB-00024575.

XX 12-OCT-2001; 2001GB-00024594.

XX (ISIS-) ISIS INNOVATIONS LTD.

XX Cookson WOCM, Moffat MF, Allen M, Lench N;

XX WPI; 2003-093132/08.

XX New nucleic acid sequence comprising DPP10 mRNA, useful for the
 PT manufacture of a medicament for regulating DPP10 protein expression or
 PT for preventing or treating inflammatory disease e.g., inflammatory bowel
 PT disease.

XX Claim 43; Page 314; 321pp; English.

XX The present invention describes a new isolated nucleic acid sequence (I)
 CC comprising a DPP10 mRNA sequence. DPP10 is a dipeptidyl peptidase (also
 CC known as prolyl oligopeptidase). (I) has antiinflammatory, antiasthmatic,
 CC antipsoriatic, antiarthritic and antirheumatic activities, and can be
 CC used in vaccines and gene therapy. A composition comprising (I) can be
 CC used for the manufacture of a medicament for regulating DPP10 expression
 CC or for preventing or treating inflammatory disease e.g., inflammatory
 CC bowel disease, asthma, atopy, rheumatoid arthritis or psoriasis. (I) can

CC also be used in an assay for detecting or measuring DPP10 in a sample. A
 CC host cell comprising (i) can be used for producing recombinant DPP10 gene
 CC products, or in drug screening systems to identify agents for diagnosis
 CC or treatment of individuals having or susceptible to inflammatory
 CC disease. Human DPP10 is located on chromosome 2, more specifically
 CC chromosome 2q14. ABQ84254 to ABQ84612 and ABP5569 to ABP55629 represent
 CC sequences used in the exemplification of the present invention
 XX
 SQ Sequence 20 BP; 8 A; 4 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 TCTTCTGGGCTCTCTCAG 132
 |||||
 Db 20 TCTTCTGGGCTCTTCCAG 1

RESULT 204
 ACC45726/C
 ID ACC45726 standard; DNA; 20 BP.

XX ACC45726;

DT 02-JUN-2003 (first entry)

DE Human HBM STS marker forward primer #153.

XX Human; high bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;
 KW gene therapy; bone density modulation; bone strength; trabecular number;
 KW bone size; bone tissue connectivity; bone disease; osteoporosis; PCR;
 KW osteomalacia; rickets; Paget's disease; neoplasm of the bone; primer; ss.

XX Homo sapiens.

XX WO200292764-A2.

XX 21-NOV-2002.

PF 13-MAY-2002; 2002WO-US014876.

PR 11-MAY-2001; 2001US-0290071P.

PR 17-MAY-2001; 2001US-0291311P.

PR 01-FEB-2002; 2002US-0353058P.

PR 04-MAR-2002; 2002US-0361293P.

XX (GENO-) GENOME THERAPEUTICS CORP.

PA (AMRP) WYETH.

XX Babijs P, Bex FJ, Yaworsky PJ, Bodine FV;

PI WPI; 2003-129278/12.

DR New transgenic animals (e.g. mice), useful as models for studying bone

XX density modulation, developing drugs for treating or preventing bone

PT diseases (e.g. osteoporosis), or diagnosing diseases characterized by

PT reduced bone density.

XX Disclosure; Page 56; 603pp; English.

XX The invention relates to novel transgenic animals expressing the high

CC bone mass (HBM) gene, expressing the corresponding wild type HBM gene,

CC comprising an alteration of the gene encoding LRP5 or LRP6, or expressing

CC an LRP5 that is modulated by an altered gene control sequence introduced

CC by homologous or non-homologous recombination. The transgenic animals are

CC for the study of bone density modulation or bone mass modulation. The

CC transgenic animals, nucleic acids and methods are useful for identifying
 CC molecules involved in bone development, and for developing pharmaceutical
 CC compositions, which may be employed for treating or preventing bone
 CC diseases, e.g. osteoporosis, osteomalacia, rickets, Paget's disease, or
 CC neoplasms of the bone. The transgenic animals and nucleic acids are also
 CC useful in methods for diagnosing diseases involved in bone development, is
 CC or characterised by reduced bone density or mass. The present sequence is
 CC used in the exemplification of the invention

XX Sequence 20 BP; 8 A; 4 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 2.1e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 CTGTTCTGTTCTTAAATAG 2750
 |||||
 Db 20 CTGTTCTGTTCTCAATCAG 1

RESULT 205

AAD49364/C

ID AAD49364 standard; DNA; 20 BP.

XX AAD49364;

XX 07-MAR-2003 (first entry)

DE Mouse phospholipid scramblase I antisense oligo, ISIS #120574.

XX Mouse; antisense; phospholipid scramblase I; immune disorder; cancer;

KW inflammation; hyperproliferative; antisense therapy; phosphorothioate;

KW ss.

XX Mus musculus.

OS Synthetic.

XX Key

FT modified_base

FT 1..20

FT /tag= a

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone"

FT modified_base

FT 1..5

FT /tag= b

FT /mod_base= OTHER

FT /note= "2'methoxyethyl nucleotides"

FT modified_base

FT 1

FT /tag= d

FT /mod_base= m5c

FT modified_base

FT 4

FT /tag= e

FT /mod_base= m5c

FT modified_base

FT 13

FT /tag= f

FT /mod_base= m5c

FT modified_base

FT 16..20

FT /tag= c

FT /mod_base= OTHER

FT /note= "2'methoxyethyl nucleotides"

FT modified_base

FT 16

FT /tag= g

FT /mod_base= m5c

XX WO200281495-A1.

XX 17-OCT-2002.

XX 02-APR-2002; 2002WO-US010529.

XX 05-APR-2001; 2001US-00828344.

XX (ISIS-) ISIS PHARM INC.

PI Bennett CF, Wyatt JR;
 DR WPI; 2003-058495/05.
 XX
 XX Novel antisense compounds targeted to nucleic acids encoding phospholipid
 PT scramble I, for modulating gene expression and treating inflammation,
 PT immune disorders and hyperproliferative conditions e.g. cancer.
 XX
 XX Claim 3; Page 80; 131pp; English.
 XX
 XX The invention relates to an antisense compound targetted to a nucleic
 CC acid molecule encoding phospholipid scramble I and which specifically
 CC hybridises with and inhibits the expression of phospholipid scramble I,
 CC or which hybridises with at least an 8-nucleobase portion of an active
 CC site on a nucleic acid molecule encoding phospholipid scramble I. The
 CC invention is useful for inhibiting the expression of human phospholipid
 CC scramble I in cells or tissues and for treating an animal having a
 CC disease or condition associated with phospholipid scramble I, such as
 CC inflammation, an immune disorder and a hyperproliferative condition, e.g.
 CC cancer. The invention is useful for diagnostics, therapeutics and as
 CC research reagent. The present sequence is mouse phospholipid scramble I
 CC antisense oligonucleotide
 XX
 SQ Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1693 TCAAGCAGCTAAACATGAAG 1712
 DB 20 TCAAGCTGTATACATGAAG 1
 RESULT 206
 ABT15991/c
 ID ABT15991 standard; DNA; 20 BP.
 XX
 XX AC ABT15991;
 XX
 XX 28-MAR-2003 (first entry)
 XX
 XX Pathogen variant detection related PCR primer #2.
 XX
 XX Primer extension chain reaction; reverse; forward; target nucleic acid;
 KW variant; HIV; HCV; HBV; Parvovirus B19; PCR primer; ss.
 XX
 XX Unidentified.
 OS
 XX WO200283927-A2.
 XX
 XX 24-OCT-2002.
 PD
 XX
 XX 17-APR-2002; 2002WO-US012035.
 PF
 XX
 XX 17-APR-2001; 2001US-0284334P.
 PR
 XX
 XX (NYBL-) NEW YORK BLOOD CENT INC.
 PA
 XX
 XX Andrus L, Nichols CN;
 PI
 XX
 XX WPI; 2003-103374/09.
 DR
 XX
 XX Detecting presence of target nucleic acid molecule e.g. human
 PT immunodeficiency virus, hepatitis B or C virus in a sample, by using a
 PT universal multi-variant detection system.
 XX
 XX Disclosure; Fig 2; 63pp; English.
 PS
 XX
 XX The invention relates to a novel method for a primer extension chain
 CC reaction for determining presence of a target nucleic acid molecule in a
 CC sample, where the nucleotide at 3' end of the reverse primer hybridises
 CC with nucleotide at 5' end of the forward primer extension product or a

CC nucleotide separated from the nucleotide at 5' end of the forward primer
 CC extension product by a gap comprising a highly conserved nucleotide
 CC sequence. The method is useful for determining presence of a target
 CC nucleic acid molecule known to have variant sequences, in a sample. The
 CC target nucleic acid is preferably a virus including human
 CC immunodeficiency virus (HIV), hepatitis C virus (HCV), hepatitis B virus
 CC (HBV) or Parvovirus B19. This polynucleotide sequence represents a PCR
 CC primer used in the primer extension chain reaction method of the
 CC invention
 XX
 SQ Sequence 20 BP; 4 A; 6 C; 2 G; 8 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 2.1e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 282 AAAACATGAATAATGCTGGG 301
 DB 20 AAAAGATGGATATCCTGGG 1
 RESULT 207
 ADB65803
 ID ADB65803 standard; DNA; 20 BP.
 XX
 XX AC ADB65803;
 XX
 XX 04-DEC-2003 (first entry)
 DT
 XX
 XX Clone specific PCR primer #4.
 XX
 XX KW Pharmaceutical; diagnostic; gene therapy; tissue regeneration;
 KW cell regeneration; membrane protein; signal transduction-related protein;
 KW transcription-related protein; osteoporosis; neurological disease;
 KW cancer; tumour; primer; PCR; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 XX EP1308459-A2.
 PN
 XX
 XX 07-MAY-2003.
 PD
 XX
 XX 28-MAR-2002; 2002EP-00007401.
 PF
 XX
 XX 05-NOV-2001; 2001JP-00379298.
 PR
 XX 25-JAN-2002; 2002US-00350978.
 PR
 XX
 XX (HELI-) HELIX RES INST.
 PA
 XX
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX
 XX WPI; 2003-450961/43.
 DR
 XX
 XX New polynucleotides and polypeptides, useful for developing a diagnostic
 PT marker or medicines for regulation of their expression and activity, or
 PT as targets of gene therapy.
 XX
 XX Example 8; Page 125; 222pp; English.
 PS
 XX
 XX The invention discloses a polynucleotide comprising a sequence selected
 CC from 1970 fully defined nucleotide sequences which encode novel
 CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
 CC or its partial peptide, an antibody binding to the polypeptide or peptide
 CC of the polynucleotide, immunologically assaying the polypeptide or
 CC peptide of the polynucleotide by contacting the polypeptide or peptide
 CC with the antibody of the encoded protein, and observing the binding
 CC between the two, a transformant carrying the polynucleotide in an
 CC expressible manner and an antisense polynucleotide. The oligonucleotide
 CC is useful as a primer for synthesising the polynucleotide, or as a probe
 CC for detecting the polynucleotide. The polynucleotides and encoded

CC proteins are useful as pharmaceutical agents and many disease-related
 CC genes may be included in them, for developing a diagnostic marker or
 CC medicines for regulation of their expression and activity, or as targets
 CC of gene therapy. The genes are involved in tissue and/or cell
 CC regeneration. Membrane proteins, signal transduction-related proteins,
 CC transcription-related proteins, disease-related proteins and genes
 CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
 CC neurological diseases, cancer, tumours. The cDNA may be used to regulate
 CC the activity or expression of the encoded protein to treat diseases. The
 CC sequence presented is clone specific PCR primer which was used in the
 CC expression analysis of the genes of the invention. Note: Some of the
 CC sequence data for this patent is not represented in the printed
 CC specification, but is based on sequence information supplied by the
 CC European Patent Office.

XX Sequence 20 BP; 3 A; 4 C; 4 G; 9 T; 0 U; 0 Other;
 CC
 CC Query Match 0.4%; Score 15.2; DB 1; Length 20;
 CC Best Local Similarity 85.0%; Pred. No. 2.1e+02;
 CC Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 888 TCCCTGCTCATTTGCTTGGT 907
 DB 1 TACGTGCTCATTTACTTGGT 20

RESULT 208
 ADB98424/C
 ID ADB98424 standard; DNA; 20 BP.

XX AC ADB98424;

XX DT 04-DEC-2003 (first entry)

XX Sequence tagged site #305 used to prepare Zmax1 (LRP5) gene region map.
 DE Osteopathic; Gene therapy; High Bone Mass; HBM; LRP5; Zmax1; LRP6;
 KW bone mass modulation; osteoporosis; STS; sequence tagged site; ds.

XX OS Homo sapiens.

XX PN WO200292000-A2.

XX PD 21-NOV-2002.

XX PF 13-MAY-2002; 2002WO-US014877.

XX PR 11-MAY-2001; 2001US-0290071P.

XX PR 17-MAY-2001; 2001US-0291311P.

XX PR 01-FEB-2002; 2002US-0353058P.

XX PR 04-MAR-2002; 2002US-0361293P.

XX (GENO-) GENOME THERAPEUTICS CORP.
 PA (AMHP) WYETH.

XX PI Allen K, Anisowicz A, Graham JR, Morales A, Yaworsky PJ, Liu W;
 XX WPI; 2003-129214/12.

XX New nucleic acid comprising a mutation in LRP5 or LRP6, useful for
 PT diagnosing a HBM-like phenotype in a subject and for preparing a
 PT composition for modulating bone mass and/or lipid levels in a subject
 PT suffering from e.g. osteoporosis.

XX Example 2; Page 63; 629pp; English.

XX The present invention relates to High Bone Mass (HBM), LRP5 (Zmax1) and
 CC LRP6 mutants, which results in a HBM-like phenotype when expressed in a
 CC cell. The HBM-like phenotype results in bone mass modulation and/or lipid
 CC level modulation. The invention is useful for diagnosing a HBM-like
 CC phenotype in a subject and for preparing a composition for modulating
 CC bone mass and/or lipid levels in a subject suffering from e.g.
 CC osteoporosis. The present sequence is a Sequence Tagged Site (STS)

CC marker, which was used to prepare a physical map of the Zmax1 (LRP5) gene
 CC region.
 XX Sequence 20 BP; 8 A; 4 C; 5 G; 3 T; 0 U; 0 Other;

CC Query Match 0.4%; Score 15.2; DB 1; Length 20;
 CC Best Local Similarity 85.0%; Pred. No. 2.1e+02;
 CC Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 CTGTTCTGTTCTTAAATAG 2750
 DB 20 CTGTTCTGTTCTTCAATCAG 1

RESULT 209
 AAQ75641/C
 ID AAQ75641 standard; DNA; 21 BP.

XX AC AAQ75641;

XX DT 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; Gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

XX PS Disclosure; Page 6; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

XX Query Match 0.4%; Score 15.2; DB 1; Length 21;
 XX Best Local Similarity 85.0%; Pred. No. 2.3e+02;
 XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3386 ACACACTCAAAAAAAAAA 3405
 DB 21 ACACAAAAAAAAAAAAAAAA 2

RESULT 210
 AAA48686
 ID AAA48686 standard; cDNA; 21 BP.

XX AC AAA48686;

XX DT 20-SEP-2000 (first entry)

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XX DE PCR primer B13M126.3 targeted to chicken MHC BFIV13.
XX KW Chicken; MHC; major histocompatibility complex; BFIV; antisera;
XX KW PCR primer; ss.
XX OS Gallus gallus.
XX PN US6075125-A.
XX PD 13-JUN-2000.
XX PF 09-JUL-1997; 97US-00890719.
XX PS 10-JUL-1996; 96US-0021685P.
XX PA (USDA ) US SEC OF AGRIC.
XX PI Hunt HD, Bacon LD, Fulton JE;
XX DR WPI; 2000-411285/35.
XX CC Producing antisera specific to major histocompatibility complex (MHC)
XX CC proteins in chickens involves administering transfected cells expressing
XX CC heterologous chicken MHC class I protein capable of eliciting immune
XX CC response.
XX PS Example 2; Col 23-24; 40pp; English.
XX CC The chicken Major Histocompatibility Complex (MHC) B-complex is comprised
XX CC of three classes of loci. Class I was mutated by site directed
XX CC mutagenesis. Transfected cells containing the mutant sequence may be
XX CC generated. The heterologous BFIV protein produced by these cells may be
XX CC used as an immunogen to produce chicken MHC class I specific antisera.
XX CC This antisera may then be used to determine the BF haplotype of any
XX CC chicken. BFIV specific antisera may be used to determine the B haplotype
XX CC of chickens with reduced cross reaction with class I and class IV MHC
XX CC proteins. The present sequence is the PCR primer B13M126.3, targeted to
XX CC mutagenise BFIV13 at positions 126 to 128
XX PS Sequence 21 BP; 3 A; 5 C; 4 G; 9 T; 0 U; 0 Other;
XX SQ
XX
Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 815 GAACATCTTCATGCTATGT 834
Db 1 GAACGTCTTCATGCTTTGT 20

RESULT 211
AAA48684/C
ID AAA48684 standard; cDNA; 21 BP.
XX AC AAA48684;
XX CC
XX DT 20-SEP-2000 (first entry)
XX DE
XX PF PCR primer B13M126.5 targeted to chicken MHC BFIV13.
XX KW Chicken; MHC; major histocompatibility complex; BFIV; antisera;
XX KW PCR primer; ss.
XX OS Gallus gallus.
XX PN US6075125-A.
XX PD 13-JUN-2000.
XX PF 09-JUL-1997; 97US-00890719.
XX PS
XX SQ

```

```

PR 10-JUL-1996; 96US-0021685P.
XX
XX PA (USDA ) US SEC OF AGRIC.
XX PI Hunt HD, Bacon LD, Fulton JE;
XX DR WPI; 2000-411285/35.
XX CC Producing antisera specific to major histocompatibility complex (MHC)
XX CC proteins in chickens involves administering transfected cells expressing
XX CC heterologous chicken MHC class I protein capable of eliciting immune
XX CC response.
XX PS Example 2; Col 23-24; 40pp; English.
XX CC The chicken Major Histocompatibility Complex (MHC) B-complex is comprised
XX CC of three classes of loci. Class I was mutated by site directed
XX CC mutagenesis. Transfected cells containing the mutant sequence may be
XX CC generated. The heterologous BFIV protein produced by these cells may be
XX CC used as an immunogen to produce chicken MHC class I specific antisera.
XX CC This antisera may then be used to determine the BF haplotype of any
XX CC chicken. BFIV specific antisera may be used to determine the B haplotype
XX CC of chickens with reduced cross reaction with class I and class IV MHC
XX CC proteins. The present sequence is the PCR primer B13M126.5, targeted to
XX CC mutagenise BFIV13 at positions 126 to 128
XX PS Sequence 21 BP; 9 A; 4 C; 5 G; 3 T; 0 U; 0 Other;
XX SQ
XX
Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 815 GAACATCTTCATGCTATGT 834
Db 21 GAACGTCTTCATGCTTTGT 2

RESULT 212
AAZ74972/C
ID AAZ74972 standard; DNA; 21 BP.
XX AC AAZ74972;
XX CC
XX DT 10-SEP-2001 (first entry)
XX DE Human biallelic marker downstream amplification primer SEQ ID NO:9328.
XX KW Human genome; biallelic marker; high density disequilibrium map;
XX KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX KW haplotyping; hybridisation; identification; characterisation;
XX KW amplification; single nucleotide polymorphism; SNP; PCR primer;
XX KW diagnosis; ss.
XX OS Homo sapiens.
XX PN WO954500-A2.
XX PD 28-OCT-1999.
XX PF 21-APR-1999; 99WO-IB000822.
XX KW 21-APR-1998; 98US-0082614P.
XX PR 23-NOV-1998; 98US-0109732P.
XX CC (GEST ) GENSET.
XX PA Cohen D, Blumenfeld M, Chumakov I;
XX PI WPI; 2000-013267/01.
XX DR
XX KW Novel biallelic markers used to construct a high density disequilibrium
XX KW map of the human genome.
XX PT

```

XX PS Claim 8; Page 2219; 2745pp; English.

XX CC AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. CC Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment. CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the present invention

XX SQ Sequence 21 BP; 9 A; 1 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2699 TCAGTATTATTTCGTCTC 2718
||| ||||| ||||| |||||
Db 20 TCACAAATTATTTCGTCTC 1

RESULT 213

AAZ71795

ID AAZ71795 standard; DNA; 21 BP.

AC AAZ71795;

XX 10-SEP-2001 (first entry)

XX Human biallelic marker upstream amplification primer SEQ ID NO:6151.

XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; Genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.

XX Homo sapiens.

OS WO9954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-IB000822.

XX 21-APR-1998; 98US-0082614P.

PR 23-NOV-1998; 98US-0109732P.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;
WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium map of the human genome.

XX Claim 8; Page 1542; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the

CC human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. CC Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment. CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the present invention

XX SQ Sequence 21 BP; 7 A; 3 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 181 GACATTTTGGACAGTTTA 200
||||| ||||| ||||| |||||
Db 1 GACATTTTGAACAGTATA 20

RESULT 214

AAZ76309

ID AAZ76309 standard; DNA; 21 BP.

XX AAZ76309;

XX 10-SEP-2001 (first entry)

XX Human biallelic marker downstream amplification primer SEQ ID NO:10665.

XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; Genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.

XX Homo sapiens.

OS WO9954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-IB000822.

XX 21-APR-1998; 98US-0082614P.

PR 23-NOV-1998; 98US-0109732P.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;
WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium map of the human genome.

XX Claim 9; Page 2504; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. CC Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment. CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and

CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention
 XX
 SQ Sequence 21 BP; 10 A; 5 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2628 GACTCTGTTTCAGAAAAA 2647
 ||||| ||||| ||||| |||||
 Db 1 GACTCTCATCAGAAAAA 20

RESULT 215

AAZ75996

ID AAZ75996 standard; DNA; 21 BP.

XX

AC AAZ75996;

XX

DT 10-SEP-2001 (first entry)

XX

DE Human biallelic marker downstream amplification primer SEQ ID NO:10352.

XX

KW Human genome; biallelic marker; high density disequilibrium map;

KW genomic map; haplotype; phenotype; polymorphic base; genotyping;

KW haplotyping; hybridisation; identification; characterisation;

KW amplification; single nucleotide polymorphism; SNP; PCR primer;

KW diagnosis; ss.

XX

OS Homo sapiens.

XX

PN WO9954500-A2.

XX

PD 28-OCT-1999.

XX

PF 21-APR-1999; 99WO-IB000822.

XX

PR 21-APR-1998; 98US-0082614P.

XX

PR 23-NOV-1998; 98US-0109732P.

XX

PA (GEST) GENSET.

XX

PI Cohen D, Blumenfeld M, Chumakov I;

XX

DR WPI; 2000-013267/01.

XX

XX

XX

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XX

CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention
 XX
 SQ Sequence 21 BP; 10 A; 5 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 2.3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2628 GACTCTGTTTCAGAAAAA 2647
 ||||| ||||| ||||| |||||
 Db 1 GACTCTCATCAGAAAAA 20

RESULT 216

AAC70918/c

ID AAC70918 standard; DNA; 21 BP.

XX

AC AAC70918;

XX

DT 09-FEB-2001 (first entry)

XX

DE Single nucleotide polymorphism PCR primer #499.

XX

KW Single nucleotide polymorphism; SNP; human; genetic disease;

KW disease susceptibility; cardiovascular system; endocrine system;

KW neurological system; forensic testing; paternity testing; ss.

KW

OS Homo sapiens.

XX

PN WO200058519-A2.

XX

PD 05-OCT-2000.

XX

PF 30-MAR-2000; 2000WO-US008440.

XX

PR 31-MAR-1999; 99US-0127248P.

XX

XX

XX

XX

XX

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Qy 3144 TCCAGAGTGCTTGATCAACA 3163
 ||||| ||||| ||||| |||||
 Db 1 TCCAGAGTGCTTGATCAACA 20

RESULT 217
 AAC70918/c

ID AAC70918 standard; DNA; 21 BP.

XX

AC AAC70918;

XX

DT 09-FEB-2001 (first entry)

XX

DE Single nucleotide polymorphism PCR primer #499.

XX

KW Single nucleotide polymorphism; SNP; human; genetic disease;

KW disease susceptibility; cardiovascular system; endocrine system;

KW neurological system; forensic testing; paternity testing; ss.

KW

OS Homo sapiens.

XX

PN WO200058519-A2.

XX

PD 05-OCT-2000.

XX

PF 30-MAR-2000; 2000WO-US008440.

XX

PR 31-MAR-1999; 99US-0127248P.

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Qy 3144 TCCAGAGTGCTTGATCAACA 3163
 ||||| ||||| ||||| |||||
 Db 1 TCCAGAGTGCTTGATCAACA 20

RESULT 217
 AAC70918/c

ID AAC70918 standard; DNA; 21 BP.

XX

AC AAC70918;

XX

DT 09-FEB-2001 (first entry)

XX

DE Single nucleotide polymorphism PCR primer #499.

XX

KW Single nucleotide polymorphism; SNP; human; genetic disease;

KW disease susceptibility; cardiovascular system; endocrine system;

KW neurological system; forensic testing; paternity testing; ss.

KW

OS Homo sapiens.

XX

PN WO200058519-A2.

XX

PD 05-OCT-2000.

XX

PF 30-MAR-2000; 2000WO-US008440.

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PR 31-MAR-1999; 99US-0127248P.

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Qy 3144 TCCAGAGTGCTTGATCAACA 3163
 ||||| ||||| ||||| |||||
 Db 1 TCCAGAGTGCTTGATCAACA 20

RESULT 217
 AAC70918/c

ID AAC70918 standard; DNA; 21 BP.

XX

AC AAC70918;

XX

DT 09-FEB-2001 (first entry)

XX

DE Single nucleotide polymorphism PCR primer #499.

XX

KW Single nucleotide polymorphism; SNP; human; genetic disease;

KW disease susceptibility; cardiovascular system; endocrine system;

KW neurological system; forensic testing; paternity testing; ss.

KW

OS Homo sapiens.

XX

PN WO200058519-A2.

XX

PD 05-OCT-2000.

XX

PF 30-MAR-2000; 2000WO-US008440.

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PR 31-MAR-1999; 99US-0127248P.

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Qy 3144 TCCAGAGTGCTTGATCAACA 3163
 ||||| ||||| ||||| |||||
 Db 1 TCCAGAGTGCTTGATCAACA 20

RESULT 217
 AAC70918/c

ID AAC70918 standard; DNA; 21 BP.

XX

AC AAC70918;

XX

DT 09-FEB-2001 (first entry)

XX

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XX Human gene single nucleotide polymorphism #2042.
DE
XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
XX polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation Replace(11,C)
FT /*tag= a
FT /standard_name="single nucleotide polymorphism"
XX
PN WO200118250-A2.
XX
PD 15-MAR-2001.
XX
XX 07-SEP-2000; 2000WO-US024503.
PF
XX 10-SEP-1999; 99US-0153357P.
PR 26-JUL-2000; 2000US-0220947P.
PR 16-AUG-2000; 2000US-0225724P.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (MILL-) MILLENNIUM PHARM INC.
XX
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JU;
PI WPI; 2001-226749/23.
DR
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis.
XX
XX Example; Page 186; 242pp; English.
XX
XX The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPs shown in the specification
XX
SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1120 TCAGAAAGCAGTCTGCCATC 1139
Db 2 TCATGAAGAGTCTGCCATC 21
/// ||| ||||| |||||
RESULTS 218
AAS22011/c
ID AAS22011 standard; DNA; 21 BP.
XX
XX AAS22011;
AC
XX 24-OCT-2001 (first entry)
DT
XX Human COL1A1 PCR primer for Exon 13 #1.
DE
XX Human; collagen; COL1A1; COL1A2; COL9A1; COL9A2; COL9A3; ss;
KW

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KW osteoporosis; multiple epiphyseal dysplasia; osteogenesis imperfecta;
XX shortness of stature; low bone density; gene therapy; PCR primer.
XX
OS Homo sapiens.
XX
XX US265157-B1.
PN
XX 24-JUL-2001.
PD
XX
XX 03-OCT-1997; 97US-00943731.
PF
XX 03-DEC-1991; 91US-00803628.
PR 13-MAR-1994; 94US-00212322.
XX
XX (UYAL-) UNIV ALLEGHENY HEALTH SCI.
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX (UYOU-) UNIV OULU.
XX
XX Prockop DJ, Spotila LD, Deltas CD, Sereda L;
PI Westerhausen Larson A, Pack M, Collige A, Early J, Koerkhoe J;
PI Ala-Kokko L, Annunen S, Pihlajamaa T, Vuoristo M, Paasilta P;
XX
XX WPI; 2001-432201/46.
DR
XX Detecting collagen gene alteration, useful for diagnosing osteoporosis,
XX multiple epiphyseal dysplasia, osteogenesis imperfecta, shortness of
XX stature and low bone density in humans.
XX
XX Example 4; Fig 21; 617pp; English.
XX
XX The invention relates to Detecting a collagen gene alteration associated
CC with a pathological condition in a human subject by obtaining from the
CC subject a sample nucleic acid containing a portion of at least 15
CC consecutive nucleotides of the segment of the COL1A1 gene extending in
CC the 5' to 3' direction from 78 nucleotides of intron 27 located adjacent
CC exon 28 through the 3' end of intron 51, where the portion contains an
CC intronic nucleotide and a first and second site, determining the sequence
CC of the portion and comparing the sequence of the portion with the
CC corresponding consensus sequence of the COL1A1 gene where a difference
CC between the sequence of the portion and the consensus sequence indicates
CC the presence of the collagen alteration in the subject. The method is
CC used for detecting abnormalities in a COL1 or COL9 gene is useful for
CC determining whether a subject is afflicted with pathological conditions
CC associated with an altered collagen gene such as osteoporosis, multiple
CC epiphyseal dysplasia, osteogenesis imperfecta, shortness of stature and
CC low bone density. Identification of an abnormality in a collagen gene is
CC also useful for designing a therapeutic nucleotide or gene therapy agent
CC which can be administered to the subject to correct or alleviate the
CC abnormality. The method is useful for detecting mutations in both the
CC coding and non-coding sequences of any of the COL1 or COL9 genes.
CC Therefore the method can be used to detect collagen gene alterations
CC which affect either the primary sequence of a collagen protein chain,
CC splicing of the mRNA encoding such chains or regulation of expression of
CC the genes encoding such chains. The present sequence is a PCR primer
CC which amplifies a nucleic acid from a collagen gene of the invention
XX
XX Sequence 21 BP; 6 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2501 GATGTTTCAGACCTCCCTTTTA 2520
Db 21 GATGTTTCAGACACGCTCTTA 2
/// ||||| ||||| |||||
RESULTS 219
AAL4630/c
ID AAL4630 standard; DNA; 21 BP.
XX
XX AAL4630;
AC
XX

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DT 05-AUG-2002 (first entry)
DE H influenzae BASB201 coding sequence PCR primer NTNLPD1014.
KW BASB201; otitis media; pneumonia; sinusitis; nosocomial infection;
KW auditory nerve damage; delayed speech learning; vaccine; antibacterial;
KW auditory; antiinflammatory; PCR; primer; ss.
OS Haemophilus influenzae.
XX WO200230967-A2.
XX 18-APR-2002.
XX 05-OCT-2001; 2001WO-EP011561.
XX 13-OCT-2000; 2000GB-00025169.
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX Thonnard J;
XX WPI; 2002-426267/45.
XX New isolated non-typeable Haemophilus influenzae BASB201 polypeptides,
XX useful as components of vaccines for treating bacterial infection such as
XX otitis media, delayed speech learning and inflammation of middle ear.
XX Example 1; Page 60; 90pp; English.
XX The present invention provides the protein and coding sequences of
XX several versions of the BASB201 protein from non-typeable Haemophilus
XX influenzae. These can be used in the production of vaccines against H.
XX influenzae infection, which can cause otitis media in infants and
XX children, pneumonia in elders, sinusitis, nosocomial infections, or
XX invasive diseases, chronic otitis media with hearing loss, fluid
XX accumulation in the middle ear, auditive nerve damage, delayed speech
XX learning, infections of the upper respiratory tract and inflammation of
XX the middle ear. The present sequence is a PCR primer used to isolate a
XX version of the BASB201 coding sequence of the invention
XX SQ Sequence 21 BP; 3 A; 3 C; 5 G; 10 T; 0 U; 0 Other;
Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1680 AACGAGCACTTCTCAGCA 1699
Db |||||||
21 AACAGCACTTCGTCAGAA 2
RESULT 220
ABL51497/C
ID ABL51497 standard; DNA; 21 BP.
XX ABL51497;
XX 01-JUL-2002 (first entry)
XX Human mitochondrial DNA polymorphism analysis PCR primer C 15983.
DE Human; mitochondrial DNA; mtDNA; polymorphism; geographic origin;
XX ethnic origin; medicine; evolutionary biology; PCR primer; ss.
KW Homo sapiens.
OS WO200222873-A1.
XX 21-MAR-2002.
XX 01-AUG-2001; 2001WO-SE001691.
XX

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PR 15-SEP-2000; 2000SE-00003286.
XX (GYLL/) GYLLENSTEN U.
PA (INGM/) INGMAN M.
PA (ALLE/) ALLEN M.
XX (ANDR/) ANDREASSON H.
PI Gyllensten U, Ingman M, Allen M, Andreasson H;
XX WPI; 2002-362359/39.
XX Determining origin and identity of humans, useful e.g. for evolutionary
XX studies, by analysis of polymorphisms in the complete mitochondrial
XX genome.
XX Claim 7; Page 20; 38pp; English.
XX The present invention describes a method for determining the origin or
XX identity of a human by: (i) determining polymorphic sites in the complete
XX mitochondrial genome; and (ii) relating the results to mitochondrial
XX sequence data of known origin. Also described is a kit for the process
XX comprising a system for analysing all informative sites in the
XX mitochondrial genome. The method is used for determining the geographical
XX and ethnic origins of humans, also in medicine (identification of disease
XX -related mutations) and evolutionary biology (e.g. estimation of mutation
XX rates). Analysis of the entire mitochondrial genome provides more
XX accurate results than (as previously) analysis of the D-loop only,
XX particularly it defines clear haplotypes whereas the D-loop shows a
XX jumbled arrangement of polymorphic sites. The present sequence represents
XX a PCR primer used in the analysis of mitochondrial DNA (mtDNA)
XX polymorphisms in the present invention
XX SQ Sequence 21 BP; 5 A; 4 C; 5 G; 7 T; 0 U; 0 Other;
Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 568 TTTAGACTACATCAGGAGGC 587
Db |||||||
21 TTTATACACAGGACAGGC 2
RESULT 221
AAL54433
ID AAL54433 standard; DNA; 21 BP.
XX AAL54433;
XX 03-APR-2003 (first entry)
XX Candidate HPV16 E6 siRNA sequence #3.
DE Virucide; cytostatic; anti-HIV; dermatological; small interfering RNA;
XX selective post-translational silencing; siRNA; oncogene; genital wart;
XX human papilloma virus; HPV gene; cancer; human cervical cancer; HIV;
XX smallpox; flu; common cold; cervical cancer; penile cancer;
XX malignant squamous cell carcinoma; verruca vulgaris; gene therapy;
XX DNA/RNA; ss.
XX Human papilloma virus.
XX Key Location/Qualifiers
XX misc_feature 20..21
XX /*tag= a
XX /note= "Two thymine nucleotides in the RNA sequence"
XX WO2003008573-A2.
XX 30-JAN-2003.
XX 17-JUL-2002; 2002WO-GB003300.
XX

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PR 17-JUL-2001; 2001GB-00017358.
PR 14-JAN-2002; 2002GB-00000688.
PR 17-JUN-2002; 2002GB-00013855.
XX (MILN/) MILNER A J.
PA
XX
XX
PI Milner AJ;
DR
XX
XX WPI; 2003-221850/21.
XX
XX selective post-transcriptional silencing of an exogenous viral gene (e.g.
PT human papilloma virus (HPV) E6), for treating e.g. cancer, comprises
PT using a small interfering RNA (siRNA) construct homologous to an mRNA of
PT the gene.
XX
XX
PS Disclosure; Fig 1B; 44pp; English.
XX
XX The invention relates to a novel method for selective post-translational
CC silencing in a mammalian cell of the expression of an exogenous gene of
CC viral origin. The method comprises introducing into the cell a small
CC interfering RNA (siRNA) construct that is homologous to a part of the
CC mRNA sequence of the gene. The method is useful for the selective post-
CC transcriptional silencing of an exogenous gene of viral origin (e.g. an
CC oncogene or human papilloma virus (HPV) gene) in a mammalian cell. The
CC method or the siRNA is particularly useful for treating cancer, human
CC cervical cancer, human immunodeficiency virus (HIV), smallpox, flu,
CC common cold, or a disease caused by a HPV (e.g. genital warts, cervical
CC cancer, penile cancer, malignant squamous cell carcinomas or verruca
CC vulgaris). An siRNA construct or vector is useful for use as a medicament
CC for the diseases mentioned. The polynucleotide sequence of the invention
CC can be used to treat disorders by gene therapy. This polynucleotide
CC sequence represents a candidate HPV16 E6 siRNA sequence of the invention
XX
XX
SQ Sequence 21 BP; 4 A; 2 C; 5 G; 2 T; 8 U; 0 Other;
Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3119 AGGTAGAGGACATTCGCTTTT 3138
DB 2 AGGUAUAGCAUUGCUUUTT 21
||||| ||| ||| ||| |||
RESULT 222
ADE87529
ID ADE87529 standard; DNA; 21 BP.
XX
XX
AC ADE87529;
XX
XX 29-JAN-2004 (first entry)
DT
XX
XX Bovine lactate dehydrogenase gene primer #26.
DE
XX
XX lactic acid; lactate dehydrogenase; ethanol; pyruvic acid;
XX pyruvate decarboxylase; bovine; codon optimisation; yeast; ss; primer.
XX
XX Bos taurus.
OS
XX
XX WO2003076630-A1.
PN
XX
XX 18-SEP-2003.
PD
XX
XX 11-MAR-2003; 2003WO-JP002833.
PR
XX
XX 11-MAR-2002; 2002JP-00065880.
PR
XX (TOYT ) TOYOTA JIDOSHA KK.
PA
XX Saito S, Sactome O, Yasutani N, Matsuo Y, Ishida N, Hirai M;
PI Imaeda T, Miyazaki C, Tokuhiko K;
XX
XX WPI; 2003-713140/67.
DR

XX
XX
XX Method for producing lactic acid comprises culturing a transformant
PT carrying DNA encoding a foreign protein which has a lactate dehydrogenase
PT activity, in a culture bed containing glucose while controlling the
PT production of ethanol.
XX
XX
PS Disclosure; SEQ ID NO 30; 76pp; Japanese.
XX
XX The invention relates to a method of producing lactic acid comprising
CC utilizing a transformant carrying DNA encoding a foreign protein which
CC has a lactate dehydrogenase activity while controlling production of
CC ethanol. The transformant also exhibits an affinity for a pyruvic acid
CC substrate which is comparable to or even exceeds the affinity for a
CC pyruvic acid substrate of the intrinsic pyruvate decarboxylase in the
CC host. The foreign protein is a lactate dehydrogenase originating from
CC cows, or its homologue. The method is for use for mass production of
CC lactic acids. This sequence represents a PCR primer used to amplify a
CC bovine lactate dehydrogenase gene which is codon optimised for expression
CC in yeast cells.
XX
XX
SQ Sequence 21 BP; 8 A; 3 C; 3 G; 7 T; 0 U; 0 Other;
Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2077 AAAAAATCAGATGATTCCTTT 2096
DB 1 AAAAAATCTGCTGATCTTT 20
||||| ||| ||| ||| |||
RESULT 223
AAF49043/C
ID AAF49043 standard; DNA; 15 BP.
XX
XX
XX AAF49043;
XX
XX 30-MAR-2001 (first entry)
DT
XX
XX IGF-I oligonucleotide #3.
DE
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX Growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200078341-A1.
PN
XX
XX 28-DEC-2000.
PD
XX
XX 21-JUN-2000; 2000WO-AU000693.
PR
XX
XX 21-JUN-1999; 99US-0140345P.
PR
XX (MURD-) MURDOCH CHILDRENS RES INST.
PA
XX
XX Wraight CJ, Werther GA, Edmondson SR;
PI
XX
XX WPI; 2001-041421/05.
DR
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
XX Example 8; Page 60; 201pp; English.
PS
XX

```

CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAP45151 and AAP45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, seborrheoa, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX Sequence 15 BP; 1 A; 0 C; 2 G; 12 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3391 CTCACAAAAAARAAA 3405

Db 15 CTCACAAAAAARAAA 1

RESULT 224

ABT36291/C
 ID ABT36291 standard; DNA; 17 BP.

XX AC ABT36291;

XX DT 12-JUN-2003 (first entry)

XX DE Tumour suppression related human fukutin oligo SEQ ID No 1928.

XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.

XX OS Homo sapiens.

XX PN WO2003025175-A2.

XX PD 27-MAR-2003.

XX PF 17-SEP-2002; 2002WO-IB004208.

XX PR 17-SEP-2001; 2001FR-00011978.

XX PA (MOLE-) MOLECULAR ENGINES LAB.

XX PI Telerman A, Amson R, Tuijnder M;

XX DR WPI; 2003-313353/30.

XX PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.

XX PS Disclosure; Page 258; 720pp; French.

XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15 consecutive
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 CC hybridizes to them under highly stringent conditions, or the complement
 CC of any of them, or the corresponding RNA. The novel isolated nucleic
 CC acids of the invention are useful as probes and primers for detecting,
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 CC component of a gene chip, in vitro as (anti)sense reagents, and for

CC production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention

XX Sequence 17 BP; 3 A; 5 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2845 GTTCGAAACACAGGAT 2859

Db 16 GTTCGAAACACAGGAT 2

RESULT 225

ADB04274/C
 ID ADB04274 standard; DNA; 17 BP.

XX AC ADB04274;

XX DT 20-NOV-2003 (first entry)

XX DE Human MDZ7 scanning oligonucleotide SEQ ID 5260.

XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.

XX OS Homo sapiens.

XX PN EP1281758-A2.

XX PD 05-FEB-2003.

XX PF 30-JUL-2002; 2002EP-00016874.

XX PR 02-AUG-2001; 2001US-00922181.

XX PA (ABOM-) AEOMICA INC.

XX PI Shannon M, Gu Y, Nguyen C;

XX DR WPI; 2003-423107/40.

XX PT New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MDZ3,
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.

XX PS Example 8; SEQ ID NO 5260; 103pp; English.

XX CC The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
 CC encoded on chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder,
 CC associated with decreased or increased expression or activity of MDZ3,
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic

CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 1 A; 0 C; 2 G; 14 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3391 CTCAAAAAATAAAA 3405
DB 17 CTCAAAAAATAAAA 3

RESULT 226
ADB04276/c
ID ADB04276 standard; DNA; 17 BP.
XX AC ADB04276;
XX DT 20-NOV-2003 (first entry)
XX DE Human MDZ7 scanning oligonucleotide SEQ ID 5262.
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
XX KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX KW developmental disorder; ss.
XX OS Homo sapiens.
XX PN EP1281758-A2.
XX PD 05-FEB-2003.
XX PF 30-JUL-2002; 2002EP-00016874.
XX PR 02-AUG-2001; 2001US-00922181.
XX PA (AEOM-) AEOMICA INC.
XX PI Shannon M, Gu Y, Nguyen C;
XX PI WPI; 2003-423107/40.
XX PT New zinc finger-containing proteins and nucleic acids, useful in
XX PT manufacturing a medicament for treating or preventing a disorder
XX PT associated with decreased or increased expression or activity of MDZ3,
XX PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX PS Example 8; SEQ ID NO 5262; 103pp; English.

CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 2 A; 1 C; 2 G; 12 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3391 CTCAAAAAATAAAA 3405
DB 15 CTCAAAAAATAAAA 1

RESULT 227
ADB04275/c
ID ADB04275 standard; DNA; 17 BP.
XX AC ADB04275;
XX DT 20-NOV-2003 (first entry)
XX DE Human MDZ7 scanning oligonucleotide SEQ ID 5261.
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
XX KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX KW developmental disorder; ss.
XX OS Homo sapiens.
XX PN EP1281758-A2.
XX PD 05-FEB-2003.
XX PF 30-JUL-2002; 2002EP-00016874.
XX PR 02-AUG-2001; 2001US-00922181.
XX PA (AEOM-) AEOMICA INC.
XX PI Shannon M, Gu Y, Nguyen C;
XX PI WPI; 2003-423107/40.
XX PT New zinc finger-containing proteins and nucleic acids, useful in
XX PT manufacturing a medicament for treating or preventing a disorder
XX PT associated with decreased or increased expression or activity of MDZ3,
XX PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX PS Example 8; SEQ ID NO 5261; 103pp; English.

CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 2 A; 0 C; 2 G; 13 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3391 CTCAAAAAATAAAA 3405
DB 16 CTCAAAAAATAAAA 2

```
RESULT 228
ADB45229/c
ID ADB45229 standard; DNA; 17 BP.
XX
XX
AC ADB45229;
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX Tumour suppression/reversion associated nucleotide #5552.
DE
XX
XX cytosatic; antiviral; neuroprotective; nontropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
XX Homo sapiens.
OS
XX
XX WO2003040369-A2.
PN
XX
XX 15-MAY-2003.
PD
XX
XX 17-SEP-2002; 2002WO-IB004219.
PF
XX
XX 17-SEP-2001; 2001FR-00011981.
PR
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX
XX Telerman A, Amson R, Tuijnder M;
PI
XX
XX WPI; 2003-441574/41.
DR
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
XX Disclosure; Page 681; 771pp; French.
XX
XX The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and/or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
XX Sequence 17 BP; 4 A; 2 C; 3 G; 8 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2123 AATTGAAACCAAGA 2137
Db 17 AATTGAAACCAAGA 3
RESULT 229
ABQ84610/c
ID ABQ84610 standard; DNA; 18 BP.
```

```
XX
AC ABQ84610;
XX
XX 20-FEB-2003 (first entry)
DT
XX
XX DPP10 related PSQ assay oligonucleotide #95.
DE
XX
XX DPP10; dipeptidyl peptidase; prolyl oligopeptidase; enzyme; asthma;
KW antiinflammatory; antiasthmatic; antipruritic; antiarthritic;
KW antineumatic; vaccine; gene therapy; inflammatory disease;
KW inflammatory bowel disease; atopy; rheumatoid arthritis; psoriasis;
KW chromosome 2q14; PCR primer; ss.
XX
XX Synthetic.
OS
XX
XX WO200286113-A2.
PN
XX
XX 31-OCT-2002.
PD
XX
XX 24-APR-2002; 2002WO-GB001887.
PF
XX
XX 24-APR-2001; 2001GB-00010044.
PR
XX
XX 24-APR-2001; 2001GB-00010046.
PR
XX
XX 12-OCT-2001; 2001GB-00024575.
PR
XX
XX 12-OCT-2001; 2001GB-00024594.
XX
XX (ISIS-) ISIS INNOVATIONS LTD.
PA
XX
XX Cookson WOCM, Moffat MF, Allen M, Lench N;
XX
XX WPI; 2003-093132/08.
XX
XX New nucleic acid sequence comprising DPP10 mRNA, useful for the
PT manufacture of a medicament for regulating DPP10 protein expression or
PT for preventing or treating inflammatory disease e.g., inflammatory bowel
PT disease.
XX
XX Disclosure; Page 321; 321pp; English.
XX
XX The present invention describes a new isolated nucleic acid sequence (I)
CC comprising a DPP10 mRNA sequence. DPP10 is a dipeptidyl peptidase (also
CC known as prolyl oligopeptidase). (I) has antiinflammatory, antiasthmatic,
CC antipruritic, antiarthritic and antirheumatic activities, and can be
CC used in vaccines and gene therapy. A composition comprising (I) can be
CC used for the manufacture of a medicament for regulating DPP10 expression
CC or for preventing or treating inflammatory disease e.g., inflammatory
CC bowel disease, asthma, atopy, rheumatoid arthritis or psoriasis. (I) can
CC also be used in an assay for detecting or measuring DPP10 in a sample. A
CC host cell comprising (I) can be used for producing recombinant DPP10 gene
CC products, or in drug screening systems to identify agents for diagnosis
CC or treatment of individuals having or susceptible to inflammatory
CC disease. Human DPP10 is located on chromosome 2, more specifically
CC chromosome 2q14. ABQ84254 to ABQ84612 and ABP55569 to ABP55629 represent
CC sequences used in the exemplification of the present invention
XX
XX Sequence 18 BP; 4 A; 2 C; 5 G; 7 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2488 CCAAAACACTGATGA 2502
Db 18 CCAAAACACTGATGA 4
RESULT 230
ABQ84611/c
ID ABQ84611 standard; DNA; 18 BP.
XX
XX AC ABQ84611;
XX
XX 20-FEB-2003 (first entry)
DT
```

XX DE DPP10 related PSQ assay oligonucleotide #96.

XX KW DPP10; dipeptidyl peptidase; prolololigopeptidase; enzyme; asthma;

XX KW antiinflammatory; antiasthmatic; antipsoriatic; antiarthritic;

XX KW antirheumatic; vaccine; gene therapy; inflammatory disease;

XX KW inflammatory bowel disease; atopy; rheumatoid arthritis; psoriasis;

XX KW chromosome 2q14; PCR primer; ss.

XX OS Synthetic.

XX FN WO200286113-A2.

XX PD 31-OCT-2002.

XX PF 24-APR-2002; 2002WO-GB001887.

XX PR 24-APR-2001; 2001GB-00010044.

XX PR 24-APR-2001; 2001GB-00010046.

XX PR 12-OCT-2001; 2001GB-00024575.

XX PR 12-OCT-2001; 2001GB-00024594.

XX PA (ISIS-) ISIS INNOVATIONS LTD.

XX PI Cookson WOCM, Moffat MF, Allen M, Lench N;

XX WIPI; 2003-093132/08.

XX PT New nucleic acid sequence comprising DPP10 mRNA, useful for the

XX PT manufacture of a medicament for regulating DPP10 protein expression or

XX PT for preventing or treating inflammatory disease e.g., inflammatory bowel

XX PT disease.

XX PS Disclosure; Page 321; 321pp; English.

XX CC The present invention describes a new isolated nucleic acid sequence (I)

XX CC comprising a DPP10 mRNA sequence. DPP10 is a dipeptidyl peptidase (also

XX CC known as prolololigopeptidase). (I) has antiinflammatory, antiasthmatic,

XX CC antipsoriatic, antiarthritic and antirheumatic activities, and can be

XX CC used in vaccines and gene therapy. A composition comprising (I) can be

XX CC used for the manufacture of a medicament for regulating DPP10 expression

XX CC or for preventing or treating inflammatory disease e.g., inflammatory

XX CC bowel disease, asthma, atopy, rheumatoid arthritis or psoriasis. (I) can

XX CC also be used in an assay for detecting or measuring DPP10 in a sample. A

XX CC host cell comprising (I) can be used for producing recombinant DPP10 gene

XX CC products, or in drug screening systems to identify agents for diagnosis

XX CC or treatment of individuals having or susceptible to inflammatory

XX CC disease. Human DPP10 is located on chromosome 2, more specifically

XX CC chromosome 2q14. ABQ84254 to ABQ84612 and ABP55569 to ABP55629 represent

XX CC sequences used in the exemplification of the present invention

XX CC

XX CC Sequence 18 BP; 4 A; 2 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2488 CCAAAACACTGATCA 2502

DB 18 CCAAAACACTGATCA 4

RESULT 231

AAAB2895/c

ID AAA82895 standard; DNA; 19 BP.

AC AAA82895;

XX 04-DEC-2000 (first entry)

DT cdk4 ribozyme binding site #76.

DE Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.

KW

XX OS Mammalia.

XX PN WO200032765-A2.

XX PD 08-JUN-2000.

XX PF 06-DEC-1999; 99WO-US028772.

XX PR 04-DEC-1998; 98US-0110954P.

XX PA (IMMU-) IMMUSOL INC.

XX PI Tritz R, Welch PJ, Barber JR, Robbins JM;

XX WIPI; 2000-412314/35.

XX DR New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves

XX PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,

XX PT PCNA and Cyclin B1.

XX PS Disclosure; Page 53; 109pp; English.

XX CC The present invention relates to a hairpin or hammerhead ribozyme,

XX CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase

XX CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.

XX CC Representative examples of ribozyme recognition sites are given in

XX CC AAA82415 to AAA86787. The ribozyme of the invention is useful for

XX CC inhibiting restenosis by introduction of the ribozyme into cells. The

XX CC ribozyme is resistant to endonuclease activity and hence is efficient in

XX CC restenosis treatment

XX CC

XX CC Sequence 19 BP; 2 A; 2 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2281 GATACAGCCCAACT 2295

DB 19 GATACAGCCCAACT 5

RESULT 232

AAH58057/c

ID AAH58057 standard; DNA; 19 BP.

XX AAH58057;

XX 10-SEP-2001 (first entry)

DT Cell-cycle dependent kinase cdk4 ribozyme binding site SEQ ID NO:481.

XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;

XX recognition site; target; ribozyme binding site; eye disease; vulnery;

XX proliferative disease; skin disease; psoriasis; diabetic retinopathy;

XX cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;

XX matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;

XX antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;

XX atopic dermatitis; actinic keratosis; gene therapy; viral wart;

XX basal cell carcinoma; seborrhic wart; vitreoretinopathy; scar;

XX sickle cell retinopathy; ss.

XX OS Homo sapiens.

OS Synthetic.

XX PN WO200130362-A2.

XX PD 03-MAY-2001.

XX PF 26-OCT-2000; 2000WO-US029500.

XX


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SQ Sequence 20 BP; 7 A; 8 C; 2 G; 3 T; 0 U; 0 Other;
  Query Match      0.4%; Score 15; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 2.2e+02;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 3166 TCCTGTGACACACAA 3180
  Db 1 TCCTGTGACACACAA 15

RESULT 235
AAD00252
ID AAD00252 standard; DNA; 20 BP.
XX
AC AAD00252;
XX
DT 09-AUG-2000 (first entry)
XX
DE Nested gene-specific primer DHRD.91.s4, to amplify human pNEU60 cDNA.
XX
XX pNEU60; neuronal-specific 7 transmembrane protein; human; therapy; AMD;
KW age-related macular degeneration; ophthalmological; screening; diagnosis;
KW mutation carrier; prenatal screening; gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200024888-A1.
XX
PD 04-MAY-2000.
XX
PF 20-OCT-1999; 99WO-EP007969.
XX
PR 26-OCT-1998; 98EP-00120231.
XX
PA (MULT-) MULTIGENE BIOTECH GMBH.
XX
PI Weber BHF, Sauer C;
XX
DR WPI; 2000-350730/30.
XX
PT Neuronal-specific 7 transmembrane protein used for diagnosis and
PT treatment of patients with macular degeneration.
XX
PS Disclosure; Fig 5; 37pp; English.
XX
XX The present DNA sequence is the nested gene-specific primer DHRD.91.s4,
CC used for amplification of human neuronal-specific 7 transmembrane cDNA,
CC pNEU60. The major site of pNEU60 expression is the sensory neuroretina.
CC Mutations of this gene is associated with the etiology of age-related
CC macular degeneration (AMD). This sequence has ophthalmological activity.
CC The pNEU60 polypeptides and polynucleotides are used for screening,
CC diagnosis and therapy of macular degeneration. The DNA sequences are
CC useful for detection of pNEU60 mutation carriers, prenatal pNEU60
CC screening and diagnosis of AMD, and in gene therapy
XX
SQ Sequence 20 BP; 11 A; 2 C; 6 G; 1 T; 0 U; 0 Other;
  Query Match      0.4%; Score 15; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 2.2e+02;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1388 CAAGAAGACAATGAA 1402
  Db 5 CAAGAAGACAATGAA 19

RESULT 236
AAC73763/c
ID AAC73763 standard; DNA; 20 BP.
XX
AC AAC73763;
XX

SQ Sequence 20 BP; 2 A; 6 C; 6 G; 6 T; 0 U; 0 Other;
  Query Match      0.4%; Score 15; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 2.2e+02;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1005 CCTGGGATGCACAGA 1019
  Db 15 CCTGGGATGCACAGA 1

RESULT 237
AAF24525
ID AAF24525 standard; DNA; 20 BP.
XX
AC AAF24525;
XX
DT 20-APR-2001 (first entry)
XX
DE Primer used to amplify human Barx2 gene mutations.
XX
XX Barx2; ras-responsive transcription factor; ovarian cancer;
KW tumour suppressor gene; cancer; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200077252-A1.
XX
PD 21-DEC-2000.
XX
PF 15-JUN-2000; 2000WO-GB002328.
XX
PR 15-JUN-1999; 99US-0139320P.

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DT 02-FEB-2001 (first entry)
XX
DE Mouse IL-5 receptor-alpha antisense oligonucleotide ISIS #17658.
XX
KW Mouse; interleukin-5; IL-5; signal transduction;
KW antisense oligonucleotide; antiasthmatic; immunosuppressive; cytostatic;
KW IL-5 receptor-alpha; asthma; eosinophilic syndrome; infection;
KW inflammation; cancer; ss.
XX
OS Mus musculus.
OS Synthetic.
XX
PN WO200058512-A1.
XX
PD 05-OCT-2000.
XX
PF 17-MAR-2000; 2000WO-US007318.
XX
PR 26-MAR-1999; 99US-00280799.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dean NM, Karras JG, McKay R;
XX
DR WPI; 2000-594648/56.
XX
PT Antisense oligonucleotide compound used to treat asthma and eosinophilic
PT syndrome in humans modulates interleukin-5 signal transduction.
XX
PS Example 23; Page 71; 156pp; English.
XX
XX The present sequence is an oligonucleotide used for antisense modulation
CC of interleukin-5 (IL-5) signal transduction. Oligonucleotides were
CC designed to target nucleic acids encoding IL-5 and IL-5 receptor-alpha.
CC The antisense oligonucleotides may be used for the treatment of diseases
CC associated with IL-5 signal transduction, IL-5 expression or IL-5
CC receptor-alpha expression. Such diseases include asthma and eosinophilic
CC syndrome. The oligonucleotides are also useful for research uses and to
CC prevent or delay infection, inflammation or tumour formation
XX
SQ Sequence 20 BP; 2 A; 6 C; 6 G; 6 T; 0 U; 0 Other;
  Query Match      0.4%; Score 15; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 2.2e+02;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1005 CCTGGGATGCACAGA 1019
  Db 15 CCTGGGATGCACAGA 1

RESULT 237
AAF24525
ID AAF24525 standard; DNA; 20 BP.
XX
AC AAF24525;
XX
DT 20-APR-2001 (first entry)
XX
DE Primer used to amplify human Barx2 gene mutations.
XX
XX Barx2; ras-responsive transcription factor; ovarian cancer;
KW tumour suppressor gene; cancer; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200077252-A1.
XX
PD 21-DEC-2000.
XX
PF 15-JUN-2000; 2000WO-GB002328.
XX
PR 15-JUN-1999; 99US-0139320P.

```

```

PR 08-MAR-2000; 2000GB-00005466.
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
PA (UJJO ) UNIV JOHNS HOPKINS.
XX
PI Nelkin BD, Gabra H, Sellar GC, Watson JEV, Porteous DJ;
XX
XX WPI; 2001-061876/07.
XX
XX Diagnosing cancer, or susceptibility to it, in a patient comprising
PT obtaining a nucleic acid containing sample and contacting it with a
PT nucleic acid which selectively hybridizes to the Barx2 gene.
XX
XX Example 7; Page 116; 191pp; English.
XX
XX The present PCR primer was used to amplify mutations of the human Barx2
CC gene. Barx2 is a ras-responsive transcription factor. The Barx2 gene is
CC mutated in ovarian cancer, and the 5' end of the Barx2 transcript is not
CC expressed in several ovarian cancer cell lines. It is believed that the
CC Barx2 gene is involved in ovarian cancer as a tumour suppressor gene. The
CC specification describes a method for diagnosing cancer (or susceptibility
CC to it) in a patient. The method comprises contacting a nucleic acid
CC sample with an oligonucleotide which selectively hybridises to the Barx2
CC gene (or mutant allele) or Barx2 cDNA. The methods are useful for
CC diagnosing, determining susceptibility to, and treating cancer
XX
XX Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 15; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.2e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 2914 AGGACAGTGCTGGG 2928
DB 1 AGGACAGTGCTGGG 15
|||||
XX
RESULT 238
AAC82915/c
ID AAC82915 standard; DNA; 20 BP.
XX
AC AAC82915;
XX
XX 21-MAR-2001 (first entry)
XX
XX Human beta-actin derived oligonucleotide #8.
XX
XX Recognition system; screening; identification; pharmaceutical; toxin;
KW Plant protection agent; toxin; venom; carcinogen; venom; teratogen;
KW herbicide; fungicide; pesticide; beta-actin; human; ss.
XX
XX Homo sapiens.
XX
XX DE19923966-A1.
XX
XX 30-NOV-2000.
XX
XX 25-MAY-1999; 99DE-01023966.
XX
XX 25-MAY-1999; 99DE-01023966.
XX
XX (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
XX Boekenkamp D, Hoppe H, Burgstaller P;
XX
XX WPI; 2001-050938/07.
XX
XX Recognition system, e.g. for identifying nucleic acids, comprises at
PT least one recognition unit comprising a region with a defined structure
PT adjacent to a region with a randomized structure.
XX
XX Example; Fig 1; 8pp; German.
XX
XX

```

```

CC This invention describes a novel recognition system comprising at least 1
CC recognition unit bound to a support, each recognition unit comprising a
CC region A with a defined structure adjacent to a region B with a
CC randomized structure. The recognition system is useful for screening,
CC identifying, or characterizing at least 1 component of a sample,
CC especially nucleic acids and/or proteins, and for screening for and/or
CC identifying cellular or synthetic binding partners, preferably proteins,
CC peptides, nucleic acids, chemical agents, preferably organic compounds,
CC pharmaceuticals, plant protection agents, toxins, venoms, carcinogens,
CC teratogens, herbicides, fungicides or pesticides
XX
XX Sequence 20 BP; 1 A; 0 C; 4 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 15; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.2e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 3391 CTCAAAAA 3405
DB 16 CTCAAAAA 2
|||||
XX
RESULT 239
ABZ89872
ID ABZ89872 standard; DNA; 20 BP.
XX
AC ABZ89872;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 5114; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC

```


CC IL-5 expression or IL-5 receptor a expression, where the disease or
 CC condition include eosinophilic syndrome or asthma. An antisense compound
 CC which alters splicing of an RNA encoding IL-5 receptor a is also useful
 CC for treating a mammal having a disease or condition. The present sequence
 CC is an antisense oligonucleotide targeting mouse IL-5 receptor
 XX

SQ Sequence 20 BP; 2 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1005 CCTGGGATGCACAGA 1019
 |||||
 DB 15 CCTGGGATGCACAGA 1

RESULT 242

AAQ75626/c

ID AAQ75626 standard; DNA; 21 BP.

AC AAQ75626;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;

OS aggregate; restriction enzyme; ss.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

PS WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 by digestion with restriction enzymes.

PS Disclosure; Page 6; lipp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3391 CTCAAAAA 3405
 |||||
 DB 20 CTCAAAAA 6

RESULT 243

AAQ75624/c

ID AAQ75624 standard; DNA; 21 BP.

XX

AC AAQ75624;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;

OS aggregate; restriction enzyme; ss.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

PS WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 by digestion with restriction enzymes.

PS Disclosure; Page 6; lipp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

SQ Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3391 CTCAAAAA 3405
 |||||
 DB 20 CTCAAAAA 6

RESULT 244

AAQ75623/c

ID AAQ75623 standard; DNA; 21 BP.

AC AAQ75623;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;

OS aggregate; restriction enzyme; ss.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX

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DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 6; lipp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ/5547-Q/5798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3391 CTCAAAAAATAAAAA 3405
DB 20 CTCAAAAAATAAAAA 6
|||||
|||||
RESULT 245
AC88899/C
ID ACA88899 standard; DNA; 21 BP.
XX
XX ACA88899;
XX
XX 08-JUL-2003 (first entry)
XX
XX Selection and amplification of genetic markers PCR related primer #10.
XX
XX Genetic marker selection; multiplex PCR amplification;
XX prenatal diagnostic testing; foetal sex determination;
XX genetic identification; DNA profiling; DNA fingerprinting;
XX forensic analysis; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX WO2003031646-A1.
XX
XX 17-APR-2003.
XX
XX 14-OCT-2002; 2002WO-AU001388.
XX
XX 12-OCT-2001; 2001AU-00008234.
XX
XX 12-OCT-2001; 2001AU-00008235.
XX
XX (UYQU ) UNIV QUEENSLAND.
XX
XX Findlay I, Matthews PL, Mulcahy BK;
XX
XX WPI; 2003-381725/36.
XX
XX Selecting genetic markers as targets for nucleic acid sequence
PT amplification, useful for improving genetic testing, e.g. fetal sex
PT determination, comprises selecting each of the genetic markers according
PT to a heterozygosity index.
XX
XX Claim 36; Page 39; 64pp; English.
XX
XX The invention describes a method of selecting genetic markers as targets
CC for nucleic acid sequence amplification comprising selecting each of the
CC genetic markers according to a heterozygosity index of 0.5 or greater.
CC Selecting and amplification of genetic markers are useful as targets for
CC nucleic acid sequence amplification, for genetic testing or facilitating
CC multiplex PCR amplification from limiting amounts of target nucleic acid.
CC The methods are also useful for improving genetic diagnostic and
CC
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CC screening methods, such as prenatal diagnostic testing, foetal sex
CC determination or genetic identification, e.g. DNA profiling or DNA
CC fingerprinting. The nucleic acid sequence amplification is also useful in
CC forensic analysis of degraded, old, ancient and difficult samples that
CC are difficult to amplify and identify. This sequence represents a PCR
CC primer used in the selection and amplification of genetic markers
XX
XX Sequence 21 BP; 7 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3321 TGTATTGCTCACAG 3335
DB 20 TGTATTGCTCACAG 6
|||||
|||||
RESULT 246
AAQ30236
ID AAQ30236 standard; DNA; 18 BP.
XX
XX AAQ30236;
XX
XX 25-MAR-2003 (revised)
XX 07-DEC-1992 (first entry)
XX
XX Oligomer HIV18 for forming triplex with HIV target duplex.
XX
XX Human immunodeficiency virus; AIDS; modified; HIV; hepatitis; herpes;
XX hepatitis; malignancy; inflammation; ss.
XX
XX Synthetic.
XX
XX Key
FH modified_base 1 Location/Qualifiers
FT /*tag= a
FT /mod_base= OTHER
FT /*note= "OTHER= N4 N4 ethanocytosine"
FT modified_base 2
FT /*tag= b
FT /mod_base= m5C
FT modified_base 7
FT /*tag= c
FT /mod_base= OTHER
FT /*note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT modified_base 8
FT /*tag= d
FT /mod_base= m5C
FT modified_base 11
FT /*tag= e
FT /mod_base= OTHER
FT /*note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT modified_base 12
FT /*tag= f
FT /mod_base= m5C
FT modified_base 13
FT /*tag= g
FT /mod_base= OTHER
FT /*note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT misc_feature 15..16
FT /*tag= j
FT /*note= "o-xyloso dimer synthon linkage"
FT misc_feature 16..18
FT /*tag= i
FT /*label= inverted_polarity_region
FT /*note= "see comments"
FT modified_base 18
FT /*tag= h
FT /mod_base= OTHER
FT /*note= "OTHER= N6 methyl-8-oxo-2' deoxyadenine"
XX
XX WO9209705-A1.
PN
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XX PD 11-JUN-1992.
XX PF
XX PR 25-NOV-1991; 91WO-US008811.
XX PR 23-NOV-1990; 90US-00617907.
XX PR 18-JAN-1991; 91US-00643382.
XX PR 08-APR-1991; 91US-00683420.
XX PR 17-APR-1991; 91US-00686544.
XX PR 17-APR-1991; 91US-00686546.
XX PR 17-APR-1991; 91US-00686547.
XX PR 27-SEP-1991; 91US-00766733.
XX PA (GILE-) GILEAD SCI INC.
XX PF
XX PI Froehner B, Krawczyk S, Matteucci MD, Milligan J;
XX PR WPI; 1992-217083/26.
XX PR
XX PT New oligomers contg. modified bases - which form a triplex with G-C
XX PT doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
XX PT herpes malignancy and inflammation.
XX PS Claim 12; Page 65; 77pp; English.
XX CC
XX CC The synthetic oligomer is capable of forming a triplex at physiological
XX CC pH with a purine rich target sequence by coupling into the major groove
XX CC of the duplex. The specific target sequence of this oligomer is an HIV
XX CC target duplex contg. a purine-rich region concentrated on one chain of
XX CC the duplex. The oligomer, and others like it are useful in diagnosis and
XX CC therapy of diseases characterised by specific DNA duplex targets, e.g.
XX CC HIV, hepatitis, herpes, malignant tumours and inflammation. The triple
XX CC helices form under mild conditions thus assays may be carried out without
XX CC subjecting the test specimen to harsh conditions. The oligomer contains
XX CC an inverted polarity region formed from an o-xyloso dimer synthon. The
XX CC linking gp. is o-xyloso (nucleotides have the 3' positions of xylose
XX CC sugars linked via the o-xyline ring). Two nucleotides, in this case T,
XX CC are coupled through a xyline residue to form the dimer synthon. This
XX CC additional modifications may rendering the oligomer stable to nuclease
XX CC activity. The oligomer is able to inhibit gene expression, as verified by
XX CC in vitro systems. See also AAQ25452-25501 and AAQ30226-448. (Updated on
XX CC 25-MAR-2003 to correct PN field.)
XX SQ Sequence 18 BP; 4 A; 4 C; 0 G; 10 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

QY 1454 CCATTCTACTACATGTTA 1471
DB 1 CCTTTTACTTACATTIA 18

RESULT 247
AAX62670
ID AAX62670 standard; RNA; 18 BP.
XX AC AAX62670;
XX DT
XX DT 16-JUL-1999 (first entry)
XX DE Granule bound starch synthase hairpin substrate SEQ ID NO:545.
XX KW Maize; corn; Zea mays; delta-9 desaturase; GBSS; target; substrate;
XX KW granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;
XX KW modulation; gene expression; transgenic plant; cleavage; canola plant;
XX KW caffeine synthesis; coffee plant; nicotine production; tobacco;
XX KW fruit ripening; flower pigmentation; lignin production; ss.
XX OS Zea mays.
XX PN W09710328-A2.

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XX PD 20-MAR-1997.
XX PF
XX PR 12-JUL-1996; 96WO-US011689.
XX PR 13-JUL-1995; 95US-0001135P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (DOWC) DOWELANCO.
XX PI Zwick MG, Edington BE, Mcswiggen JA, Merlo PAO, Guo L, Skokut TA;
XX PI Young SA, Folkerts O, Merlo DJ;
XX PR WPI; 1997-202224/18.
XX PT Ribozyme which modulates plant gene expression - preferably modulates
XX PT expression of DELTA-9 desaturase or granule bound starch synthase in
XX PT maize or canola.
XX PS Claim 42; Page 83; 155pp; English.
XX CC
XX CC The present invention describes an enzymatic nucleic acid molecule (I)
XX CC with RNA cleaving activity, which modulates the expression of a plant
XX CC gene. Also described is a gene comprising a cDNA sequence encoding maize
XX CC Delta-9 desaturase. (I) can be used to modulate expression of a gene,
XX CC preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)
XX CC gene, in a plant (preferably a maize or canola plant). (I) can be used to
XX CC modulate caffeine synthesis in a coffee plant, nicotine production in a
XX CC tobacco plant, fruit ripening processes in an apple, tomato, pear, plum
XX CC or peach plant, flower pigmentation in a rose, petunia, chrysanthemum or
XX CC marigold plant or lignin production in a tobacco, aspen, poplar or pine
XX CC plant
XX SQ Sequence 18 BP; 2 A; 8 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 12; Conservative 4; Mismatches 2;

QY 150 CTGCTCAGTCCACCATTG 167
DB 1 CUGCUCCGUCACCAGUG 18

RESULT 248
AAV36210/C
ID AAV36210 standard; DNA; 18 BP.
XX AC AAV36210;
XX DT
XX DT 03-SEP-1998 (first entry)
XX DE Oligonucleotide used in the course of the invention.
XX KW Detection; diagnosis; 26S rRNA gene; P. carinii specific; infection;
XX KW species identification; PCR primer; probe; ss.
XX OS Synthetic.
XX OS Pneumocystis carinii.
XX PN US5776680-A.
XX PD
XX PD 07-JUL-1998.
XX PF 21-JUL-1995; 95US-00505509.
XX PR 30-JUL-1992; 92US-00922987.
XX PR 31-AUG-1994; 94US-00298087.
XX PA (UYNE-) UNIV NEW JERSEY.
XX PI Liu Y, Leibowitz MJ;
XX PN

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DR WPI; 1998-398016/34.
XX
PT Detection of Pneumocystis carinii - by amplification of nucleic acid from
PT sample with PCR primers specific for the 26S rRNA gene of Pneumocystis
PT carinii.
XX
PS Claim 1; Col 9; 42pp; English.
XX
CC Oligonucleotides AAV36181-210 are used for PCR amplification, sequencing,
CC and detection in the course of the invention. The specification describes
CC a method for the diagnosis of Pneumocystis carinii which comprises
CC detecting the presence of a nucleic acid sequence containing the 26S rRNA
CC gene specific for P. carinii in a sample. The 26S rRNA gene in a sample
CC is amplified, and the primer extension products detected by hybridisation
CC with a labelled oligonucleotide. The methods can be used for the
CC diagnosis of P. carinii infection and for the detection of various
CC species of P. carinii
XX
SQ Sequence 18 BP; 1 A; 4 C; 5 G; 8 T; 0 U; 0 Other;

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. NO. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 429 CAGAGACAGACGACAAAC 446
Db 18 CAGAGCCCAAGAGCTAAC 1

RESULT 249
AAV83002/c
ID AAV83002 standard; DNA; 18 BP.
XX
AC AAV83002;
XX
DT 23-FEB-1999 (first entry)
XX
DE Primer used for amplification and sequencing of P. carinii sequences.
XX
KW PCR amplification; sequencing; assay; inhibitor; nuclear rRNA gene;
KW catalytic Group I self-splicing intron reaction; drug screening;
KW PCR primer; ss.
XX
OS Synthetic.
OS Pneumocystis carinii.
XX
PN US5849484-A.
XX
PD 15-DEC-1998.
XX
PF 19-JUN-1995; 95US-00491690.
XX
PR 30-JUL-1992; 92US-00922987.
PR 27-MAY-1993; 93US-00068248.
XX
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI Liu Y, Leibowitz MJ;
XX
DR WPI; 1999-069716/06.
XX
PT Screening assays for drugs against Pneumocystis carinii - based on
PT inhibition of 26S rRNA gene intron self-splicing.
XX
PS Example 1; Col 13-14; 51pp; English.
XX
CC Primers AAV82973-V83002 represent oligonucleotides used for PCR
CC amplification and sequencing of Pneumocystis carinii nucleic acid
CC sequences. The primers are used in the in vitro method of the invention,
CC which assays for an inhibitor of the catalytic Group I self-splicing
CC intron reaction in the nuclear rRNA genes of P. carinii. The method is
CC useful for screening potential drugs for treating P. carinii infections
CC before more costly animal testing is conducted
XX
XX
SQ Sequence 18 BP; 1 A; 4 C; 5 G; 8 T; 0 U; 0 Other;

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. NO. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 429 CAGAGACAGACGACAAAC 446
Db 18 CAGAGCCCAAGAGCTAAC 1

RESULT 250
AAZ40877
ID AAZ40877 standard; DNA; 18 BP.
XX
AC AAZ40877;
XX
DT 26-JAN-2000 (first entry)
XX
DE Human CD40 phosphorothioate antisense oligonucleotide SEQ ID NO:26.
XX
KW Identification; genetic target; gene modulation; human; probe;
KW antisense oligonucleotide; phosphorothioate; PCR primer;
KW nucleotide sequence-based technology; antisense drug discovery;
KW target validation; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO953101-A1.
XX
PD 21-OCT-1999.
XX
PF 13-APR-1999; 99WO-US008268.
XX
PR 13-APR-1998; 98US-0081483P.
PR 28-APR-1998; 98US-00067638.
XX
PA (ISTS-) ISIS PHARM INC.
XX
PI Cowsett LM, Baker BF, Mcneil J, Freier SM, Sasmor HM, Brooks DG;
PI Ohasi C, Wyatt JR, Borchers AH, Vickers TA;
XX
DR WPI; 1999-620446/53.
XX
PT Identifying compounds which modulate expression of nucleic acids, used to
PT provide compounds having defined physical, chemical or bioactive
PT properties, e.g. antisense activity.
XX
PS Example 8; Page 77; 264pp; English.
XX
CC A method has been developed of defining a set of compounds that modulate
CC the expression of a target nucleic acid (tNA) sequence via binding of the
CC compounds with the tNA sequence. The method comprises generating a
CC library of virtual compounds in silico according to defined criteria, and
CC evaluating in silico the binding of the virtual compounds with the tNA
CC according to defined criteria. Also described are: (1) a method of
CC defining a set of oligonucleotides (ONs) that modulate the expression of
CC a tNA sequence via binding of the ONs with the tNA sequence comprising
CC generating a library of virtual compounds in silico according to defined
CC criteria, and evaluating in silico the binding of the virtual ONs with
CC the tNA according to defined criteria; and (2) a method of defining a set
CC of compounds that modulate the expression of a tNA sequence via binding
CC of the compounds with the tNA. The methods can be used for the generation
CC and identification of synthetic compounds having defined physical,
CC chemical or bioactive properties. Information gathered from assays of
CC such compounds is used to identify nucleic acid sequences that are
CC tractable to a variety of nucleotide sequence-based technologies, e.g.
CC antisense drug discovery and target validation. AAZ40852 to AAZ41220, and
CC AAY52701 to AAY52706, represent sequences used in the exemplification of
CC the present invention
XX

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SQ Sequence 18 BP; 2 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1608 CTCGTGTCATGTTCTA 1625
| | | | | | | | | | | | | | | | | |
Db 1 CTCGTGTCAGTGCTA 18

RESULT 251

AAZ57877/c

ID AAZ57877 standard; DNA; 18 BP.

XX AC AAZ57877;

XX DT 15-JUL-1999 (first entry)

DE PCR primer used in construction of yeast artificial chromosome.
XX YAC; yeast artificial chromosome; PCR primer; sexual dysfunction;
KW reporter gene; transgenic mammal; therapy; circadian function;
KW sleep disorder; eating disorder; premenstrual syndrome; birth defect;
KW autoimmune disorder; ss.

XX OS Synthetic.

XX PN GB2331752-A.

XX PD 02-JUN-1999.

XX PF 27-NOV-1998; 98GB-00026126.

XX PR 28-NOV-1997; 97GB-00025311.

XX PR 28-NOV-1997; 97GB-00025313.

XX PR 20-MAR-1998; 98GB-00006072.

XX PR 05-NOV-1998; 98GB-00024275.

XX PA (MEDI-) MEDICAL RES COUNCIL.

XX PI Shen S, Schedl A, Harmar AJ;

XX WPI; 1999-290603/25.

XX PT New reporter gene labeled YAC vectors and transgenic mammals used for
PT screening potential active agents.
XX PS Disclosure; Page 56; 98pp; English.
XX CC This sequence represents a PCR primer used in the construction of a yeast
CC artificial chromosome of the invention. The yeast artificial chromosome
CC (YAC) vectors contain a reporter gene and transgenic mammals produced
CC using them may be used to screen for an agent affecting nucleotide
CC expression and gives easier monitoring of in vivo expression. The vector
CC is used in the production of transgenic mammals for testing potential
CC pharmaceutical or veterinary agents. pYAM4 is used to amplify YAC. The
CC assay may be used to screen for agents useful in treatment of disturbance
CC of circadian function, sleep disorders, eating disorders, premenstrual
CC syndrome, autoimmune disorders, birth defects in women and/or sexual
CC dysfunction. The agents thus detected may be used for treatment of
CC disorders related to the expression pattern of a nucleotide such as those
CC above. The vectors have more concentrated YAC DNA, which allows better
CC and more reliable gene transfer. The presence of a reporter gene allows
CC easy monitoring of in vivo expression and the vectors allow for gene
CC overexpression (3-5 fold) and easy site determination. The pYAM4
CC amplification vector does not contain the thymidine kinase gene, which
CC causes male infertility in transgenic mice

XX SQ Sequence 18 BP; 8 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

SQ Sequence 18 BP; 8 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match

Best Local Similarity 88.9%; Score 14.8; DB 1; Length 18;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 236 CTGCTCTCTGGATTAT 253
| | | | | | | | | | | | | | | | | |
Db 18 CTGCTCTCTGGATTAT 1

RESULT 252

AAZ20256/c

ID AAZ20256 standard; DNA; 18 BP.

XX AC AAZ20256;

XX DT 17-JAN-2000 (first entry)

XX DE Bacillus cereus enterotoxin HBL gene PCR primer hbla-R.

XX HBL; hbla gene; enterotoxin; toxin; haemolysin BL; biocontrol;

XX biological control; plant pathogen; PCR; primer; ss.

XX OS Synthetic.

XX OS Bacillus cereus.

XX PN WO9951733-A2.

XX PD 14-OCT-1999.

XX PF 07-APR-1999; 99WO-US007649.

XX PR 07-APR-1998; 98US-0080943P.

XX PA (WISC) WISCONSIN ALUMNI RES FOUND.

XX PI Handelsman J, Klimowicz AK;

XX WPI; 1999-611040/52.

XX PT New mutant Bacillus useful as a biocontrol agent for biological control

XX of plant pathogens.

XX PS Example 1; Page 13; 45pp; English.

XX CC This primer, denoted hbla-R, was used with primer hbla-F (see AAZ20255)

CC in the PCR amplification of a 1022 bp internal fragment of the coding

CC region of the Bacillus cereus haemolysin BL (HBL) gene (hbla), using

CC genomic DNA as template. The PCR product was used as a probe in Southern

CC hybridization analysis. The invention relates to new B. cereus mutants

CC that do not produce active HBL owing to the introduction of a mutation

CC that inactivates a HBL component. The mutants are useful for biological

CC control of plant pathogens. They have the same biocontrol activity as

CC wild-type strains without the concerns for human pathogenicity

XX SQ Sequence 18 BP; 3 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 2e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1543 GAACCGAGACATAGTTGG 1560

| | | | | | | | | | | | | | | | | |

Db 18 GCAGCGAAGATAGTTGG 1

RESULT 253

AAZ47710

ID AAZ47710 standard; DNA; 18 BP.

XX AC AAZ47710;

XX DT 02-MAR-2000 (first entry)

XX DE Human CD40 antisense oligonucleotide SEQ ID NO:26.

XX XX

KW Human; CD40; antisense oligonucleotide; phosphorothioate; modulation;
 KW expression; immune disease; inflammatory disease; immunomodulatory;
 KW anti-inflammatory; anti-arthritis; anti-asthmatic; antiproliferative;
 KW anticancer; immuno-suppressive; anti-psoriatic; allograft rejection;
 KW hyperproliferative disease; autoimmune disease; rheumatoid arthritis;
 KW inflammatory bowel disease; asthma; psoriasis; cancer; tumour; ss.
 OS Synthetic.
 OS Homo sapiens.
 XX WO9957320-A1.
 PN XX
 PD 11-NOV-1999.
 PF 22-APR-1999; 99WO-US008765.
 XX 01-MAY-1998; 98US-00071433.
 XX (ISIS-) ISIS PHARM INC.
 XX Bennett CF, Cowsett LM;
 PI WPI; 2000-062158/05.
 DR Antisense molecules directed against nucleic acid encoding human CD40,
 PT for treating e.g. immune, inflammatory or hyperproliferative diseases.
 XX Claim 3; Page 43; 102pp; English.
 XX AA247685 to AA247768 represent phosphorothioate antisense
 CC oligonucleotides targeted to human CD40, which can be used to inhibit the
 CC expression of human CD40. CD40 is involved in lymphocyte activation.
 CC tumour growth and/or angiogenesis. Inhibition of CD40 is used to treat or
 CC prevent immune-associated diseases (specifically guest vs. host disease,
 CC allograft rejection or autoimmune diseases); inflammation (specifically
 CC asthma, rheumatoid arthritis, allograft rejection, inflammatory bowel
 CC disease or psoriasis) or hyperproliferation (specifically cancer and
 CC tumours). The antisense oligonucleotides are also useful as diagnostic
 CC and research reagents. AA247769 represents the human CD40 nucleotide
 CC sequence. AA247770 to AA247772 represent human CD40 forward and reverse
 CC PCR primers, and a human CD40 PCR probe, respectively. AA247773 to
 CC AA247775 represent other PCR primers and a probe used in the
 CC exemplification of the present invention
 XX Sequence 18 BP; 2 A; 5 C; 4 G; 7 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1608 CTCGTTCACATGTTCTA 1625
 Db 1 CTCGTTCACAGGTGCTA 18
 RESULT 254
 AAA92573/C
 ID AAA92573 standard; DNA; 18 BP.
 XX AC
 XX AAA92573;
 XX 04-JAN-2001 (first entry)
 DT Antisense oligonucleotide ISIS# 30283.
 DE Human; SRA; steroid receptor RNA activator; cytostatic; antiinflammatory;
 KW SRA inhibitor; cancer; infection; antisense oligonucleotide; ss.
 XX Synthetic.
 OS US6107092-A.
 PN 22-AUG-2000.
 PD New antisense compounds targeting nucleic acids encoding human Akt-3

XX 29-MAR-1999; 99US-00280409.
 XX 29-MAR-1999; 99US-00280409.
 PR (ISIS-) ISIS PHARM INC.
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX Cowsett LM, Bennett CF, O'malley BW;
 PI WPI; 2000-586211/55.
 DR Antisense compounds targeted to steroid receptor RNA activator useful for
 PT diagnosis, prophylaxis and treatment of diseases associated with the
 PT steroid activator, such as infection, inflammation or tumor formation.
 XX Claim 3; Col 41; 47pp; English.
 XX The present sequence is one of a large number of antisense
 CC oligonucleotides which is directed against one of four human steroid
 CC receptor RNA activator (SRA) nucleic acid sequences. Two series of
 CC antisense oligonucleotides were synthesised. The first series comprised 8
 CC -30 oligodeoxynucleotides with a phosphorothioate backbone. The second
 CC series comprised chimeric oligonucleotides composed of a central gap
 CC region, consisting of ten 2'-deoxynucleotides, which was flanked on both
 CC sides by four-nucleotide wings. The wings were composed of 2'-
 CC methoxyethyl (2'-MOE) nucleotides. Both series contained the same
 CC nucleotide sequences. The antisense compounds are useful for research,
 CC diagnosis, treatment and prophylaxis to prevent or delay infection,
 CC inflammation or tumour formation. Therapeutically the oligonucleotides
 CC are highly safe and are effectively administered to humans
 XX Sequence 18 BP; 3 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1334 TCTGCAGCCACACCTTAAG 1351
 Db 18 TCTGCAGCCACACCTGAG 1
 RESULT 255
 AAF79637/C
 ID AAF79637 standard; DNA; 18 BP.
 XX AC
 XX AAF79637;
 XX 29-MAY-2001 (first entry)
 DT Human Akt-3 antisense oligonucleotide, SEQ ID NO: 45.
 DE Human; Akt-3; protein kinase; cytostatic; antiinflammatory; infection;
 KW antisense therapy; inflammation; tumour; ss.
 XX Homo sapiens.
 OS US6187586-B1.
 XX 13-FEB-2001.
 PD 29-DEC-1999; 99US-00474922.
 PF 29-DEC-1999; 99US-00474922.
 XX (ISIS-) ISIS PHARM INC.
 PA Monia BP, Cowsett LM, Roth RA;
 PI WPI; 2001-264979/27.
 DR New antisense compounds targeting nucleic acids encoding human Akt-3
 XX

PT useful for treating a disease or condition associated with Akt-3
 PT expression, or in preventing or delaying inflammation or tumor formation.
 XX
 PS Example 15; Col 39; 37pp; English.

XX The present sequence is one of a number of antisense compounds of up to
 CC 30 nucleobases in length targeted to a nucleic acid encoding human Akt-3.
 CC The antisense compounds are useful for inhibiting the expression of human
 CC Akt-3 in human cells or tissues. They are also useful for modulating the
 CC expression of Akt-3, and for treating a human or an animal suspected of
 CC having, or being prone to, a disease or condition associated with Akt-3
 CC expression. The antisense compounds may also be used as research
 CC reagents, in kits and in diagnostics, e.g. to elucidate the function of a
 CC particular gene or to distinguish between functions of various members of
 CC a biological pathway; and as a prophylactic, e.g. to prevent or delay
 CC infection, inflammation or tumour formation

XX Sequence 18 BP; 1 A; 7 C; 1 G; 9 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2e+02; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 2;

Qy 2423 GCAGAGAGTGGAGAAAT 2440
 Db 18 GCAGAGAGGAGAGAAAT 1

RESULT 256

AAH19624
 ID AAH19624 standard; DNA; 18 BP.

AC AAH19624;

DT 31-JUL-2001 (first entry)

XX Complementary oligo of sequence containing a mixture of CAG/CAA codons.
 XX
 KW Polyglutamine region; polypeptide aggregation; aggregation disruption;
 KW Huntington's disease; Alzheimer's disease; Parkinson's disease;
 KW spinocerebellar ataxia; multiple myeloma; amyloidosis; anticonvulsant;
 KW spongiform encephalopathy; neuroprotective; neurotropic; antiparkinsonian;
 KW ss.

OS Synthetic.

PN WO200123412-A2.

XX 05-APR-2001.

XX 27-SEP-2000; 2000WO-US041008.

XX 27-SEP-1999; 99US-00405048.

XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX Housman DE, Preisinger EA, Kazantsev AG;

XX WPI; 2001-300097/31.

XX Screening for agents which disrupt aggregation of polypeptides for
 PT treating aggregation-associated disorders e.g. Alzheimer's disease, by
 PT using aggregation-disposed polypeptides or cell expressing the
 PT polypeptides.

PS Example 1; Page 25; 42pp; English.

XX The present sequence was used to generate a polypeptide with extended
 CC polyglutamine regions. This was performed in an example illustrating a
 CC method for identifying a compound which disrupts polypeptide aggregation.
 CC The method is carried out using a cell which has been genetically
 CC modified to express aggregation-disposed polypeptides, or using purified
 CC aggregation-disposed polypeptides. The compounds identified by this

CC method are useful for treating disorders associated with such polypeptide
 CC aggregation, including Huntington's disease, Alzheimer's disease,
 CC Parkinson's disease, spinocerebellar ataxia, multiple myeloma,
 CC amyloidosis, and spongiform encephalopathies like Creutzfeldt-Jakob
 CC disease and kuru in humans. The present sequence was annealed to its
 CC complement to generate double stranded duplex DNA with trinucleotide
 CC extensions

XX Sequence 18 BP; 0 A; 3 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 2e+02; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 2;

Qy 135 TTGTGCTGTAACGCTG 152

Db 1 TTGTGCTGTTGCTG 18

RESULT 257

AAC85250/C

ID AAC85250 standard; DNA; 18 BP.

AC AAC85250;

XX 22-MAR-2001 (first entry)

XX Reverse primer L 53534 for determining size of YAC insert.

XX Internal ribosomal entry site; IRES; yeast artificial chromosome; YAC;
 KW vector; centromere; telomere; origin of replication; transgenic;
 KW circadian function; sleep disorder; eating disorder;
 KW premenstrual syndrome; autoimmune disease; birth defect;
 KW sexual dysfunction; serotonin transporter; VIP2 receptor; SERT; VIPR2;
 KW polymerase chain reaction; PCR; primer; amplify; YAC 35D8/D6;
 KW YAC HSC7E526/V12; ss.

OS Synthetic.

PN GB2350613-A.

XX 06-DEC-2000.

XX 17-AUG-2000; 2000GB-00020335.

XX 28-NOV-1997; 97GB-00025311.

XX 28-NOV-1997; 97GB-00025313.

XX 20-MAR-1998; 98GB-00006072.

XX 05-NOV-1998; 98GB-00024275.

XX 27-NOV-1998; 98GB-00026126.

XX (MEDI-) MEDICAL RES COUNCIL.

XX Shen S, Schedl A, Harmar AJ;

XX WPI; 2001-034098/05.

XX Transgenic organism for identifying potential therapeutic agents able to
 PT modulate gene expression, comprises a yeast artificial chromosome vector.

XX Example; Page 54; 93pp; English.

XX The sequences given in AAC85227-50 are primers which were used to
 CC determine the size of the integrated YAC 35D8/D6 and YAC HSC7E526/V12
 CC constructs in a transgenic founder animal. The constructs were prepared
 CC from novel yeast artificial chromosome (YAC) vectors each of which
 CC comprises a centromere, two telomeres, at least one origin of
 CC replication, an internal ribosomal entry site (IRES), and a selection
 CC gene that is specifically removable from the vector. The resulting YAC
 CC are used to produce transgenic organisms for use in screening for agents
 CC that can affect the expression pattern of a nucleotide sequence of
 CC interest (NOI) or the activity of its expression product. The identified
 CC agents are potentially useful as pharmaceutical and veterinary agents for

CC treating disorders of circadian function; sleep or eating disorders;
 CC premenstrual syndrome; autoimmune diseases; birth defects in women and/or
 CC sexual dysfunction, and also as lead compounds for developing agents with
 CC other activities. YAC can also be used for expression, regulation and/or
 CC functional studies on NOI, in combination with other NOI, compounds or
 CC compositions. The new vectors provide high YAC copy numbers and allow
 CC easy monitoring (in vivo) of the expression pattern of NOI;
 CC (over)expression of NOI and a reporter gene; and determination of the
 CC sites where NOI is expressed. Incorporation of IRES allows expression of
 CC at least two nucleic acid sequences (e.g. NOI plus a reporter of more
 CC than one NOI)
 XX
 SQ Sequence 18 BP; 8 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
 Matches 16; Conservative 0; Indels 2; Indels 0; Gaps 0;
 QY 236 CTTGCTTCTTGGAAATAT 253
 ||||| ||||| |||||
 Db 18 CTTGCTTCTTGGAAATAT 1

RESULT 258
 ABK11199
 ID ABK11199 standard; DNA; 18 BP.
 XX
 AC ABK11199;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Oligonucleotide #2 used to generate DNA with trinucleotide extensions.
 XX
 KW Inhibition of protein-protein interaction; Alzheimer's disease;
 KW polyglutamine-containing transcription factor; hexamerisation of p53;
 KW homodimerisation of Jun; expanded trinucleotide repeat; CAG repeat;
 KW Huntington's disease; HD; primate and bulbar muscular atrophy; SBMA;
 KW dentatorubral-pallidoluysian atrophy; spinocerebellar ataxia type 1;
 KW spinocerebellar ataxia type 2; spinocerebellar ataxia type 6;
 KW spinocerebellar ataxia type 7; Machado-Joseph disease; MJD/SCA3;
 KW neurotropic; anticonvulsant; cerebroprotective; neuroprotective; ss.

OS Synthetic.
 XX
 XX WO200216644-A1.
 XX
 XX 28-FEB-2002.
 XX
 XX 20-AUG-2001; 2001WO-US026097.
 XX
 XX 18-AUG-2000; 2000US-0226502P.
 XX
 XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
 PA
 PI Kazantsev A, Thompson L, Housman DE;
 XX
 XX WPI; 2002-280948/32.
 DR
 XX
 XX Novel agent for inhibiting protein-protein interaction useful to treat
 PT Alzheimer's disease, has two domains which bind first, second proteins
 PT with seven consecutive glutamine residues and a domain separating two
 PT domains.
 XX

PS Disclosure; Page 8; 40pp; English.
 XX
 CC The present invention relates to therapeutic agents comprising a first
 CC domain (D1) that binds a protein having at least seven consecutive
 CC glutamine (Glu) residues, a second domain (D2) that binds another protein
 CC having at least 7 consecutive Glu residues, and a third domain (D3) that
 CC separates D1 from D2. The therapeutic agents of the invention are useful
 CC for inhibiting protein-protein interactions (e.g. aggregation,
 CC dimerisation or other physiologically significant association), and can
 CC be used for treating Alzheimer's disease, and disorders in which

CC polyglutamine-containing transcription factors or coactivators are
 CC desirably active (e.g. disorders associated with homodimerisation of Jun
 CC or hexamerisation of p53. The therapeutic agents can also be used to
 CC treat various disorders, including those associated with expanded
 CC trinucleotide (CAG) repeats. For example such disorders can include
 CC Huntington's disease (HD), primate and bulbar muscular atrophy (SBMA),
 CC dentatorubral-pallidoluysian atrophy, spinocerebellar ataxia type 1, type
 CC 2, type 6 or type 7, or Machado-Joseph disease (MJD/SCA3). The present
 CC sequence represents an oligonucleotide used to generate double stranded
 CC DNA with trinucleotide extensions
 XX
 SQ Sequence 18 BP; 0 A; 3 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
 Matches 16; Conservative 0; Indels 2; Indels 0; Gaps 0;
 QY 135 TTGTTGCTGTAACCTGCTG 152
 ||||| ||||| |||||
 Db 1 TTGTTGCTGTTGCTGCTG 18

RESULT 259
 ADC07721
 ID ADC07721 standard; DNA; 18 BP.
 XX
 AC ADC07721;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Enterobacteria phage M13 packaging gene PCR primer Seq ID1.
 XX
 KW bacterial strain; packaging function; filamentous bacteriophage;
 KW phage display expression vector; infectious filamentous phage particle;
 KW helper phage; capsid cylinder; filamentous phage; Pf phage; M13; fl; fd;
 KW filamentous peptide; filamentous phage; PCR; primer; ss;
 XX M13 packaging gene.
 XX
 OS Enterobacteria phage M13.
 XX
 XX US2003104604-A1.
 XX
 XX 05-JUN-2003.
 XX
 XX 02-AUG-2002; 2002US-00211296.
 XX
 XX 03-AUG-2001; 2001US-0310171P.
 XX
 XX (YANG/) YANG W.
 XX (SOME/) SOMERVILLE R.
 XX
 XX Yang W, Somerville R;
 XX
 XX WPI; 2003-708726/67.
 DR
 XX
 XX New bacterial strain comprising one or more genes that encodes a
 PT packaging function of a filamentous bacteriophage, useful for displaying
 PT filamentous peptides on filamentous phage.
 XX
 XX Example 4; SEQ ID NO 1; 30pp; English.
 XX
 CC This invention relates to a novel bacterial strain comprising one or more
 CC genes that encodes a packaging function of a filamentous bacteriophage
 CC where the one or more genes can, together with at least one other gene
 CC that resides on a phage display expression vector, produce and package
 CC the phage display expression vector in an infectious filamentous phage
 CC particle in the absence of a helper phage. Filamentous phage are
 CC characterised by having a single-stranded DNA genome that is encased by a
 CC long capsid cylinder. The invention preferably uses genes from
 CC filamentous phage (Pf phage) that infect Escherichia coli, including M13,
 CC fl and fd. The bacterial strain is useful for displaying filamentous
 CC peptides on filamentous phage, particularly for generating recombinant
 CC filamentous phage without the use of a helper phage. The present sequence

CC is that of a PCR primer which was used for the amplification of
 CC bacteriophage M13 packaging genes in the exemplification of the
 CC invention.

XX Sequence 18 BP; 3 A; 2 C; 3 G; 10 T; 0 U; 0 Other;

SQ Query Match 0.4%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2323 CATATGCTGATGTTT 2340

|||||

1 CATATGCTGTTATTT 18

RESULT 260

AAV10722/c

ID AAV10722 standard; DNA; 19 BP.

XX AC AAV10722;

XX 21-JUL-1998 (first entry)

XX Human breast cancer gene CH8-2a13-1 primer pch8-1fa.

DE Breast cancer; malignant transformation; diagnostic; therapeutic;
 XX screening; primer; ss.

XX Synthetic.

XX Homo sapiens.

XX WO9738085-A2.

XX 16-OCT-1997.

XX 09-APR-1997; 97WO-US005930.

XX 10-APR-1996; 96US-0015167P.

XX 05-JUN-1996; 96WO-US009286.

XX 06-JUN-1996; 96US-0019202P.

XX 11-JUL-1996; 96US-00678280.

XX (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.

XX Smith H, Chen L;

XX WPI; 1997-512705/47.

XX Breast cancer genes - used to develop products to design or screen
 XX diagnostic reagents or therapeutic compounds.

XX Disclosure; Fig 10; 118pp; English.

XX AAV10720-V10747 are primers used in a method to identify the novel human
 XX breast cancer gene CH8-2a13-1 by differential display. The identified
 XX genes or fragments of these genes can be used for identifying genes and
 XX gene products that are intimately related to malignant transformation or
 XX maintenance of the malignant properties of cancer cells. It can also be
 XX used to design or screen diagnostic reagents or therapeutic compounds.
 XX Kits are included within the scope of the invention

XX Sequence 19 BP; 5 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

XX Query Match 0.4%; Score 14.8; DB 1; Length 19;

XX Best Local Similarity 88.9%; Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;

XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2790 GTCTCAGGCTGTTTCAG 2807

|||||

19 GTCTCTCAGGCTGTTTCAG 2

Db

RESULT 261

AAV10742

ID AAV10742 standard; DNA; 19 BP.

XX AC AAV10742;

XX 21-JUL-1998 (first entry)

XX Human breast cancer gene CH8-2a13-1 primer pch8-1fb.

XX Breast cancer; malignant transformation; diagnostic; therapeutic;
 XX screening; primer; ss.

XX Synthetic.

XX Homo sapiens.

XX WO9738085-A2.

XX 16-OCT-1997.

XX 09-APR-1997; 97WO-US005930.

XX 10-APR-1996; 96US-0015167P.

XX 05-JUN-1996; 96WO-US009286.

XX 06-JUN-1996; 96US-0019202P.

XX 11-JUL-1996; 96US-00678280.

XX (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.

XX Smith H, Chen L;

XX WPI; 1997-512705/47.

XX Breast cancer genes - used to develop products to design or screen
 XX diagnostic reagents or therapeutic compounds.

XX Disclosure; Fig 10; 118pp; English.

XX AAV10720-V10747 are primers used in a method to identify the novel human
 XX breast cancer gene CH8-2a13-1 by differential display. The identified
 XX genes or fragments of these genes can be used for identifying genes and
 XX gene products that are intimately related to malignant transformation or
 XX maintenance of the malignant properties of cancer cells. It can also be
 XX used to design or screen diagnostic reagents or therapeutic compounds.
 XX Kits are included within the scope of the invention

XX Sequence 19 BP; 4 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

XX Query Match 0.4%; Score 14.8; DB 1; Length 19;

XX Best Local Similarity 88.9%; Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;

XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2790 GTCTCAGGCTGTTTCAG 2807

|||||

1 GTCTCTCAGGCTGTTTCAG 18

Db

RESULT 262

AAV51387

ID AAV51387 standard; DNA; 19 BP.

XX AC AAV51387;

XX 27-OCT-1998 (first entry)

XX Human TIGR PCR primer SK6A.

XX TIGR; trabecular meshwork induced glucocorticoid response protein; human;
 XX diagnosis; glaucoma; polymorphism; steroid sensitivity; PCR primer; ss.

XX Synthetic.

XX Homo sapiens.

XX WO9832850-A1.

XX

XX PD 30-JUL-1998.
 XX XX
 XX PF 09-JAN-1998; 98WO-US000468.
 XX XX
 XX PR 28-JAN-1997; 97US-00791154.
 XX PR 26-SEP-1997; 97US-00938669.
 XX XX
 XX PA (REGC) UNIV CALIFORNIA.
 XX XX
 XX PI Nguyen TD, Polansky JR, Chen P, Chen H;
 XX XX
 XX DR WPI; 1998-427946/36.
 XX XX
 XX PT Use of TIGR nucleic acid sequences - used for, e.g. developing products
 XX PT for diagnosis, prognosis and treatment of glaucoma.
 XX XX
 XX PS Claim 9; Page 9; 105pp; English.
 XX XX
 CC AAV51371-V51390 are PCR primers used in the amplification of a novel
 CC human trabecular meshwork induced glucocorticoid response protein (TIGR)
 CC promoter region which is used in a method for diagnosing glaucoma in a
 CC patient. The method involves the detection of polymorphisms whose
 CC presence is predictive of a mutation affecting TIGR response in the
 CC patient and can be diagnostic of glaucoma or steroid sensitivity. Base
 CC substitutions and base additions upstream of and within TIGR exons can
 CC also be used to diagnose glaucoma
 XX XX
 SQ Sequence 19 BP; 2 A; 9 C; 2 G; 6 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 QY 124 CCTTCTCAGCCTGTGTC 141
 DB 1 CCTTCTCAGCCTGTGTCAC 18
 XX
 RESULT 263
 AAA82506/c
 ID AAA82506 standard; DNA; 19 BP.
 XX
 AC AAA82506;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE cdk1 ribozyme binding site #92.
 XX
 KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
 XX
 OS Mammalia.
 XX
 PN WO200032765-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 06-DEC-1999; 99WO-US028772.
 XX
 PR 04-DEC-1998; 98US-0110954P.
 XX
 PA (IMMU-) IMMUSOL INC.
 XX
 PI Tritz R, Welch PJ, Barber JR, Robbins JM;
 XX
 DR WPI; 2000-412314/35.
 XX
 PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1.
 XX
 PS Disclosure; Page 47; 109pp; English.
 XX

CC The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells. The
 CC ribozyme is resistant to endonuclease activity and hence is efficient in
 CC restenosis treatment
 XX
 SQ Sequence 19 BP; 2 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3347 TGCTGAGCACAAGCAGA 3364
 DB 19 TGCTGAGCACAAGCAGA 2
 XX
 RESULT 264
 AAA57505
 ID AAA57505 standard; DNA; 19 BP.
 XX
 AC AAA57505;
 XX
 DT 20-OCT-2000 (first entry)
 XX
 DE Primer used for SSCP screening of the human TIGR gene.
 XX
 KW TIGR; trabecular meshwork inducible glucocorticoid receptor; promoter;
 KW glaucoma; steroid sensitivity; progressive ocular hypertension;
 KW vision loss; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200042220-A1.
 XX
 PD 20-JUL-2000.
 XX
 PF 11-JAN-2000; 2000WO-US000559.
 XX
 PR 11-JAN-1999; 99US-00227881.
 PR 07-MAY-1999; 99US-00306828.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Nguyen TD, Polansky JR, Chen P, Chen H;
 XX
 DR WPI; 2000-491060/43.
 XX
 PT Diagnosis, prognosis and treatment of glaucoma, based on detecting
 PT specific polymorphisms in the promoter of the trabecular meshwork
 PT inducible glucocorticoid receptor gene.
 XX
 PS Claim 9; Page 53; 122pp; English.
 XX
 CC Primers AAA57489-A57508 were used for single strand conformational
 CC polymorphism (SSCP) screening of the human TIGR (trabecular meshwork
 CC inducible glucocorticoid receptor) gene. The primers correspond to
 CC sequences found within the TIGR promoter and two of the exons of TIGR,
 CC and are used in the method of the invention. The specification describes
 CC a method for the diagnosis, prognosis and treatment of glaucoma, based on
 CC detecting specific polymorphisms in the promoter of the TIGR gene. The
 CC method is used for diagnosis and prognosis of glaucoma (of all types),
 CC steroid sensitivity and progressive ocular hypertension that leads to
 CC loss of vision. Glaucoma can be treated by administering an agent that
 CC binds to cis-acting elements within the TIGR promoter. The TIGR promoter
 CC (or other regulatory regions) can be used to express homologous or
 CC heterologous genes, particularly for tissue-specific expression of
 CC therapeutic transgenes for treating glaucoma, also to generate transgenic
 CC animals and in screening for compounds (specific modulators) with
 CC diagnostic or therapeutic potential. Fragments of the TIGR sequence can

CC be used as amplification primers or probes, e.g. for isolating related
 CC sequences in non-human animals
 XX
 SQ Sequence 19 BP; 2 A; 9 C; 2 G; 6 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 124 CCTTCTCAGCCTTGTTGC 141
 |||||
 Db 1 CCTTCTCAGCCTTGTTAC 18
 RESULT 265
 AAH57668/C
 ID AAH57668 standard; DNA; 19 BP.
 AC AAH57668;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Cell-cycle dependent kinase cdk1 ribozyme binding site SEQ ID NO:92.
 XX
 KW Human, ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnery;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antipapillary; dermatological; antiseborrheic; keratolytic; virucide;
 KW antisticking; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200130362-A2.
 XX
 PD 03-MAY-2001.
 XX
 PF 26-OCT-2000; 2000WO-US029500.
 XX
 PR 26-OCT-1999; 99US-0161532P.
 XX
 PA (IMMU-) IMMUSOL INC.
 XX
 PI Robbins JM, Tritz R;
 XX
 XX WPI; 2001-300427/31.
 XX
 DR Treating proliferative skin or eye diseases and scarring, using ribozymes
 XX that cleave RNA encoding cytokines involved in inflammation, matrix
 PT metalloproteinases, growth factors and cell-cycle dependent kinases.
 PT
 XX Example 1; Page 78; 408pp; English.
 PS
 XX The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antipapillary,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisticking,
 CC ophthalmological, vulnery, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative skin
 CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of

CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 19 BP; 2 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3347 TGCTGAGCACAAAGCAGA 3364
 |||||
 Db 19 TGCTGAGCCAAAGCAGA 2
 RESULT 266
 ABL88879/C
 ID ABL88879 standard; DNA; 19 BP.
 AC ABL88879;
 XX
 DT 22-MAY-2002 (first entry)
 XX
 DE HIV-1 related binding molecule oligonucleotide sequence SEQ ID NO:101.
 XX
 KW Binding molecule; HIV-1; human immunodeficiency virus type 1;
 KW reverse transcriptase; binding group; ss.
 XX
 OS Human immunodeficiency virus 1.
 OS Synthetic.
 XX
 PN EPI174518-A1.
 XX
 PD 23-JAN-2002.
 XX
 PF 20-JUL-2000; 2000EP-00202611.
 XX
 PR 20-JUL-2000; 2000EP-00202611.
 XX
 PA (AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.
 XX
 PI Loukachov VW, Van Gemen B, Goudsmit J;
 XX
 XX WPI; 2002-156696/21.
 XX
 DR Collection of binding groups for determining or typing samples,
 XX especially clinical samples, has groups capable to identify essentially
 PT all members of the family of nucleic acids of relatively high
 PT significance.
 PT
 XX Disclosure; Page 31; 166pp; English.
 PS
 XX The present invention describes a collection of binding groups for a
 CC family of nucleic acids comprising members of relative high and relative
 CC low significance, where the binding groups are selected to be capable to
 CC identify, alone or in combination, essentially all members of the family
 CC of nucleic acids of relatively high significance. The collection of
 CC binding groups is useful for typing of nucleic acid in a clinical sample,
 CC by contacting the nucleic acid with the collection and determining
 CC whether one or more binding groups bound to the nucleic acid of the
 CC sample. This method is useful for determining whether the sample
 CC comprises at least a part of a member of relatively high significance
 CC of a family of nucleic acids. The collection of binding groups is useful for
 CC diagnosing the severity of a disease caused by a pathogen containing a
 CC member of a family of nucleic acids. ABL8879 to ABL89321 represent
 CC oligonucleotide sequences used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 19 BP; 12 A; 2 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;

ID	ABS68532 standard; DNA; 19 BP.
XX	
XX	ABS68532;
XX	
XX	19-NOV-2002 (first entry)
DE	
XX	Clock gene Bmal2 (brain-muscle-Arnt-like protein 2)-related primer #21.
XX	
KW	Human; clock protein BMAL2; brain-muscle-Arnt-like protein 2; insomnia;
KW	sleeping disorder; non-24-hour sleep; sleep-phase forward; primer;
KW	retreat syndrome; time-zone variation syndrome; PCR; ss.
XX	
OS	Unidentified.
XX	
XX	WO200264785-A1.
XX	
XX	22-AUG-2002.
PD	
XX	
XX	23-AUG-2001; 2001WO-JP007197.
PF	
XX	
XX	13-FEB-2001; 2001JP-00035743.
PR	
XX	
XX	(NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA	
XX	
PI	Fukada Y, Okano T;
XX	
XX	WPI; 2002-667007/71.
DR	
XX	
XX	Clock gene Bmal2 and expressed clock protein BMAL2 important in clock
PT	oscillation mechanism and relating to circadian rhythm, used in diagnosis
PT	of and developing drugs for insomnia and other sleeping disorders.
XX	
XX	Example 4; Page 36; 187pp; Japanese.
PS	
XX	
CC	The invention relates to a DNA sequence encoding clock protein BMAL2
CC	(brain-muscle-Arnt-like protein 2). The gene and protein are applicable
CC	in diagnosis of and development of drugs for insomnia and other sleeping
CC	disorders e.g. non-24-hour sleep, sleep-phase forward or retreat syndrome
CC	and time-zone variation syndrome. ABS68501-ABS68552 represent BMAL2
CC	coding sequences and PCR primers of the invention
XX	
XX	Sequence 19 BP; 4 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
SQ	
	Query Match 0.4%; Score 14.8; DB 1; Length 19;
	Best Local Similarity 88.9%; Pred. No. 2.1e+02;
	Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	85 TCTTGGCTCACAGGGAC 102
Db	2 TCTTGGATCACAGGGAC 19
RESULT 269	
ABX79687/c	
ID	ABX79687 standard; cDNA; 19 BP.
XX	
XX	ABX79687;
AC	
XX	
XX	17-APR-2003 (first entry)
DT	
XX	
XX	EST polymorphic DNA repeat polynucleotide #12.
XX	
KW	EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW	polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW	Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW	Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW	Fredreich's ataxia; myotonic dystrophy; hyperandrogenaemia;
KW	spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX	
OS	Homo sapiens.
XX	
XX	US6472154-B1.
PN	
XX	

```

PD 29-OCT-2002.
XX
PF 31-DEC-1999; 99US-00475947.
XX
PR 31-DEC-1999; 99US-00475947.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Garner HR, Wren JD, Minna JD, Fondon JW;
XX
XX WPI; 2003-208818/20.
XX
XX Identifying a candidate polymorphic repeat within a coding sequence, for
XX understanding or treating genetic disease, comprises detecting tandem
XX repeats in a target coding sequence and scoring the repeats for
XX polymorphic probability.
XX
XX Example; Col 175; 588pp; English.
XX
XX The invention discloses a method for identifying a candidate polymorphic
XX repeat within a coding sequence (expressed sequence tag, EST), which
XX comprises detecting tandem repeats in a target coding sequence, scoring
XX the repeats for polymorphic probability and generating a dataset
XX correlating the repeats with polymorphic probability to identify a
XX candidate polymorphic repeat. The computational methods (polymorphic
XX marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
XX useful for identifying and detecting candidate polymorphic repeats in
XX human genes, which can be used to understand, treat or eliminate genetic
XX diseases, predispositions or adverse drug-treatment reactions. Examples
XX of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
XX syndrome, Huntington's disease, fragile-X syndrome, Friedreich's ataxia,
XX myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
XX spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
XX the polymorphic repeats identified for a search of human ESTs
XX
XX Sequence 19 BP; 0 A; 4 C; 0 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 14.8; DB 1; Length 19;
XX Best Local Similarity 88.9%; Pred. No. 2.1e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2412 AGAAAAATAAGCAAGAA 2429
Db 19 AGAAAAAGAAAGAAAGAA 2
XX
RESULT 270
AAQ39509
XX
XX AAQ39509 standard; DNA; 20 BP.
XX
XX AC AAQ39509;
XX
XX 25-MAR-2003 (revised)
XX 20-MAY-1993 (first entry)
XX
XX PCR Primer #1 for mapping EST's to specific chromosome.
XX
XX expressed sequence tag; human genome project; chromosome;
XX human gene sequencing; PCR mapping; somatic cell hybrids;
XX sublocalisation; gene tagging; tissue typing.
XX
XX Synthetic.
XX
XX WO9300353-A1.
XX
XX 07-JAN-1993.
XX
XX 19-JUN-1992; 92WO-US005222.
XX
XX 20-JUN-1991; 91US-00716831.
XX 12-FEB-1992; 92US-00837195.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICE.
XX

Venter JC, Adams MD;
WPI; 1993-036325/04.
Particular expressed sequence tags from human CDNA - corresponds to
transcription prods. of genes, useful for tagging genes, mapping
chromosomes and tissue typing.
Example 3; Page 42; 199pp; English.
This PCR primer was used together with AAQ39510 for the PCR mapping of
somatic cell hybrids. This is a method of assigning an EST (expressed
sequence tag) to a particular chromosome. ESTs are markers for human
genes actually transcribed in vivo. Unlike the random genomic DNA
sequence tagged sites (STSS), ESTs point directly to expressed genes. The
use of ESTs could facilitate the tagging of most expressed human genes
within a few years at a fraction of the cost of complete genomic
sequencing. Using these primers and disclosed methods sublocalisation can
be achieved with panels of fragments from specific chromosomes or pools
of large genomic clones in an analogous manner. This PCR primer sequence
was designed from EST00356 by the computer program INTRON (National
Institutes of Mental Health, Bethesda, MD) to minimise the chance of
amplifying through an intron using the assumptions that: 1) introns are
genomic sequences that interrupt the coding and non-coding sequences of
genes. 2) there are consensus sequences for splice junctions. 3) 90% of
the human genes studied have 3' UTR of mRNA not interrupted by introns in
the genomic DNA. This PCR primer localised EST00356 to chromosome 6.
(Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 20 BP; 3 A; 4 C; 4 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2.3e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3275 CTGTATGTTCCACCTCTG 3292
Db 2 CTGTATGTTAACCTTTG 19
XX
RESULT 271
AAQ58798
XX
XX ID AAQ58798 standard; DNA; 20 BP.
XX
XX AC AAQ58798;
XX
XX 23-NOV-1994 (first entry)
XX
XX Probe specific for 5'-end of oncogene v-myc.
XX
XX DNA hybridisation assay; improvement; detection; sensitivity;
XX oncogene v-myc; oligonucleotide probe; self-hybridisation; inhibition;
XX signal/noise ratio; MC29; avian myelocytomatosis virus 29; ss.
XX
XX Synthetic.
XX
XX JF06070799-A.
XX
XX 15-MAR-1994.
XX
XX 26-AUG-1992; 92JP-00227189.
XX
XX 26-AUG-1992; 92JP-00227189.
XX
XX (TOKE ) TOSHIBA KK.
XX
XX WPI; 1994-128691/16.
XX
XX New hybridisation method between sample nucleic acid and probe - using
XX nucleic acid chain inhibiting self-hybridisation of sample nucleic acid.
XX
XX Example 2; Page 5; 6pp; Japanese.
XX

```

XX Probe A (AAQ58798) is directed to the 5'-side of the v-myc oncogene and
 CC it was used together with a probe to the 3'-side of v-myc. An
 CC oligonucleotide was also added to the hybridisation mixt. which consisted
 CC of a sequence complementary to the sequence of the portion not
 CC complementary to the probes. Self-hybridisation of the target nucleic
 CC acid is inhibited giving an increased signal/noise ratio
 XX Sequence 20 BP; 11 A; 3 C; 5 G; 1 T; 0 U; 0 Other;
 SQ

Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2404 TCGGAGAGAGAAATAA 2421
 Db 3 TCGGAGAGAGAAAGAA 20
 |||||

RESULT 272
 AAQ67125/c
 ID AAQ67125 standard; DNA; 20 BP.
 XX
 AC AAQ67125;
 XX
 XX
 DT 25-MAR-2003 (revised)
 DT 23-MAR-1995 (first entry)
 XX
 XX CD40 ligand gene mutation detection primer #4.
 DE
 XX Probe; primer; PCR; amplify; polymerase chain reaction; detection;
 KW mutation; CD40 ligand gene; Igm; ss.
 KW
 XX Synthetic.
 OS
 XX WO9417196-A1.
 PN
 XX
 PD 04-AUG-1994.
 XX
 XX 21-JAN-1994; 94WO-US000786.
 PF
 XX 22-JAN-1993; 93US-00009258.
 PR
 PR 20-JAN-1994; 94US-00184422.
 XX
 XX (IMV) IMMUNEX CORP.
 PA
 XX Spriggs MK, Armitage RJ, Fanslow WC, Widmer MB, Davison BL;
 PI Renshaw BR;
 PI
 XX WPI; 1994-264109/32.
 DR
 XX Method for detecting mutation in CD 40 ligand gene - comprises
 PT amplification of nucleic acid, and mutational analysis.
 PT
 XX

Example 7; Page 25; 38pp; English.
 The sequences given in AAQ67117-20 are primers which were used in the
 CC method of the invention for the detecting mutation in a CD40 ligand gene.
 CC The method comprises isolating DNA from an individual and selectively
 CC amplifying the isolated DNA derived from the CD40 ligand gene. The
 CC amplification product is then analysed to determine if there is a
 CC mutation present and determining if a protein expressed from the ligand
 CC gene will bind CD40. The detection of mutations in the CD40 ligand gene
 CC allows subsequent treatment of a syndrome resulting in elevated levels of
 CC serum IgM and diminished levels of other Ig isotypes, due to mutation in
 CC the CD40 ligand gene. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 20 BP; 5 A; 2 C; 7 G; 6 T; 0 U; 0 Other;
 SQ

Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 395 CAGGCTCTTCAGAAAAT 412
 Db 19 CAAGCTCTTCAGCAATAT 2
 |||||

RESULT 273
 AAT32537
 ID AAT32537 standard; DNA; 20 BP.
 XX
 AC AAT32537;
 XX
 XX
 DT 02-DEC-1996 (first entry)
 DT
 DE Primer for exon 13 of the calpain large subunit 1 gene.
 XX
 KW Calpain; subunit; calcium; protease; mutation; treatment; detection;
 KW identification; diagnosis; limg girdle muscular dystrophy; LGMD2;
 KW calcium activated neutral protease; CANP; ss.
 KW
 XX Synthetic.
 OS
 XX WO9616175-A2.
 PN
 XX 30-MAY-1996.
 PD
 XX
 XX 21-NOV-1995; 95WO-EP004575.
 PF
 XX 22-NOV-1994; 94EP-00402668.
 PR
 XX (ASPR-) ASSOC FR CONTRE MYOPATHIES.
 PA
 XX Beckmann J, Richard I;
 PI
 XX WPI; 1996-268611/27.
 DR
 XX Human novel Calpain large subunit 1 gene encoding a calcium dependent
 PT protease - used to develop prods. for the diagnosis and treatment of limb
 PT -girdle muscular dystrophy 2 disease.
 PT
 XX Claim 16; Page 14; 66pp; English.
 PS
 XX The calpain large subunit 1 gene located on chromosome 15 codes for a
 CC calcium activated neutral protease (CANP) belonging to the calpain
 CC family. Mutations in the gene induce limb-girdle muscular dystrophy
 CC (LGMD) 2 disease. The gene, and fragments of it, can be used in the
 CC prevention, treatment, diagnosis and detection of a predisposition to
 CC LGMD2 disease. Fifty primers (AAT32510-59) were used to specifically
 CC amplify the exons and splice junctions of the calpain large subunit 1
 CC gene as well as the regions containing the putative CAT, TATA boxes and
 CC the polyadenylation signal. Two primers (AAT32536, AAT32537) were used to
 CC amplify exon 13 of the gene
 XX Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
 SQ

Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3282 TTCACCCCTCTGAAGTGGG 3299
 Db 1 TTCAACCTCTGGAGTGGG 18
 |||||

RESULT 274
 AAT51303/c
 ID AAT51303 standard; DNA; 20 BP.
 XX
 AC AAT51303;
 XX
 XX
 DT 11-NOV-1997 (first entry)
 DT
 DE Human AD4 exon 8 PCR primer INT103L.
 DE
 XX

KW Autosomal dominant early-onset Alzheimer's Disease; AD4 gene; STM2;
 KW neurodegeneration; senile dementia; human chromosome 1;
 KW Volga German kindred; VG; yeast artificial chromosome library;
 KW expressed sequence tag database; polymerase chain reaction; PCR primer;
 KW Homo sapiens; diagnosis; detection; polymorphism; ss.
 XX Synthetic.
 OS
 PN WO9703192-A2.
 PD
 XX
 XX 30-JAN-1997.
 XX
 XX 05-JUL-1996; 96WO-US011386.
 XX
 XX 07-JUL-1995; 95US-0000956P.
 PR
 PR 28-JUL-1995; 95US-0001675P.
 PR
 PR 11-AUG-1995; 95US-0002174P.
 PR
 PR 14-AUG-1995; 95US-0002328P.
 XX
 XX (DARW-) DARWIN MOLECULAR CORP.
 PA (VAME-) VA MEDICAL CENT.
 PA (GEOH) GEN HOSPITAL CORP.
 XX
 XX Levy-Lahad E, Tanzi RE, Schellenberg GD, Wasco W, Bird TD;
 PI Mulligan J, Galas DJ;
 PI
 XX WPI; 1997-119048/11.
 DR
 XX
 XX New Alzheimer's disease related gene, AD4 - used to develop prods. for
 PT detecting pre-disposition to or for diagnosis, prevention or treatment of
 PT Alzheimer's disease.
 PT
 XX Example 8; Page 53; 83pp; English.
 PS
 XX A genetically isolated group of families with autosomal dominant early-onset Alzheimer's disease (AD) has been studied and initial mapping analyses have predicted the AD4 locus (also known as STM2) resides on chromosome 1. The group of families has been designated the Volga German (VG) kindreds. The entire gene has been amplified from VG individuals and unaffected individuals (from VG and unrelated lineages). Sequence analysis has shown that affected individuals have a nucleotide change at codon 141 resulting in an amino acid alteration from Asn to Ile. Portions of a mutant AD4, especially one in which Asn at position 141 has been replaced by Ile, can be used in a peptide vaccine. Detection of mutant AD4, for example using antibodies specific for the protein or using nucleic acid probes specific for the mutant gene, provides a means of diagnosing Alzheimer's disease. In a specific example, ten pairs of primers were designed for PCR amplification of ten fragments carrying the 12 exons of the human AD4 gene to facilitate detection of polymorphisms associated with Alzheimer's Disease. The present sequence represents a primer used for amplifying exon 8
 CC
 XX Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3203 GAACTCCAGAGCATGCC 3220
 Db |||||
 18 GAGCTCTCAGAGCATGCC 1
 RESULT 275
 AAT75184/C
 ID AAT75184 standard; DNA; 20 BP.
 XX
 AC AAT75184;
 XX
 XX 11-FEB-1998 (first entry)
 DT
 XX Mouse CD34 reverse PCR primer.
 DE
 XX

KW Haematopoietin receptor; Hu-Bi.219; mouse; cancer; leukaemia; therapy;
 KW primer; PCR; CD34; ss.
 XX
 OS Synthetic.
 OS Mus musculus.
 XX
 PN WO9727286-A1.
 PD 31-JUL-1997.
 XX
 XX 21-JAN-1997; 97WO-US000767.
 PF
 XX 23-JAN-1996; 96US-00589915.
 PR
 PR 20-MAR-1996; 96US-00618957.
 PR
 PR 13-SEP-1996; 96US-00713296.
 XX
 XX (PROG-) PROGENITOR INC.
 PA
 XX Snodgrass HR, Cioffi J, Zupancic TJ, Shafer AW, Mikhail AA;
 PI Barut BA;
 PI
 XX WPI; 1997-393674/36.
 DR
 XX Using leptin to activate haematopoietic cells - to treat
 PT immunodeficiency, anaemia or myeloid deficiency.
 PT
 XX Example; Page 46; 82pp; English.
 PS
 XX A reverse primer (AAT75184) and a forward primer (AAT85183) were used to amplify mouse CD34 sequences from haematopoietic and endothelial cells. They were used in studies of Hu-Bi.219 (see AAT75172) expression by long-term repopulating haematopoietic progenitor cells. The results showed that Hu-Bi.219 is a marker of a subpopulation of early progenitor cells within the CD34+ fraction and can be used as a marker for their isolation. Hu-Bi.219 expression was also detected in a CD34+ subpopulation, and can be used as a marker to isolate CD34+ stem cells
 CC
 XX Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 595 TTGGGAAAGCTGGGATC 612
 Db |||||
 20 TTGAGAAAGCTGGGATC 3
 RESULT 276
 AAV41074
 ID AAV41074 standard; DNA; 20 BP.
 XX
 AC AAV41074;
 XX
 XX 25-SEP-1998 (first entry)
 DT
 XX Primer MYH11:1377L20 for abnormality detection.
 DE
 XX PCR primer; chromosomal abnormality; abnormality detection; leukaemia; lymphoma; carcinoma; adenocarcinoma; sarcoma; glioma; neuroblastoma; medullablastoma; malignant melanoma; malignant neoplastic condition; ss.
 KW
 KW Synthetic.
 OS
 OS Homo sapiens.
 OS
 XX WO9824928-A2.
 PN
 XX 11-JUN-1998.
 PD
 XX 08-DEC-1997; 97WO-DK000556.
 PF
 XX 06-DEC-1996; 96DK-00001401.
 PR
 XX

PA (PALL/) PALLISGAARD N.
 PI Pallisgaard N, Hokland P;
 XX WPI; 1998-333344/29.
 DR
 XX
 XX
 XX
 PT Detection of chromosomal abnormalities - by subjecting patient sample
 PT nucleic acids to a multiplex molecular amplification procedure using
 PT primers specific for characteristic nucleic acid sequence.
 XX
 XX
 PS Claim 73; Page 108; 126pp; English.
 XX
 XX
 CC This sequence represents a primer used in the method of the invention for
 CC the detection of the presence or absence of chromosomal abnormalities,
 CC each abnormality being associated with a condition in a subject and each
 CC being defined by at least one characteristic nucleic acid sequence. The
 CC method comprises: (a) obtaining a sample of nucleic acids derived from a
 CC subject which may harbour one of the chromosomal abnormalities; (b)
 CC subjecting the sample to a multiplex molecular amplification (MMA)
 CC procedure, where a number of the characteristic sequences, if present in
 CC a sufficient amount, will be amplified; (c) retrieving the product(s)
 CC from step (b), and detecting the presence and/or absence of an amplicon
 CC characteristic of the abnormal sequences to detect the presence or
 CC absence of corresponding chromosomal abnormalities; where the MMA
 CC procedure comprises the use of at least 7 mutually distinct primers (MDP)
 CC in one single reaction mixture, each of the primers defining an end of at
 CC least one characteristic nucleic acid sequence, and where at least one of
 CC the primers defines the first end of at least two characteristic nucleic
 CC acid sequences, the characteristic nucleic acid sequences each being
 CC determined in their opposite ends by MDP selected from the remainder of
 CC the MDP. The methods can be used for detecting chromosomal abnormalities
 CC associated with diseases including numerous leukaemia's, lymphoma's,
 CC carcinoma's, adenocarcinoma's, sarcoma's, glioma's, neuroblastoma's,
 CC medullablastoma, malignant melanoma, and malignant neoplastic conditions
 XX
 XX
 SQ Sequence 20 BP; 1 A; 5 C; 7 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2788 TGGTCTTCACGGCTGTC 2805
 Db 3 TGGTCTTCACGGCTGTC 20
 RESULT 277
 AA240467
 ID AA240467 standard; DNA; 20 BP.
 XX
 AC AA240467;
 XX
 DT 18-FEB-2000 (first entry)
 XX
 DE Primer #1 for external intergene spacer region.
 XX
 XX
 KW PCR; primer; amplification; intergene spacer region; analysis; ITS;
 KW internal transcribed spacer; eukaryote; ribosomal DNA; 18S; 28S; rDNA;
 KW taxonomy; ss.
 XX
 OS Synthetic.
 XX
 PN RU2113481-C1.
 XX
 PD 20-JUN-1998.
 XX
 PF 28-AUG-1996; 96RU-00117336.
 XX
 PR 28-AUG-1996; 96RU-00117336.
 XX
 PA (ASGE=) AS USSR GEN GENETICS INST.
 PA (AUG=) AS UKR AGROBIOLOGY BIOTECHN INST.
 XX

PI Zakharov IA, Mukha DV, Sidorenko AP;
 XX WPI; 1999-618437/53.
 XX
 PT Method of investigation of structural-functional organization of dna of
 PT eucaryotic ribosomal claster.
 XX
 PS Claim; Col 6; 6pp; Russian.
 XX
 CC The invention relates to the use of PCR using the universal primers
 CC AA240465-240466 for an internal intergene spacer region and primers
 CC AA240467-240468 for an external intergene spacer region. The invention
 CC can be used for the amplification and analysis of internal transcribed
 CC and external non-transcribed spacer regions from eukaryotic ribosomal DNA
 CC genes (especially 18S and 28S rDNA genes) from a wide range of taxonomic
 CC groups
 XX
 SQ Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2622 AACTATGACTCTGTCAG 2639
 Db 1 AACTATGACTCTCTTAAAG 18
 RESULT 278
 AA289480
 ID AA289480 standard; DNA; 20 BP.
 XX
 AC AA289480;
 XX
 DT 03-DEC-1999 (first entry)
 XX
 DE Human ptc-2 PCR primer P107.
 XX
 KW Patched-2; ptc-2; human; hedgehog receptor; nootropic; neuroprotective;
 KW antiinflammatory; antiparkinsonian; cardiant; antiarthritic; screening;
 KW modulator; antagonist; agonist; cellular proliferation; neuronal tissue;
 KW testicular tissue; osteogenic tissue; chondrogenic tissue; disease;
 KW graft; transplant; treatment; nervous system injury; chemical injury;
 KW nasal injury; infection; inflammatory; tumor-induced injury; ageing;
 KW Alzheimer's disease; chronic neurodegenerative disease; innervation;
 KW Parkinson's disease; Huntington's chorea; amyotrophic lateral sclerosis;
 KW spinocerebellar degeneration; multiple sclerosis; autonomic disorders;
 KW peripheral nervous system; smooth muscle; endocrine tissue; tachycardia;
 KW atrial cardiac arrhythmia; cell differentiation; chronic pain syndrome;
 KW lesion-induced death; neuron regeneration; damage repair; skeletal;
 KW cartilage; osteogenesis; arthritis; bone fracture; hereditary disease;
 KW prosthetic cartilage device; spermatogenesis; fertility enhancer;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO929854-A1.
 XX
 PD 17-JUN-1999.
 XX
 PF 08-DEC-1998; 98WO-US026009.
 XX
 PR 08-DEC-1997; 97US-0067940P.
 XX
 PA (ONTO-) ONTOGENY INC.
 XX
 PI Bumcrot DA;
 XX
 XX WPI; 1999-561298/47.
 XX
 PT New human patched-2 (ptc-2) genes and proteins, useful in the treatment,
 PT prevention and/or reduction of the severity of neurological conditions.

```

XX PS Example 1; Page 62; 80pp; English.
XX
XX This invention describes a novel recombinantly produced human patched-2
XX (ptc-2) polypeptide which has nontropic, neuroprotective, cardiant,
XX antiinflammatory, antiparkinsonian and antiarthritic activity. The ptc-2
XX protein is a hedgehog receptor and is therefore capable of modulating
XX hedgehog signalling, and so affect a number of hedgehog-mediated
XX biological activities. The human patched-2 (ptc-2) protein can be used to
XX screen for modulators, antagonists and agonists, which are likely to play
XX an important role in the modulation of cellular proliferation and
XX maintenance of, e.g. neuronal, testicular, osteogenic or chondrogenic
XX tissues during disease states. Modulators of ptc-2 protein can be used
XX for in vivo reformation of tissue; to improve grafting and morphology of
XX transplanted tissue; for the treatment, prevention and/or reduction of
XX the severity of neurological conditions deriving from: injury to the
XX nervous system including traumatic injury, chemical injury, vascular injury
XX and deficits (such as ischemia resulting from stroke), together with
XX infectious/inflammatory and tumor-induced injury; ageing of the nervous
XX system including Alzheimer's disease; chronic neurodegenerative diseases
XX of the nervous system including Parkinson's disease, Huntington's chorea,
XX amyotrophic lateral sclerosis, as well as spinocerebellar degenerations;
XX and chronic immunological diseases of the nervous system including
XX multiple sclerosis. ptc-2 therapeutics can also be used in the treatment
XX of autonomic disorders of the peripheral nervous system, including
XX disorders affecting the innervation of smooth muscle and endocrine
XX tissue, e.g. to treat tachycardia or atrial cardiac arrhythmias.
XX Antagonists of ptc-2 protein can be used to prevent differentiation of
XX cells in culture, as well as for treatment of chronic pain syndromes.
XX Agonists may be used to rescue neurons from lesion-induced death as well
XX as neuron regeneration, in diseases such as CNS trauma infarction, (viral)
XX infection, metabolic disease, nutritional deficiency, toxic agents, and
XX so on. ptc-2 therapeutics may also be used for the repair of central and
XX peripheral nerve damage, for repair and regeneration of non-neuronal
XX tissue, e.g. skeletal and cartilage tissue, e.g. in the treatment of
XX osteogenesis, arthritis, bone fractures, hereditary disease, as well as
XX for generation of prosthetic cartilage devices, and to induce
XX spermatogenesis and as fertility enhancers. This sequence represents a
XX PCR primer used to amplify the human ptc-2 protein described in the
XX invention
XX
XX Sequence 20 BP; 8 A; 7 C; 4 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2.3e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 203 CACGAAGCCGAGACCTG 220
XX Db 1 CACAAAGCCGAGACCTG 18
XX
XX RESULT 279
XX AAZ37557/c
XX ID AAZ37557 standard; DNA; 20 BP.
XX XX AAZ37557;
XX XX
XX XX 07-JAN-2000 (first entry)
XX XX
XX XX Human mdm2 phosphorothioate oligodeoxynucleotide #87.
XX XX
XX XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
XX KW antisenase; modulation; oligonucleotide; expression; inhibition;
XX KW hyperproliferation; blood cancer; brain cancer; breast cancer;
XX KW lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;
XX KW restenosis; ss.
XX XX
XX XX Synthetic.
XX OS Homo sapiens.
XX XX
XX XX WO9949065-A1.
XX XX
XX XX

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PD 30-SEP-1999.
XX
XX 26-MAR-1999; 99WO-US006702.
XX
XX 26-MAR-1998; 98US-00048810.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsett LM;
XX WPI; 1999-610754/52.
XX
XX New antisense compounds used to treat eg. hyperproliferative conditions.
XX
XX Example 9; Page 49; 157pp; English.
XX
XX AAZ37473-237738 represent human mdm2 phosphorothioate oligonucleotides.
XX AAZ37471, AAZ37472, AAZ37739, AAZ37740 and AAZ37741 are used in the
XX exemplification of the present invention. The present invention describes
XX novel nucleotide antisense compounds, targeted to the 5' untranslated,
XX translation termination codon, or 3' untranslated region of a nucleic
XX acid encoding human mdm2, that modulates expression of human mdm2. The
XX oligonucleotides mediate their effect by antisense inhibition of
XX hyperproliferative gene expression. The antisense compound is used to
XX treat an animal having a disease or condition associated with mdm2,
XX particularly a hyperproliferative condition, more particularly cancer,
XX especially of the blood, brain, breast, lung or soft tissue, or
XX psoriasis, fibrosis, atherosclerosis or restenosis
XX
XX Sequence 20 BP; 7 A; 3 C; 2 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2.3e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 799 GATTAAACCATATATGA 816
XX Db 19 GACTAAACGATTATATGA 2
XX
XX RESULT 280
XX AAZ03775/c
XX ID AAZ03775 standard; DNA; 20 BP.
XX
XX AC AAZ03775;
XX
XX DT 07-OCT-1999 (first entry)
XX
XX DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
XX KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
XX KW paratrachoma; inclusion conjunctivitis; genital disease; perihhepatitis;
XX KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
XX KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
XX OS Synthetic.
XX OS Chlamydia trachomatis.
XX
XX XX WO9928475-A2.
XX XX
XX XX 10-JUN-1999.
XX
XX XX 27-NOV-1998; 98WO-IB001939.
XX
XX XX 28-NOV-1997; 97FR-00015041.
XX PR 17-DEC-1997; 97FR-00016034.
XX PR 04-NOV-1998; 98US-0107077P.
XX
XX XX (GEST ) GENSET.
XX
XX XX Griffais R;
XX
XX WPI; 1999-371125/31.
XX

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XX Genome sequence of Chlamydia trachomatis.
XX Disclosure; Page 1634; 1755pp; English.
XX
XX PCR primers AA201426-206209 were used to amplify open reading frames
XX (ORFs) of the genome of Chlamydia trachomatis (see AA201425). These ORFs
XX encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
XX against Chlamydia trachomatis. Antisense and ribozyme sequences can also
XX be used to control growth of the microorganism. Chlamydia trachomatis is
XX responsible for a large number of diseases, e.g. eye diseases such as
XX conjunctival trachoma, non-demic trachoma, paratrachoma, and inclusion
XX epidymitis; genital diseases such as nongonococcal urethritis,
XX pneumopathy in breast feeding infants; perihepatitis, Bartholinitis;
XX The polypeptides of the invention may be of use in treating these
XX diseases
XX
XX Sequence 20 BP; 5 A; 2 C; 8 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2.3e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2377 CATCTGATCTTCACCTGG 2394
XX 18 CATCTCATCATCTGG 1
XX
XX RESULT 281
XX AA237011
XX ID AAZ37011 standard; DNA; 20 BP.
XX AC AAZ37011;
XX XX
XX DT 13-MAR-2000 (first entry)
XX
XX DE Probe for peripheral benzodiazepine receptor associated protein-1 DNA.
XX
XX KW Human; peripheral benzodiazepine receptor associated protein-1; PRAX-1;
XX peripheral benzodiazepine receptor; chromosome 17;
XX KW central nervous system; immune system; gene therapy;
XX KW PRAX-1 deficiency condition; endocrine system; probe; PCR primer; ss.
XX
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX PN WO9960117-A2.
XX
XX PD 25-NOV-1999.
XX
XX PF 06-MAY-1999; 99WO-FR001070.
XX
XX PR 15-MAY-1998; 98FR-00006190.
XX
XX PA (SNFI ) SANOFI-SYNTHELABO.
XX
XX PI Casellas P, Galiegue S, Jbilo O, Le Fur G;
XX WPI; 2000-062455/05.
XX
XX PT New PRAX-1 polypeptide that interact with peripheral benzodiazepine
XX receptor, used to treat e.g. immune, central nervous or endocrine
XX disorders.
XX
XX PS Claim 14; Page 21; 44pp; French.
XX
XX AA236990-237023 represent probes for the polynucleotides encoding a human
XX peripheral benzodiazepine receptor associated protein-1, designated PRAX-
XX 1. The probes may also function as PCR primers. PRAX-1 interacts
XX specifically with the peripheral benzodiazepine receptor. The PRAX-1 gene
XX is localised on chromosome 17 in the q22-q23 region. The gene is
XX associated with markers of pathologies of the central nervous system or
XX immune system. The PRAX-1 nucleic acid is useful in gene therapy (of PRAX
XX -1 deficiency conditions, e.g. disorders of the central nervous, immune
XX or endocrine systems; as a source of diagnostic primers and probes (see
XX AA236990-237023) and of antisense therapeutics; for recombinant
XX production of the PRAX-1 protein; and for detecting allelic variants,
XX mutations, deletions, insertions, loss of heterozygosity and gene
XX rearrangements in the PRAX-1 gene. The PRAX-1 protein is used to raise
XX specific antibodies and to screen for specific modulators (potential
XX therapeutic agents). The antibodies are used as immunoassay reagents,
XX e.g. for diagnosis of abnormal expression or accumulation of PRAX-1
XX
XX Sequence 20 BP; 2 A; 8 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 14.8; DB 1; Length 20;

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PD 19-OCT-2000.
XX
XX
XX 06-APR-2000; 2000WO-US009355.
XX
XX 09-APR-1999; 99US-0128521P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Smith MW, Shin HD, O'brien SJ;
XX
XX WPI; 2000-687051/67.
XX
XX Predicting susceptibility to HIV infection or progression useful for
XX selection of therapeutic treatment for persons infected with HIV virus,
XX comprises detecting polymorphism in human interleukin-10 promoter.
XX
XX Example 1; Page 11; 40pp; English.
XX
XX The present invention describes a method for predicting susceptibility to
XX HIV infection or HIV progression in a subject. The method involves
XX detecting a polymorphism in a human interleukin-10 (IL-10) promoter,
XX where the presence of the polymorphism indicates susceptibility to HIV
XX infection or HIV progression. The method provides prognostic information
XX to persons infected with HIV virus and is useful to help select
XX treatments (such as administration of IL-10 or gene therapy with IL-10).
XX The presence of polymorphism is useful as predictor that very aggressive
XX treatment could substantially eradicate the virus from the infected
XX person. The method is useful for the generation of normograms or other
XX predictive algorithms that can be used, in association with allele
XX status, to prognose probable survival or years to development of AIDS
XX following HIV seroconversion. It indicates that increased expression of
XX the IL-10 gene helps to reduce HIV-1 infection and pathogenic progression
XX and enables a variety of new therapeutic interventions in the treatment
XX of HIV disease. The present sequence represents a short tandem repeat
XX (STR) primer which is used in an example from the present invention
XX
XX Sequence 20 BP; 5 A; 1 C; 10 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2.3e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2299 ACTCTTAACAGCCCC 2316
XX Db 20 ACTCTTATCAGCTCC 3
XX
XX RESULT 288
XX AAD14792
XX ID AAD14792 standard; DNA; 20 BP.
XX
XX AC AAD14792;
XX
XX 01-NOV-2001 (first entry)
XX
XX Human glycoen synthase kinase 3 alpha antisense oligo ISIS #116633.
XX
XX Human; glycoen synthase kinase 3 alpha; antidiabetic; cytostatic;
XX antisense therapy; diabetes; hyperproliferative disorder; inflammation;
XX neurological disorder; tumour; haematopoietic disorder; infection;
XX hyperproliferative disorder; developmental disorder; antisense;
XX phosphorothioate backbone; ss.
XX
XX Homo sapiens.
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone"
XX modified_base 1..5
XX /tag= b
```

```
FT /mod_base= OTHER
FT /note= "Methoxyethyl residues"
FT modified_base 1
FT /tag= d
FT /mod_base= m5C
FT modified_base 4
FT /tag= e
FT /mod_base= m5C
FT modified_base 6
FT /tag= f
FT /mod_base= m5C
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "Methoxyethyl residues"
XX
XX WO200152865-A1.
XX
XX 26-JUL-2001.
XX
XX 16-JAN-2001; 2001WO-US001411.
XX
XX 21-JAN-2000; 2000US-00488856.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Mckay R, Butler MW, Wyatt JR;
XX
XX WPI; 2001-442247/47.
XX
XX Antisense compound 8 to 30 nucleobases in length comprising a compound
XX that is targeted to a nucleic acid molecule encoding glycogen synthase
XX kinase 3 alpha, useful for the treatment of e.g. diabetes and
XX hyperproliferative disorders.
XX
XX Example 15; Page 83; 115pp; English.
XX
XX The invention relates to an antisense compound 8 to 30 nucleobases in
XX length targeted to a nucleic acid encoding glycogen synthase kinase 3
XX alpha. The antisense compound specifically hybridises with and inhibits
XX the expression of glycogen synthase kinase 3 alpha. The antisense
XX compound is useful for the treatment of a disease associated with
XX glycogen synthase kinase 3 alpha such as diabetes, a neurological
XX disorder, a haematopoietic disorder, a hyperproliferative disorder or a
XX developmental disorder. The antisense compounds may also be used
XX prophylactically to prevent or delay infection, inflammation or tumour
XX formation. The present sequence is a phosphorothioate antisense
XX oligonucleotide targeted to human glycogen synthase kinase 3 alpha DNA
XX
XX Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 2.3e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2192 AGAAGTGAAGTTGAAG 2209
XX Db 2 AGCACTGAAGTTGAAGAG 19
XX
XX RESULT 289
XX AAF73034/c
XX ID AAF73034 standard; DNA; 20 BP.
XX
XX AC AAF73034;
XX
XX 24-APR-2001 (first entry)
XX
XX Human daxx inhibitory antisense phosphorothioate oligonucleotide SEQ:135.
XX
XX Antisense oligonucleotide; daxx; inhibition; phosphorothioate;
XX Fas binding protein; CENP-C binding protein; gap6; EAP; cytostatic;
XX antiinflammatory; death associated protein 6; Ets-1 associated protein;
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infection; inflammation; tumour formation; ss.
KW OS Homo sapiens.
XX PN US6180353-B1.
XX PD 30-JAN-2001.
XX PF 24-JAN-2000; 2000US-00490692.
XX PR 24-JAN-2000; 2000US-00490692.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Dean NM, Cowser LM;
XX DR WPI; 2001-217744/22.
XX PT Novel antisense compounds capable of modulating expression of daxx useful
PT for diagnosis, prophylaxis and treatment of diseases associated with
PT expression of daxx.
XX PS Claim 1; Col 47; 59pp; English.
XX CC The present invention describes an antisense compound (I) up to 30
CC nucleobases in length, where (I) inhibits expression of daxx (also known
CC as Fas binding protein, CENP-C binding protein, dap6 for death associated
CC protein 6 and EAP for Ets-1 associated protein). (I) has cytostatic and
CC antiinflammatory activity, and can be used in antisense therapy and as a
CC modulator of daxx. (I) is useful for inhibiting the expression of daxx in
CC cells or tissues in vitro. (I) can be utilised for diagnostics,
CC therapeutics for the treatment of diseases associated with the expression
CC of daxx, prophylaxis e.g. to prevent or delay infection, inflammation or
CC tumour formation and as research reagent. The present sequence represents
CC an inhibitory human daxx antisense phosphorothioate oligonucleotide which
CC is used in the exemplification of the present invention
XX SQ Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 384 AGCTTCAGTCGAGGCTC 401
Db ||||| ||||| |||||
19 AGCTTCAGTCGAGGCTC 2

RESULT 290
AAS45736/c
ID AAS45736 standard; DNA; 20 BP.
XX AC AAS45736;
XX DT 18-DEC-2001 (first entry)
XX DE Human PARP-2 antisense inhibitor ISIS #126176.
XX KW Human; ss; PARP; Poly (ADP-ribose) polymerase; antisense oligonucleotide;
KW cytostatic; neutropic; neuroprotective; antiinflammatory; antidiabetic;
KW immunosuppressant; hyperproliferative disorder; cancer; cellular injury;
KW oxidative stress; neurological disorder; parkinsonism; apoptosis;
KW menigitis-associated intracranial complication; ischaemia; probe;
KW inflammatory disorder; autoimmune disorder; arthritis; diabetes.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..20

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/*tag= b
/mod_base= OTHER
/note= "All cytidine residues are 5-methyl cytidine"
modified_base 1..5
/*tag= c
/mod_base= OTHER
/note= "2'-methoxyethyl nucleotides"
modified_base 16..20
/*tag= d
/mod_base= OTHER
/note= "2'-methoxyethyl nucleotides"
WO200164955-A1.
07-SEP-2001.
01-MAR-2001; 2001WO-US006572.
02-MAR-2000; 2000US-00517467.
(ISIS-) ISIS PHARM INC.
Popoff I, Cowser LM;
WPI; 2001-602570/68.
Antisense compound useful for treating hyperproliferative, neurological,
inflammatory and autoimmune disorders and diabetes inhibits human PARP.
Claim 3; Page 86; 168pp; English.
The invention relates to antisense oligonucleotides targeted to human
PARP nucleic acid and inhibiting expression of human PARP. PARP (Poly
(ADP-ribose) polymerase plays an important role in chromatin
decondensation, DNA replication, DNA repair, gene expression, malignant
transformation, cellular differentiation and apoptosis. The antisense
oligonucleotide inhibitors are useful for inhibiting the expression of
PARP in human cells or tissues. They are also useful for treating a human
with a disease associated with PARP especially hyperproliferative
disorders (e.g. cancer), cellular injury resulting from oxidative stress,
neurological (e.g. parkinsonism, menigitis-associated intracranial
complications and ischaemia), inflammatory and autoimmune disorders (e.g
arthritis) and diabetes. The present sequence is an antisense
oligonucleotide of the invention
XX SQ Sequence 20 BP; 5 A; 9 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1474 GAAGTGGAGGTGGATGGT 1491
Db ||||| ||||| |||||
18 GAAGTGGAGAGGATGGT 1

RESULT 291
AAF92850/c
ID AAF92850 standard; DNA; 20 BP.
XX AC AAF92850;
XX DT 17-MAY-2001 (first entry)
XX DE Human ABC1 transcription factor binding site #12.
XX KW High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.
XX OS Homo sapiens.
XX PN WO200115676-A2.
XX PD 08-MAR-2001.

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XX PF 01-SEP-2000; 2000WO-IB001492.
XX PR 01-SEP-1999; 99US-0151977P.
XX PR 15-MAR-2000; 2000US-00526193.
XX PR 23-JUN-2000; 2000US-0213958P.
XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX PA (XENO-) XENON GENETICS INC.
XX PI Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;
XX DR WPI; 2001-244356/25.
XX XX
XX XX Treating a lower than normal high density lipoprotein-cholesterol (HDL-C)
XX PT level, a higher than normal triglyceride level, or a cardiovascular
XX PT disease, by administering a compound that modulates LXR- or RXR-mediated
XX PT transcriptional activity.
XX XX
XX PS Disclosure; Fig 3; 317pp; English.
XX XX
XX XX The present invention relates to a method for treating a patient
XX CC diagnosed as having a lower than normal high density lipoprotein-
XX CC cholesterol (HDL-C) level, a higher than normal triglyceride level, or a
XX CC cardiovascular disease, involving administering a compound that modulates
XX CC LXR- or RXR-mediated transcriptional activity or ABCI expression or
XX CC activity. The LXR gene product may be used in an assay to identify
XX CC compounds useful for the treatment of a disease or condition selected a
XX CC lower than normal HDL cholesterol level, a higher than normal
XX CC triglyceride level, and a cardiovascular disease
XX XX
XX SQ Sequence 20 BP; 6 A; 8 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 78 GATGTGATCTGGCTCAC 95
Db 18 GGTGTGATCTGGCTCAC 1
RESULT 292
AAH27935/C
ID AAH27939 standard; DNA; 20 BP.
XX AC AAH27939;
XX DT 05-SEP-2001 (first entry)
XX DE PCR primer for a minimal deletion in FRA16D oxidoreductase gene.
XX KW Cancer associated protein; FOR gene; FRA16D; fragile site; aphidicolin;
XX KW chromosomal rearrangement; cancer; splice variant; DNA instability;
XX KW FRA16D oxidoreductase; neoplasia; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200144466-A1.
XX PD 21-JUN-2001.
XX PF 15-DEC-2000; 2000WO-AU001539.
XX PR 16-DEC-1999; 99AU-00004711.
XX PR 19-APR-2000; 2000AU-00007025.
XX XX
XX PA (WOMB-) WOMEN'S & CHILDREN'S HOSPITAL.
XX PI Richards R, Ried K, Finnis M, Hobson L, Mangelsdorf M, Dayan S;
XX PI Nancarrow J, Woollatt E, Baker E;
XX XX
XX DR WPI; 2001-398151/42.

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XX XX Novel isolated 16q23.2 nucleic acid molecule, FRA16D oxidoreductase (FOR)
XX PT gene associated with FRA16D site, useful for early diagnosis and
XX PT assessment of risk of cancers associated with the FRA16D region.
XX PS Example 1; Page 46; 150pp; English.
XX XX
XX XX PCR primers AAH27888-AAH28055 represent PCR primers used to amplify and
XX CC identify minimal deletions in the human FRA16D oxidoreductase (FOR) gene.
XX CC The FOR gene encodes a cancer associated protein. The FRA16D site is a
XX CC fragile site induced by aphidicolin, which is located within the FOR
XX CC gene. The fragile site is the location of breakpoints of a variety of
XX CC chromosomal rearrangements, and other mutations associated with cancers.
XX CC The FOR protein is expressed as a number of splice variants. FOR gene
XX CC polynucleotide fragments are capable of acting as specific primers or
XX CC probes for detecting cancer associated variations of DNA sequence such as
XX CC a point mutation or small DNA rearrangement associated with the tumour, a
XX CC breakpoint of one or more chromosomal rearrangements associated with the
XX CC tumour and a pause site within the FRA16 gene. FOR nucleic acid molecules
XX CC are useful as markers to identify relationship between the fragile site
XX CC (FRA16D) and the DNA instability in neoplasia which allows better
XX CC diagnosis of cancers associated with the region
XX XX
XX SQ Sequence 20 BP; 8 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 229 AAGTTCACTGCTCTCTG 246
Db 20 AGTTCACTGCTCTCTG 3
RESULT 293
AAF80711/C
ID AAF80711 standard; DNA; 20 BP.
XX AC AAF80711;
XX DT 02-MAY-2001 (first entry)
XX DE Human mdm2 phosphorothioate oligonucleotide #85.
XX KW Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX OS Homo sapiens.
XX PN US6184212-B1.
XX PD 06-FEB-2001.
XX PF 26-MAR-1999; 99US-00280805.
XX PR 26-MAR-1998; 98US-00048810.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsett LM;
XX XX
XX DR WPI; 2001-190948/19.
XX XX
XX XX Novel antisense compound 8-30 nucleobases in length targeted to a nucleic
XX PT acid molecule encoding human mdm-2 useful for modulating the expression
XX PT of human mdm-2 and reducing hyperproliferation of human cells.
XX XX
XX PS Example 9; Col 27; 77pp; English.
XX XX
XX XX The present invention relates to an antisense compound 8-30 nucleobases
XX CC in length targeted to nucleobases 1-308 of the 5' untranslated region, the
XX CC 1776-1806 of the translation termination codon region or 1818-2370 of the
XX CC 3' untranslated region of a nucleic acid molecule encoding human mdm-2.
XX CC The invention is useful for reducing hyperproliferation of human cells,

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CC modulating the expression of mdm2 in human cells or tissues or in vitro.
CC The hyperproliferative disorder includes cancer or psoriasis
XX
SQ Sequence 20 BP; 7 A; 3 C; 2 G; 8 T; 0 U; 0 Other;

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 799 GATTAAACCATATATGA 816
Db 19 GACTAAACGATTATATGA 2

RESULT 294
AAF74765/c
ID AAF74765 standard; DNA; 20 BP.
XX
XX AAF74765;
AC
XX 17-MAY-2001 (first entry)
DT
XX Human hDPP PCR primer SEQ ID NO:5.
DE
XX Human; hDPP; diacylglycerol pyrophosphate phosphatase; DPP; detection;
KW PCR primer; ss.
XX
XX Homo sapiens.
OS
XX CN1271009-A.
FN
XX 25-OCT-2000.
PD
XX
XX 17-MAR-2000; 2000CN-00114952.
PF
XX 17-MAR-2000; 2000CN-00114952.
PR
XX (SREN-) SOUTHERN RES CENT NAT HUMAN GENE GROUP.
PA
PI Li N, Xiao H, Liu F;
XX
XX WPI; 2001-081384/10.
DR
XX
XX New human diacyl glyceropyrophosphate phosphatase protein and its code
PT sequence.
PT
XX
PS Example 1; Page 10; 19pp; Chinese.
XX
XX The present invention describes a human diacylglycerol pyrophosphate
CC phosphatase (DPP) designated hDPP. hDPP is expressed in normal tissue
CC near cancerous liver cells of a human body. Also described are methods
CC for the preparation and detection of hDPP nucleotide and protein
CC sequences. The present sequence represents a PCR primer for human hDPP,
CC which is used in an example from the present invention
XX
XX Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1117 TGTTCAAGAGCAGTCTG 1134
Db 18 TGTTCAAGAGCACTG 1

RESULT 295
AAF75704
ID AAF75704 standard; DNA; 20 BP.
XX
XX AAF75704;
AC
XX 11-MAY-2001 (first entry)
DT
```

```
XX
DE
XX Marine Xist gene peptide nucleic acid primer D2.
KW Primer; peptide nucleic acid; PNA; polyamide backbone; murine; Xist; ss.
XX
XX Mus sp.
OS
XX
XX Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /note= "This sequence is a peptide nucleic acid (PNA),
FT i.e. it contains a polyamide backbone instead of a
FT deoxyribose backbone"
XX
XX WO200112852-A2.
PN
XX
XX 22-FEB-2001.
PD
XX
XX 09-AUG-2000; 2000WO-US021880.
PF
XX
XX 13-AUG-1999; 99US-00373845.
PR
XX (PEPE-) PE CORP.
PA
XX Egholm M, Chen C;
PI
XX WPI; 2001-211233/21.
DR
XX
XX Producing non-radioisotopically labeled PNA-DNA chimeras for nucleic acid
PT analysis, comprises extending the chimera using a polymerase and an
PT extension reagent with non-radioisotopically labeled nucleotide 5'-
PT triphosphate.
XX
XX Example 3; Page 26; 59pp; English.
PS
XX The present invention relates to a method for producing a non-
CC radioisotopically labelled chimera. The method comprises enzymatically
CC extending a PNA-DNA chimera in the presence of a template nucleic acid, a
CC polymerase and a primer extension reagent comprising a non-
CC radioisotopically labeled nucleotide 5'-triphosphate capable of effecting
CC enzymatic chimera primer extension. The present sequence is a primer used
CC in the method of the present invention
XX
XX Sequence 20 BP; 7 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1006 CTGGGATGCACAGAGAT 1023
Db 2 CTGGGATGCAAGAGCAT 19

RESULT 296
AAC67718/c
ID AAC67718 standard; DNA; 20 BP.
XX
XX AAC67718;
AC
XX 16-FEB-2001 (first entry)
DT
XX Oligonucleotide #29 ISIS #116897.
DE
XX
XX Antiinflammatory; cytostatic; antibacterial; methionine aminopeptidase 2;
KW inhibitor; MetAP2; eukaryotic initiation factor associated protein; p67;
KW eIF-2; protein synthesis; antisense oligonucleotide; infection; human;
KW inflammation; tumour; phosphorothioate; 2-methoxyethyl wing; ss.
XX
XX Homo sapiens.
OS
XX US6136604-A.
PN
XX
```

```

PD 24-OCT-2000.
XX
XX
PF 27-OCT-1999; 99US-00428584.
XX
PR 27-OCT-1999; 99US-00428584.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Wyatt J;
XX
XX WPI; 2001-030942/04.
XX
XX New antisense compounds which specifically hybridize with and inhibit
PT human methionine aminopeptidase 2 expression, useful for treating
PT methionine aminopeptidase 2 related disorders and preventing inflammation
PT or tumor formation.
XX
XX Claim 14; Col 41-42; 39pp; English.
XX
XX Methionine aminopeptidase 2 (also known as MetAP2 and eukaryotic
XX initiation factor [eIF-2] associated protein, p67) is a cellular
XX glycoprotein that promotes protein synthesis in the presence of active
XX eIF-2 kinases by protecting the eIF-2 alpha subunit from phosphorylation.
XX The present invention relates to antisense oligonucleotides (AAC67690-
XX C67767) which inhibit human methionine aminopeptidase 2 coding sequence
XX expression (see AAC67683). The present sequence is one such antisense
XX oligonucleotide. The present sequence may be used for treating a patient
XX suspected of having or being prone to a disease or condition associated
XX with expression of MetAP2. In addition, the present sequence can also be
XX used as research reagents, diagnostics and to distinguish between
XX functions of various members of a biological pathway. The antisense
XX oligonucleotide may further be used prophylactically, e.g. to prevent or
XX delay infection, inflammation or tumour formation. Note: the present
XX sequence may have a phosphorothioate backbone and 2-methoxyethyl (2'-MOE)
XX wings
XX
XX Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;
XX
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 996 TGGACCAAGCGCTGGGATG 1013
DB 19 TGGATCAAGCTGGGATG 2
RESULT 297
AAH91454
ID AAH91454 standard; DNA; 20 BP.
XX
XX AAH91454;
XX
XX 09-OCT-2001 (first entry)
XX
XX Human inflammatory bowel disease associated polymorphic site #529.
XX
XX Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
XX single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
XX chromosome 5q31-33; forensic test; gene therapy; ds.
XX
XX Homo sapiens.
XX
XX Key misc_feature 12 Location/Qualifiers
XX
XX modified_base 1.20
XX
XX /mod base= OTHER
XX /note= "SNP, optionally insertion or deletion at this
XX position"
XX
XX WO200142511-A2.
XX
XX 14-JUN-2001.
XX

```

```

PF 11-DEC-2000; 2000WO-US033632.
XX
XX 10-DEC-1999; 99US-0170257P.
XX 10-APR-2000; 2000US-0196046P.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX
XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
XX
XX WPI; 2001-367874/38.
XX
XX Testing for the presence of polymorphisms associated with inflammatory
XX bowel disease, using a hybridization assay.
XX
XX Claim 1; Page 61; 463pp; English.
XX
XX The present invention describes a method for detecting the presence of
XX polymorphisms associated with inflammatory bowel diseases such as
XX ulcerative colitis and Crohn's disease. The methods can be used to detect
XX the presence of genetic polymorphisms associated with inflammatory bowel
XX disease and correlating their occurrence with disease states. They may be
XX used in this way for phenotypic correlations, forensics, paternity
XX testing, medicine and genetic analysis. The present sequence is a
XX polymorphic site described in the exemplification of the invention
XX
XX Sequence 20 BP; 17 A; 0 C; 2 G; 0 T; 0 U; 1 Other;
XX
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2408 AAGAAGAAAAATAAAGCAA 2426
DB 1 AAAAAGAAAAAAGAAA 19
RESULT 298
AAS29326/c
ID AAS29326 standard; DNA; 20 BP.
XX
XX AAS29326;
XX
XX 21-NOV-2001 (first entry)
XX
XX Human mdm2 antisense oligonucleotide 31727.
XX
XX Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
XX atherosclerosis; tumour; cytostatic; anti psoriatic;
XX anti arteriosclerotic; vasotropic; antisense; phosphorothioate; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX
XX modified_base 1.20
XX
XX /mod base= OTHER
XX /note= "OTHER= All phosphorothioate linkages,
XX additionally bases 1-6 and bases 15-20 are 2'-O-
XX methoxyethyl bases, and bases 7-14 are deoxynucleotides"
XX
XX US2001016575-A1.
XX
XX 23-AUG-2001.
XX
XX 02-JAN-2001; 2001US-00752983.
XX
XX 26-MAR-1998; 98US-00048810.
XX 26-MAR-1999; 99US-00280805.
XX
XX (MIRA/) MIRAGLIA L J.
XX (NERO/) NERO P.
XX (GRAH/) GRAHAM M J.
XX

```

PA (MONI/) MONIA B P.
 XX (COWS/) COWSERT L M.
 PT Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsert LM;
 XX WPI; 2001-535565/59.
 DR
 XX
 XX An antisense compound, useful for treating e.g. cancer, comprises
 PT nucleobases targeted a region (e.g. translation termination codon region)
 PT of a nucleic acid encoding human mdm2.
 XX
 XX Example 9; Page 15; 81pp; English.
 PS
 XX The present invention relates to antisense compounds, 8-30 nucleobases in
 CC length targeted to the 5' untranslated region, translation termination
 CC codon region, 3' untranslated region, coding region or translation start
 CC site of a nucleic acid encoding human mdm2, where the antisense compound
 CC modulates the expression of human mdm2. The antisense oligonucleotides of
 CC the invention are useful for encoding human mdm2 and for inhibiting the
 CC expression of human mdm2. They may be used for treating an animal having
 CC a disease or condition associated with amplification of mdm2 gene or
 CC overexpression of mdm2 e.g. a hyperproliferative disorder such as cancer
 CC (blood, brain, breast, lung, or a soft tissue cancer) and psoriasis,
 CC fibrosis, atherosclerosis or restenosis, tumours, colorectal carcinoma
 CC and chronic myelogenous leukemia. The antisense compound may be
 CC administered with a chemotherapeutic agent to overcome drug resistance.
 CC The antisense compound reduces hyperproliferation of human cells. The
 CC method, which involves the use of the antisense compound, is also useful
 CC for detecting the role of mdm2 expression in various cell functions and
 CC physiological processes and useful in both clinical research and
 CC diagnostic tools. AAS29242-AAS29507 represent the human mdm2 antisense
 CC oligonucleotides of the present invention
 XX
 XX Sequence 20 BP; 7 A; 3 C; 2 G; 8 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 799 GATTAACCATTTATGA 816
 DB 19 GACTAACGATTATATGA 2
 |||||||
 RESULT 299
 AAH80637/c
 ID AAH80637 standard; cDNA; 20 BP.
 XX
 XX AAH80637;
 XX
 XX 11-SEP-2003 (revised)
 DT 19-SEP-2001 (first entry)
 XX
 XX Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 601.
 DE Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
 KW disease diagnosis; ss.
 XX
 XX Human immunodeficiency virus 1.
 OS
 XX USG251588-B1.
 PN 26-JUN-2001.
 PD 10-FEB-1998; 98US-00021701.
 XX
 XX 10-FEB-1998; 98US-00021701.
 PF (AGIL-) AGILENT TECHNOLOGIES INC.
 XX
 XX Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
 PI WPI; 2001-424456/45.
 XX
 XX Predicting the potential of an oligonucleotide to hybridize to a target
 PT nucleotide sequence, useful for evaluating oligonucleotide probe
 PT sequences, by identifying a oligonucleotides based on the evaluation of
 PT parameters.
 XX
 XX Example 2; Col 67; 342pp; English.
 PS
 XX The present invention describes a method for predicting the potential of
 CC an oligonucleotide to hybridize to a (complementary) target nucleotide
 CC sequence, involving identifying a subset of oligonucleotides within the
 CC predetermined number of unique oligonucleotides based on the evaluation
 CC of the parameter. Oligonucleotides in the subset are identified that are
 CC clustered along a region of the nucleotide sequence that is hybridisable
 CC to the target nucleotide sequences. This is useful for evaluating
 CC oligonucleotide probe sequences. The present sequence is an
 CC oligonucleotide described in the exemplification of the invention.
 CC (Updated on 11-SEP-2003 to standardise OS field)
 XX
 XX Sequence 20 BP; 5 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1073 ACTCAGGATTCTGGAA 1090
 DB 20 ACTCAAGACTTCTGGAA 3
 |||||||
 RESULT 300
 AAH80639/c
 ID AAH80639 standard; cDNA; 20 BP.
 XX
 XX AAH80639;
 XX
 XX 11-SEP-2003 (revised)
 DT 19-SEP-2001 (first entry)
 XX
 XX Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 603.
 DE Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
 KW disease diagnosis; ss.
 XX
 XX Human immunodeficiency virus 1.
 OS
 XX USG251588-B1.
 PN 26-JUN-2001.
 PD 10-FEB-1998; 98US-00021701.
 XX
 XX 10-FEB-1998; 98US-00021701.
 PF (AGIL-) AGILENT TECHNOLOGIES INC.
 XX
 XX Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
 PI WPI; 2001-424456/45.
 XX
 XX Predicting the potential of an oligonucleotide to hybridize to a target
 PT nucleotide sequence, useful for evaluating oligonucleotide probe
 PT sequences, by identifying a oligonucleotides based on the evaluation of
 PT parameters.
 XX
 XX Example 2; Col 67; 342pp; English.
 PS
 XX The present invention describes a method for predicting the potential of
 CC an oligonucleotide to hybridize to a (complementary) target nucleotide
 CC sequence, involving identifying a subset of oligonucleotides within the
 CC predetermined number of unique oligonucleotides based on the evaluation
 CC of the parameter. Oligonucleotides in the subset are identified that are
 CC clustered along a region of the nucleotide sequence that is hybridisable

XX
 PT Predicting the potential of an oligonucleotide to hybridize to a target
 PT nucleotide sequence, useful for evaluating oligonucleotide probe
 PT sequences, by identifying a oligonucleotides based on the evaluation of
 PT parameters.
 XX
 XX Example 2; Col 67; 342pp; English.
 PS
 XX The present invention describes a method for predicting the potential of
 CC an oligonucleotide to hybridize to a (complementary) target nucleotide
 CC sequence, involving identifying a subset of oligonucleotides within the
 CC predetermined number of unique oligonucleotides based on the evaluation
 CC of the parameter. Oligonucleotides in the subset are identified that are
 CC clustered along a region of the nucleotide sequence that is hybridisable
 CC to the target nucleotide sequences. This is useful for evaluating
 CC oligonucleotide probe sequences. The present sequence is an
 CC oligonucleotide described in the exemplification of the invention.
 CC (Updated on 11-SEP-2003 to standardise OS field)
 XX
 XX Sequence 20 BP; 5 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1073 ACTCAGGATTCTGGAA 1090
 DB 20 ACTCAAGACTTCTGGAA 3
 |||||||
 RESULT 300
 AAH80639/c
 ID AAH80639 standard; cDNA; 20 BP.
 XX
 XX AAH80639;
 XX
 XX 11-SEP-2003 (revised)
 DT 19-SEP-2001 (first entry)
 XX
 XX Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 603.
 DE Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
 KW disease diagnosis; ss.
 XX
 XX Human immunodeficiency virus 1.
 OS
 XX USG251588-B1.
 PN 26-JUN-2001.
 PD 10-FEB-1998; 98US-00021701.
 XX
 XX 10-FEB-1998; 98US-00021701.
 PF (AGIL-) AGILENT TECHNOLOGIES INC.
 XX
 XX Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
 PI WPI; 2001-424456/45.
 XX
 XX Predicting the potential of an oligonucleotide to hybridize to a target
 PT nucleotide sequence, useful for evaluating oligonucleotide probe
 PT sequences, by identifying a oligonucleotides based on the evaluation of
 PT parameters.
 XX
 XX Example 2; Col 67; 342pp; English.
 PS
 XX The present invention describes a method for predicting the potential of
 CC an oligonucleotide to hybridize to a (complementary) target nucleotide
 CC sequence, involving identifying a subset of oligonucleotides within the
 CC predetermined number of unique oligonucleotides based on the evaluation
 CC of the parameter. Oligonucleotides in the subset are identified that are
 CC clustered along a region of the nucleotide sequence that is hybridisable

CC to the target nucleotide sequence. This is useful for evaluating
 CC oligonucleotide probe sequences. The present sequence is an
 CC oligonucleotide described in the exemplification of the invention.
 CC (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1073 ACTCAAGACTTCTGGGAA 1090
 Db 18 ACTCAAGACTTCTGGGAA 1

RESULT 301
 AAH80638/c
 ID AAH80638 standard; cDNA; 20 BP.
 AC AAH80638;
 XX
 XX 11-SEP-2003 (revised)
 DT 19-SEP-2001 (first entry)
 XX
 DE Oligonucleotide hybridisation potential related cDNA SEQ ID NO: 602.
 XX
 XX Nucleic acid hybridisation; probe; primer; human; rabbit; HIV-1;
 KW disease diagnosis; ss.
 KW
 XX Human immunodeficiency virus 1.
 OS
 XX US6251588-B1.
 PN
 XX 26-JUN-2001.
 PD
 XX 10-FEB-1998; 98US-00021701.
 PF
 XX 10-FEB-1998; 98US-00021701.
 PR
 XX (AGIL-) AGILENT TECHNOLOGIES INC.
 PA
 XX Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;
 PI WPI; 2001-424456/45.
 XX
 DR Predicting the potential of an oligonucleotide to hybridize to a target
 XX nucleotide sequence, useful for evaluating oligonucleotide probe
 PT sequences, by identifying a oligonucleotides based on the evaluation of
 PT parameters.
 PT
 XX Example 2; Col 67; 342pp; English.

The present invention describes a method for predicting the potential of
 an oligonucleotide to hybridize to a (complementary) target nucleotide
 sequence, involving identifying a subset of oligonucleotides within the
 predetermined number of unique oligonucleotides based on the evaluation
 of the parameter. Oligonucleotides in the subset are identified that are
 clustered along a region of the nucleotide sequence that is hybridisable
 to the target nucleotide sequence. This is useful for evaluating
 CC oligonucleotide probe sequences. The present sequence is an
 CC oligonucleotide described in the exemplification of the invention.
 CC (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1073 ACTCAAGACTTCTGGGAA 1090
 Db 19 ACTCAAGACTTCTGGGAA 2

CC to the target nucleotide sequence, by altering the function of a plastid
 gene, selecting plants expressing altered phenotype, transforming plants
 with a vector capable of restoring function and separating transformed
 plants.
 Example 4; Page 36; 56pp; English.
 The invention relates to producing multicellular plants, organs or
 tissues transformed on their plastome, comprising altering/disrupting the
 function of a gene in a plastid genome for producing a selectable
 phenotype and selecting plants with plastids expressing the phenotype.
 CC transforming the plastid genomes of selected plants with a transformation
 vector with a restoring sequence for restoring function and separating
 CC transformed plants. This method is useful for producing multicellular
 CC plants, organs or tissues transformed on their plastome and for selection
 CC of antibiotics and herbicide resistance genes. Sequences ABS52237-
 CC ABS52269 represent PCR primers used to amplify plant vector genes of the
 CC invention
 XX
 SQ Sequence 20 BP; 1 A; 7 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 878 ATTGGATGCTCTCCCTGCT 895
 Db 1 ATTGTTGCTCTCCCTGCT 18

RESULT 303
 ABS73901/c
 ID ABS73901 standard; DNA; 20 BP.
 AC ABS73901;
 XX
 XX 06-DEC-2002 (first entry)
 DT
 XX Human cytohesin-1 coding region antisense oligonucleotide, ISIS#110994.
 DE
 XX Human; antisense; cytohesin-1; guanine nucleotide exchange protein; ARF;
 KW ADP ribosylation factor; inflammation; antiinflammatory; tumour;

KW cytostatic; ss.
 XX Homo sapiens.
 OS WO200268584-A2.
 PN 06-SEP-2002.
 PD 30-OCT-2001; 2001WO-US047583.
 PF 22-FEB-2001; 2001US-00791243.
 PR (ISIS-) ISIS PHARM INC.
 PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
 XX Bennett CF, Rothlein R, Kishimoto TK, Cowseert LM;
 DR WPI; 2002-723198/78.
 XX New antisense oligonucleotide encoding human cytohesin-1, useful for
 PT preventing or treating a disease or condition associated with cytohesin-1
 PT expression e.g. tumor or inflammation.
 XX Example 15; Page 80; 107pp; English.
 XX The invention relates to a new antisense compound, comprising 8-30
 CC nucleobases targeted to a nucleic acid molecule encoding human cytohesin-
 CC 1, specifically hybridises with, and inhibits the expression of, human
 CC cytohesin-1, a guanine nucleotide exchange protein for ARF (ADP
 CC ribosylation factor). The antisense compound may be used in a
 CC pharmaceutical composition for inhibiting the expression of cytohesin-1
 CC in human cells or tissues, and in treating a disease or condition
 CC associated with cytohesin-1 by administering to the human the antisense
 CC compound e.g. tumour or inflammation. The antisense compound is also
 CC useful for diagnostics, therapeutics, prophylaxis and as research
 CC reagents and kits. The present sequence is an antisense oligonucleotide
 CC targeting human cytohesin-1
 XX
 SQ Sequence 20 BP; 2 A; 6 C; 5 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1005 CCTGGGATGCACAGAGAA 1022
 DB 18 CCTGGGATCCACAGAGGA 1
 RESULT 304
 ABL43907/c
 ID ABL43907 standard; DNA; 20 BP.
 XX ABL43907;
 AC 11-APR-2002 (first entry)
 DT Human chromosome 1p36-35 PCR primer SEQ ID NO:951.
 XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
 KW PCR primer; ss.
 XX Homo sapiens.
 OS JP2001321190-A.
 PN 20-NOV-2001.
 XX 12-MAR-2001; 2001JP-00068285.
 PF 10-MAR-2000; 2000JP-00066716.
 PR (RIKA) RIKAGAKU KENKYUSHO.
 PA

PA (GENO-) GENOTEX YG.
 XX WPI; 2002-144136/19.
 DR Arraying genome clones.
 PT Claim 4; Page 23; 528pp; Japanese.
 PS
 XX
 CC The present invention describes a method of arraying genome clones. The
 CC method comprises: (a) clones of the genomic libraries contained in
 CC multiwell plates numbered for discrimination are mixed in each of the
 CC multiwell plates; (b) a primer designed based on the chromosome marker
 CC sequence is added to the mixture to carry out an amplification reaction;
 CC (c) a signal corresponding to the marker is detected from the resultant
 CC amplified product to specify the discrimination Nos. of the multiwell
 CC plates containing the clones having said marker sequence; (d) the order
 CC of the markers is changed so that the same discrimination Nos. succeed to
 CC the maximum in the specified discrimination Nos. to array the multiwell
 CC plates; (e) the clones in the multiwell plates of the specified
 CC discrimination Nos. are mixed respectively in each wells of longitudinal
 CC and lateral directions; (f) the mixed clones are cultured and the
 CC resultant cultures are amplified by using the above primer; (g) signals
 CC are detected from the amplified products; (h) the clones in the multiwell
 CC plates are specified from the detected result; and (i) the clones are
 CC reconstituted as the positions on the chromosome and arrayed. The
 CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
 CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
 CC represent PCR primers for human chromosome 21q22.1, which are
 CC specifically claimed for use in the present invention
 XX
 SQ Sequence 20 BP; 5 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 947 ACAGTTCCTTGACAG 964
 DB 19 ACAGTTCCTGTGCACAG 2
 RESULT 305
 ABQ66437/c
 ID ABQ66437 standard; DNA; 20 BP.
 XX ABQ66437;
 AC 22-AUG-2002 (first entry)
 DT Human cytohesin-1 mRNA levels inhibitor #6.
 XX Cytohesin-1; CT1; inhibit; cytostatic; antiinflammatory; cytostatic;
 KW anti-infective; antisense gene therapy; infection; inflammation; tumour;
 KW human; ss; inhibitor.
 XX Synthetic.
 OS US6383809-B1.
 XX 07-MAY-2002.
 PD 30-OCT-2000; 2000US-00702246.
 PF 30-OCT-2000; 2000US-00702246.
 PR (ISIS-) ISIS PHARM INC.
 XX Bennett CF, Cowseert LM;
 PI WPI; 2002-478385/51.
 XX New antisense compounds directed against human cytohesin-1, useful for
 PT treating and preventing infection, inflammation and tumors.

XX Claim 14; Col 41; 40pp; English.

PS The invention relates to a novel antisense compound of 16-30 nucleotides

XX targeted to any of 71 specified regions of the sequence that encodes

CC human cytohesin-1 (CTL), where the compound hybridizes and inhibits

CC expression of human CTL. The compound of the invention has

CC antiinflammatory, cytostatic, and anti-infective activity. The antisense

CC compounds may have a use in antisense gene therapy. The antisense

CC compounds are useful for treating or preventing disorders associated with

CC expression of human CTL, e.g. infections, inflammation and tumours, and

CC as research and diagnostic reagents. Sequences ABQ66432-ABQ66511

CC represent chimeric phosphorothioate oligonucleotides, with 2'-MOE wings

CC and a deoxy gap. The claimed sequences inhibit production of cytohesin-1

CC mRNA

XX Sequence 20 BP; 2 A; 6 C; 5 G; 7 T; 0 U; 0 Other;

SQ

Query Match 0.4%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 2.3e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1005 CCTGGGATCCACAGAGAA 1022

DB 18 CCTGGGATCCACAGAGGA 1

RESULT 306

AA149188

ID AAL49188 standard; DNA; 20 BP.

AC AAL49188;

XX 30-OCT-2002 (first entry)

DT Porcine CD 151 coding sequence PCR primer #12.

DE

XX CD 151; porcine reproductive and respiratory syndrome virus; PRRSV; pig;

KW selective breeding; xenotransplant; anti-RNA entry protein; anti-REP;

KW anti-viral; vaccine; PCR; primer; ss.

XX Sus scrofa.

OS

XX WO200260924-A2.

PN

XX 08-AUG-2002.

PD

XX 29-JAN-2002; 2002WO-US002868.

XX

XX 29-JAN-2001; 2001US-00772044.

PR

XX 28-JAN-2002; 2002US-00772044.

PR

XX (UNIV) UNIV KANSAS STATE RES FOUND.

PA

XX Kapil S, Shanmukhappa K;

PI

XX WPI; 2002-619225/66.

DR

XX Determining susceptibility and resistance to porcine reproductive and

PT respiratory syndrome virus (PRRSV), useful for improving swine breeding,

PT by assaying for CD 151 in a sample of cellular material of known origin

PT from the animal.

XX

XX Example 17; Page 35; 77pp + Sequence Listing; English.

PS

XX The present invention relates to a method of determining the

CC susceptibility or resistance of an animal to porcine reproductive and

CC respiratory syndrome virus (PRRSV). This involves assaying for CD 151 in

CC a sample of cellular material of known origin from the animal. In

CC addition, coding sequences of CD 151 are described, and anti-viral

CC compounds designated anti-RNA entry proteins (anti-REPs). The method is

CC useful for determining susceptibility and resistance to PRRSV in an

CC animal. This is particularly useful for improving swine breeding or for

CC screening different pig breeding lines. The method is also useful for

CC developing non-simian recombinant cell lines for propagating the virus,

CC for producing anti-viral compounds or vaccines for inducing immunity

CC against PRRSV, and for diagnosing PRRSV infection in a swine. The present

CC sequence is a PCR primer used to isolate the porcine CD 151 coding

CC sequence. Note: The sequence data for this patent did not form part of

CC the printed specification, but was obtained in electronic format directly

CC from WIPO at fp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 20 BP; 2 A; 7 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 2.3e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 386 CTTGAGCTGCAGGCTCTT 403

DB 1 CTCCAGCTTCAGGCTCTT 18

RESULT 307

ABZ87594/C

ID ABZ87594 standard; DNA; 20 BP.

XX

AC ABZ87594;

XX

XX 17-OCT-2003 (first entry)

DT

XX Human oligonucleotide sequence.

DE

XX Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

KW lung inflammation; respiratory disease; db.

XX

OS Homo sapiens.

XX WO200285308-A2.

PN

XX 31-OCT-2002.

PD

XX 23-APR-2002; 2002WO-US013135.

PF

XX 24-APR-2001; 2001US-0286137P.

PR

XX (EPIG-) EPIGENESIS PHARM INC.

PA

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

PI

XX WPI; 2003-229219/22.

DR

XX Pharmaceutical composition for treating ailments associated with impaired

PT respiration, has oligo(s) antisense to specific gene(s) or its

PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

PT ubiquinone.

XX

XX Disclosure; SEQ ID NO 2836; 872pp; English.

PS

XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the

CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or

CC nasal airway dysfunction and a second active agent comprising an

CC antiinflammatory steroid and ubiquinone. A composition of the invention

CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or

CC preventing a respiratory, lung or malignant disease or condition, also

CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 4 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3194 GGCTCCGTCGAACTCCCA 3211
 Db 18 GGCTCCGTCGAACTCCCA 1

RESULT 308
 ABZ88879
 ID ABZ88879 standard; DNA; 20 BP.

XX
 AC ABZ88879;

XX
 DT 17-OCT-2003 (first entry)

XX
 DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX
 PD 31-OCT-2002.

XX
 PF 23-APR-2002; 2002WO-US013135.

XX
 PR 24-APR-2001; 2001US-0286137P.

XX
 PA (EPIG-) EPIGENESIS PHARM INC.

XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;

XX
 DR WPI; 2003-229219/22.

XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX
 PS Disclosure; SEQ ID NO 4121; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 20 BP; 16 A; 1 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3388 ACACCTCAAAAAA 3405
 Db 2 AAACCTTAAAAA 19

RESULT 309
 ABZ85771
 ID ABZ85771 standard; DNA; 20 BP.

XX
 AC ABZ85771;

XX
 DT 17-OCT-2003 (first entry)

XX
 DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX
 PD 31-OCT-2002.

XX
 PF 23-APR-2002; 2002WO-US013135.

XX
 PR 24-APR-2001; 2001US-0286137P.

XX
 PA (EPIG-) EPIGENESIS PHARM INC.

XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;

XX
 DR WPI; 2003-229219/22.

XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX
 PS Claim 15; SEQ ID NO 1013; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 14 A; 1 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2409 AGAAGAAATAAAGCAA 2426
 |||||
 Db 1 AAAAGAAATAAAGCTA 18

RESULT 310

ABZ94088
 ID ABZ94088 standard; DNA; 20 BP.

AC ABZ94088;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 PI

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX Disclosure; SEQ ID NO 9330; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 2 A; 8 C; 3 G; 6 T; 0 U; 1 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 114 CTTCTGGCTCTCTTCAG 132

Db 1 CTNCCCTGGCTCTCTTCAGT 19

RESULT 311

ABZ93102
 ID ABZ93102 standard; DNA; 20 BP.

XX AC ABZ93102;

XX 17-OCT-2003 (first entry)

XX Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 PI

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX Disclosure; SEQ ID NO 8344; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 6 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2822 TAAATGCTGTCGAATTT 2839

Db 3 TAAATGCTGTCGAATTT 20

RESULT 312
 ABZ92034/C
 ID ABZ92034 standard; DNA; 20 BP.

AC ABZ92034;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.

XX WO200285308-A2.

PN 31-OCT-2002.

PD 23-APR-2002; 2002WO-US013135.

PF 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

PS Disclosure; SEQ ID NO 7276; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 20 BP; 1 A; 5 C; 2 G; 12 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2411 AAGAAAAATAAGCAAGA 2428

Db 19 AAGAAAGATAGAGCAAGA 2

RESULT 313

ABZ88937

ID ABZ88937 standard; DNA; 20 BP.

XX AC ABZ88937;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.

XX WO200285308-A2.

PN 31-OCT-2002.

PD 23-APR-2002; 2002WO-US013135.

PF 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

PS Disclosure; SEQ ID NO 4179; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 13 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3387 CACACTCAAAAAA 3404
||| |||||
Db 3 CACTGTCAAAAAA 20

RESULT 314
ABZ93343
ID ABZ93343 standard; DNA; 20 BP.
XX
AC ABZ93343;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antiense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antiense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 8585; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 6 A; 1 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1518 AGTGGATGAAAAAGTGGT 1535
||| |||||
Db 3 AGTGGATGCAAAAGTGGT 20

RESULT 315
ABX09085/C
ID ABX09085 standard; DNA; 20 BP.
XX
AC ABX09085;
XX
DT 22-JAN-2003 (first entry)
XX
DE Human dual specific phosphatase 5 phosphorothioate oligonucleotide #24.
XX
KW Human; dual specific phosphatase 5; ss; developmental disorder;
KW hyperproliferative disorder; inflammatory disorder aberrant apoptosis;
KW antiinflammatory; cytostatic; antiapoptotic; antiproliferative;
KW phosphorothioate oligonucleotide.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200297108-A2.
XX
XX 05-DEC-2002.
XX
PF 15-MAY-2002; 2002WO-US015305.
XX
PR 25-MAY-2001; 2001US-00865993.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Watt AT;
XX
DR WPI; 2003-041418/03.
XX
PT Antisense modulation of dual specific phosphatase 5 expression used in
PT treating disorders e.g. inflammatory diseases.
XX
XX Example 15; Page 84; 110pp; English.
XX
CC The invention relates to a compound 8-50 nucleobases in length targeted
CC to a nucleic acid molecule encoding dual specific phosphatase 5, where
CC the compound specifically hybridizes with and inhibits the expression of
CC dual specific phosphatase 5. The compound is used for treating an animal
CC having a disease or condition associated with dual specific phosphatase 5
CC such as a hyperproliferative disorder, a developmental disorder, an
CC inflammatory disorder or a disease which arises from aberrant apoptosis.
CC Sequences ABX09062-ABX09139 represent human dual specific phosphatase 5
CC phosphorothioate oligonucleotides of the invention
XX
SQ Sequence 20 BP; 4 A; 2 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1672 CCAGTTTCAAGGAGCACT 1689
 Db 19 CCACCTTCAAGAAGCAAT 2

RESULT 316
 ABTL13634
 ID ABTL13634 standard; DNA; 20 BP.
 XX
 AC ABTL13634;
 XX
 XX
 DT 07-FEB-2003 (first entry)
 XX
 DE Liver regeneration-related gene panel PCR primer #156.
 XX
 KW PCR; primer; ss; liver regeneration; gene panel; expression profile;
 KW drug screening; drug development; hepatitis; liver transplantation.
 XX
 OS Unidentified.
 XX
 XX WO200277222-A1.
 PN
 XX 03-OCT-2002.
 PD
 XX
 XX 13-MAR-2002; 2002WO-JP002372.
 PF
 XX
 XX 13-MAR-2001; 2001JP-00070940.
 PR
 XX
 PA (AJIN) AJINOMOTO CO INC.
 PI
 PI Yokoya F, Okutsu T, Mori M, Takahara Y, Fukuda H, Aburatani H;
 PI Sonaka I;
 XX
 DR WPI; 2003-018922/01.
 XX
 XX
 PT Gene panel participating in liver regeneration, applicable in providing
 PT expression data, diagnosis and development of drugs for promoting liver
 PT regeneration e.g. after transplantation or removal of liver during
 PT cancer.
 XX
 XX Example 2; Page 89; 101pp; Japanese.
 PS
 XX
 CC The invention comprises a gene panel constructed from the expression
 CC profile of known genes which show a change in expression level between
 CC normal liver cells and liver cells under regeneration. The gene panel is
 CC useful for providing expression data and screening/development of drugs
 CC for liver regeneration (e.g. when treating hepatitis, after
 CC transplantation or removal of the liver during cancer or hepatitis
 CC therapy). The present DNA sequence represents a PCR primer used in the
 CC invention
 CC
 XX
 SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 99 GGACGATGTCAGCTCTT 116
 Db 2 GGACGCTGTCATGCTCTT 19

RESULT 317
 ABTL16110
 ID ABTL16110 standard; DNA; 20 BP.
 XX
 AC ABTL16110;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE NOVX related reverse PCR primer SEQ ID No 167.
 XX
 KW Antidiabetic; anorectic; virucide; antibacterial; fungicide; nootropic;
 KW NOVX-associated disorder. The nucleic acid molecules, preferably a

protozoacide; neuroprotective; antiparkinsonian; antilipaseic;
 NOVX-associated disorder; metabolic disorder; diabetes; anorexia;
 obesity; infectious disease; cancer-associated cachexia; immune disorder;
 neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 haematopoietic disorder; cancer; dyslipidaemia; metabolic disturbance;
 neurogenesis; cell differentiation; cell proliferation; haematopoiesis;
 wound healing; angiogenesis; gene therapy; chromosome mapping;
 tissue typing; preventive medicine; pharmacogenomic; NOVX; PCR; primer;
 ss.

Unidentified.
 OS
 XX WO200299062-A2.
 PN
 XX 12-DEC-2002.
 PD
 XX
 XX 04-JUN-2002; 2002WO-US017559.
 PF
 XX
 XX 04-JUN-2001; 2001US-0295607P.
 PR
 XX 06-JUN-2001; 2001US-0296404P.
 PR
 XX 06-JUN-2001; 2001US-0296418P.
 PR
 XX 07-JUN-2001; 2001US-0296575P.
 PR
 XX 11-JUN-2001; 2001US-0297414P.
 PR
 XX 12-JUN-2001; 2001US-0297567P.
 PR
 XX 12-JUN-2001; 2001US-0297573P.
 PR
 XX 14-JUN-2001; 2001US-0298285P.
 PR
 XX 15-JUN-2001; 2001US-0298528P.
 PR
 XX 18-JUN-2001; 2001US-0299133P.
 PR
 XX 19-JUN-2001; 2001US-0299230P.
 PR
 XX 21-JUN-2001; 2001US-0299499P.
 PR
 XX 22-JUN-2001; 2001US-0300177P.
 PR
 XX 28-JUN-2001; 2001US-0301530P.
 PR
 XX 28-JUN-2001; 2001US-0301550P.
 PR
 XX 03-JUL-2001; 2001US-0302951P.
 PR
 XX 12-SEP-2001; 2001US-0318771P.
 PR
 XX 25-SEP-2001; 2001US-0324687P.
 PR
 XX 24-OCT-2001; 2001US-0339266P.
 PR
 XX 16-NOV-2001; 2001US-0337524P.
 PR
 XX 14-DEC-2001; 2001US-0341143P.
 PR
 XX 21-FEB-2002; 2002US-0358643P.
 PR
 XX 28-FEB-2002; 2002US-0359151P.
 PR
 XX 05-MAR-2002; 2002US-0361195P.
 PR
 XX 10-APR-2002; 2002US-0361964P.
 PR
 XX 10-APR-2002; 2002US-0371346P.
 PR
 XX 03-JUN-2002; 2002US-0371523P.
 XX
 XX 03-JUN-2002; 2002US-00161493.
 PA
 XX (CURA-) CURAGEN CORP.
 XX
 XX Anderson DW, Zerhusen BD, Li L, Zhong M, Casman SJ, Gerlach VL;
 PI Shinkets RA, Gorman L, Pena CEA, Kekuda R, Patturajan M, Szytek KA;
 PI Leite MW, Rastelli L, Macdougall JR, Taupier RJ, Guo X, Miller CE;
 PI Shenoy SG, Hjalt T, Voss EZ, Boldog FL, Malyankar UM, Padigaru M;
 PI Ji W, Smithson G, Edinger SR, Millet I, Ellerman K;
 XX
 DR WPI; 2003-140607/13.
 XX
 XX New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
 PT obesity, cancer, Parkinson's disease, infections, immune disorders, or
 PT various dyslipidemias.
 XX
 PS Example C; Page 286; 461pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising any of the 36
 CC 86-1370 residue amino acid sequences, given in the specification, a
 CC mature form of them, or a sequence that is at least 95 % identical to, or
 CC having one or more conservative amino acid substitutions in one of the 36
 CC amino acid sequences. The polypeptides, nucleic acid molecules and
 CC antibodies of the invention are useful in the manufacture of a medicament
 CC for treating a syndrome associated with a human disease, preferably a
 CC NOVX-associated disorder. The nucleic acid molecules, polypeptides and

Tue Sep 28 08:41:40 2004

CC antibodies are useful for treating, preventing or diagnosing diseases
 CC such as metabolic disorders, diabetes, obesity, infectious diseases
 CC (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer-
 CC associated cachexia, neurodegenerative disorders, Alzheimer's disease,
 CC Parkinson's disease, immune disorders, haematopoietic disorders, cancer
 CC and various dyslipidaemias, or metabolic disturbances associated with
 CC obesity, metabolic X syndrome, and wasting disorders. The nucleic acids
 CC and polypeptides may also be used as targets for the identification of
 CC small molecules that modulate or inhibit e.g. neurogenesis, cell
 CC differentiation, cell proliferation, haematopoiesis, wound healing and
 CC angiogenesis. In gene therapy, in generation of antibodies that bind
 CC immunospecifically to NOX substances for use in therapeutic or
 CC diagnostic methods. The nucleic acids are further used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine, and
 CC pharmacogenomics. This polynucleotide represents a NOX related reverse
 CC PCR primer of the invention
 XX
 SQ Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1221 ATCATGATGGGGCATA 1238
 ||||| ||||| ||||| |||||
 Db 3 ATCAGGACATGGGGCATA 20
 RESULT 318
 AAD55467
 ID AAD55467 standard; DNA; 20 BP.
 AC AAD55467;
 XX
 DT 07-AUG-2003 (first entry)
 XX
 DE Human FGFR-3 antisense oligonucleotide, ISIS #125171.
 XX
 KW Human; antisense; fibroblast growth factor receptor 3; prophylaxis;
 KW developmental disorder; hyperproliferative disorder; antisense therapy;
 KW FGFR-3; ACH; JTK4; CEK2; cancer; phosphorothioate; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone; All cytidine residues
 FT are 5-methylcytidines"
 FT 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 XX
 FN WO2003023004-A2.
 XX
 PD 20-MAR-2003.
 XX
 PF 06-SEP-2002; 2002WO-US028549.
 XX
 PR 10-SEP-2001; 2001US-00953047.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Wyatt JR;
 XX
 XX WPI; 2003-313244/30.

XX Novel compound targeted to a nucleic acid molecule encoding fibroblast
 PT growth factor receptor 3, useful for inhibiting the expression of the
 PT receptor and for treating an animal having cancer or developmental
 PT disorder.
 XX
 PS Claim 3; Page 79; 120pp; English.
 XX
 CC The invention relates to antisense compounds targetted to a nucleic acid
 CC molecule encoding fibroblast growth factor (FGF) receptor 3 (also known
 CC as FGFR-3, ACH, JTK4 and CEK2) to inhibit its expression. Antisense
 CC compounds of the invention are useful for treating diseases or conditions
 CC associated with FGFR-3 such as developmental disorders or
 CC hyperproliferative disorders, especially cancer of colorectal, bladder,
 CC bone, lung, cervical, breast or skin. They are useful as research
 CC reagents, therapeutics, prophylaxis, kits and diagnostics, and as tools
 CC in differential and/or combinatorial analyses to elucidate expression
 CC patterns of a portion of the genes expressed within cells and tissues.
 CC They are also useful in antisense therapy. The present sequence is an
 CC antisense oligonucleotide targetted to human FGFR-3
 XX
 SQ Sequence 20 BP; 3 A; 4 C; 5 G; 8 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2084 CAGATGATCTCTTTTGGG 2101
 ||||| ||||| ||||| |||||
 Db 2 CAGATGATCTCTTTTGGG 19
 RESULT 319
 AAL61748
 ID AAL61748 standard; DNA; 20 BP.
 AC AAL61748;
 XX
 DT 22-SEP-2003 (first entry)
 XX
 DE Human PCTAIRE protein kinase 1 antisense oligo, ISIS 204185.
 XX
 KW Human; PCTAIRE protein kinase 1; PCTAIRE-1; sideroblastic anaemia;
 KW hyperproliferative disease; neurological disease; thrombocytopaenia;
 KW retinitis pigmentosa; X-linked Charcot-Marie-Tooth disease; therapy;
 KW mental retardation; Wiskott-Aldrich syndrome; dystonia; Parkinsonism;
 KW PTK1; crk5; incontinentia pigmenti; phosphorothioate backbone;
 KW antisense; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone; All cytidines are 5-
 FT methylcytidines"
 FT 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotides"
 FT 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl nucleotides"
 XX
 FN WO2003049691-A2.
 XX
 PD 19-JUN-2003.
 XX
 PF 06-DEC-2002; 2002WO-US039138.
 XX
 XX

PI Baker BF, Cowser LM;
 XX WPI; 2003-393515/37.
 XX
 XX New compounds, particularly antisense oligonucleotides targeted to a
 PT nucleic acid encoding matrix metalloproteinase 1 (MMP1), useful for
 PT treating a disease/condition associated with MMP1, such as
 PT hyperproliferative disorder.
 XX
 XX Claim 3; Page 75; 99pp; English.
 XX
 XX The invention relates to antisense compounds, compositions and methods
 CC used for modulating the expression of matrix metalloproteinase 1 (MMP1).
 CC Specifically claimed, are antisense oligonucleotides capable of
 CC modulating the expression of MMP1, and which comprise any of the 55
 CC sequences of 20 bp, fully defined in the specification. The compound,
 CC composition and methods are useful for treating a disease or condition
 CC associated with MMP1, such as hyperproliferative disorder, e.g. cancer,
 CC inflammatory disorder or atherosclerosis, by inhibiting the expression of
 CC MMP1. They are also useful in research and diagnostics for modulating the
 CC expression of MMP1. The antisense compounds can act as MMP1 inhibitors
 CC and have the following activities: cytostatic, antiinflammatory, and
 CC antiarteriosclerotic. This polynucleotide sequence represents one of the
 CC antisense compounds used for modulating the expression of matrix
 CC metalloproteinase 1 of the invention.
 XX
 XX Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2673 AGAGAGCAGCTTCAGTGA 2690
 Db 18 AGAGAGCAGCTTCAGTGA 1
 RESULT 322
 ADD21522/C
 ID ADD21522 standard; DNA; 20 BP.
 XX
 XX ADD21522;
 AC
 DT 15-JAN-2004 (first entry)
 XX
 XX Human mdm2 antisense oligonucleotide #85.
 DE
 KW antisense oligonucleotide; human; mdm2; hyperproliferation;
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;
 KW atherosclerosis; restenosis; apoptosis modulation; p21; ss;
 KW 2'-methoxyethoxy-residue; phosphorothioate backbone.
 XX
 XX Homo sapiens.
 OS
 XX WO2003048315-A2.
 PN
 XX 12-JUN-2003.
 PD
 XX 02-DEC-2002; 2002WO-US038281.
 PF
 XX 04-DEC-2001; 2001US-00005344.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Miraglia LJ, Nero PS, Graham MJ, Monia BP, Koller E, Chiang MY;
 PI Manoharan M;
 XX
 XX WPI; 2003-577263/54.
 DR
 XX Novel antisense compound targeted to 5' untranslated region, coding
 PT region, or intron:exon junction of nucleic acid molecule encoding mdm2,
 PT useful for treating e.g. cancer, psoriasis or restenosis by inhibiting
 PT mdm2 expression.
 PT

XX
 PS Example 9; SEQ ID NO 87; 289pp; English.
 XX
 CC The invention comprises antisense oligonucleotides which are targeted to
 CC the human mdm2 gene. The antisense oligonucleotides of the invention are
 CC useful for reducing hyperproliferation of human cells. The antisense
 CC oligonucleotides are also useful for treating: hyperproliferative
 CC disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or
 CC restenosis. The antisense oligonucleotides are also useful for modulating
 CC apoptosis, and for increasing expression of p21. The present DNA sequence
 CC represents a human mdm2 gene antisense oligonucleotide of the invention.
 CC The present sequence contains 2'-methoxyethoxy-residues and has a
 CC phosphorothioate backbone.
 XX
 XX Sequence 20 BP; 7 A; 3 C; 2 G; 8 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 2.3e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 799 GATTAAACCATTTATGCA 816
 Db 19 GACTAAACGATTATGCA 2
 RESULT 323
 AAD61223
 ID AAD61223 standard; DNA; 20 BP.
 XX
 XX AAD61223;
 AC
 DT 15-JAN-2004 (first entry)
 XX
 XX Human Ship-1 antisense oligonucleotide ISIS #168304.
 DE
 KW Human; Ship-1; SH2-containing phosphatidylinositol phosphatase-1; INPP5D;
 KW insensitivity to apoptotic signal; developmental disorder; inflammation;
 KW immunosuppressive; autoimmune disorder; antisense therapy; antisense;
 KW phosphorothioate backbone; ss.
 XX
 XX Homo sapiens.
 OS
 XX Synthetic.
 OS
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone; All cytidines are 5-
 FT methyl cytidines"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl (2'-MOE) nucleotides"
 XX
 XX US2003114401-A1.
 PN
 XX 19-JUN-2003.
 PD
 XX 06-DEC-2001; 2001US-00003919.
 PF
 XX 06-DEC-2001; 2001US-00003919.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Bennett CF, Freier SM;
 PI WPI; 2003-801302/75.
 XX
 XX Antisense compounds targeted to nucleic acid molecule encoding Ship-1,
 DR
 PT

PT useful for treating diseases associated with expression of Ship-1, such
 XX as autoimmune and developmental disorders.

PS Claim 3; Page 25; Opp; English.

XX The present invention provides antisense compounds targetted to nucleic
 CC acid molecule encoding Ship-1 (also known as SH2-containing
 CC phosphatidylinositol phosphatase-1 and INPP5D) to modulate/inhibit the
 CC expression of Ship-1. The invention is useful in treatment of diseases
 CC such as insensitivity to apoptotic signals, autoimmune disorders,
 CC developmental disorders and inflammatory disorders. The present sequence
 CC is human Ship-1 antisense oligonucleotide

XX Sequence 20 BP; 6 A; 6 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 2.3e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 953 CCCCTTGGACAGAAACCA 970

DB 2 CCCCTTGGACAGAAACCA 19

RESULT 324

ADD81530/c

ID ADD81530 standard; DNA; 20 BP.

XX AC ADD81530;

XX DT 29-JAN-2004 (first entry)

XX DE HIV PRT antisense derived probe #459.

XX ss; oligonucleotide hybridisation potential; efficient hybridisation;
 KW large array; minimum oligonucleotide synthesis; probe.

XX OS Human immunodeficiency virus.

XX PN US2003054346-A1.

XX PD 20-MAR-2003.

XX PF 15-FEB-2001; 2001US-00784674.

XX PR 10-FEB-1998; 98US-00021701.

XX (SHAN/) SHANNON K W.

XX (WOLB/) WOLBER P K.

XX (DELE/) DELENSTARR G C.

XX (WEBB/) WEBB P G.

XX (KINC/) KINCAID R H.

XX Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;

XX WPI; 2003-743746/70.

XX Predicting potential of oligonucleotides to hybridize to target
 PT nucleotide sequence comprises determining and evaluating for each
 PT oligonucleotide a parameter predictive of the oligonucleotides ability to
 PT hybridize with target.

XX Example 2; SEQ ID NO 603; 423bp; English.

XX The invention relates to a method of predicting the potential of
 CC oligonucleotides to hybridise to target nucleotide sequences. The method
 CC is useful for predicting the potential of an oligonucleotide to hybridise
 CC to a target nucleotide sequence, e.g. RNA or DNA or a sequence that
 CC contains chemically modified nucleotides. The method is also useful for
 CC predicting the potential of the oligonucleotides to hybridise to a
 CC complementary target nucleotide sequence. The method is useful to predict
 CC efficient hybridisation oligonucleotides for each of multiple target
 CC sequences therefore very large arrays may be constructed and tested with

CC minimum synthesis of oligonucleotides. The present sequence represents a
 CC HIV PRT antisense derived probe.

XX Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

Query Match

Best Local Similarity 0.4%; Score 14.8; DB 1; Length 20;

Matches 16; Conservative 88.9%; Pred. No. 2.3e+02;

0; Mismatches 2; Indels 0; Gaps 0;

QY 1073 ACTCAAGGATTCTGGGAA 1090

DB 18 ACTCAAGGATTCTGGGAA 1

RESULT 325

ADD81529/c

ID ADD81529 standard; DNA; 20 BP.

XX AC ADD81529;

XX DT 29-JAN-2004 (first entry)

XX DE HIV PRT antisense derived probe #458.

XX ss; oligonucleotide hybridisation potential; efficient hybridisation;
 KW large array; minimum oligonucleotide synthesis; probe.

XX OS Human immunodeficiency virus.

XX PN US2003054346-A1.

XX PD 20-MAR-2003.

XX PF 15-FEB-2001; 2001US-00784674.

XX PR 10-FEB-1998; 98US-00021701.

XX (SHAN/) SHANNON K W.

XX (WOLB/) WOLBER P K.

XX (DELE/) DELENSTARR G C.

XX (WEBB/) WEBB P G.

XX (KINC/) KINCAID R H.

XX Shannon KW, Wolber PK, Delenstarr GC, Webb PG, Kincaid RH;

XX WPI; 2003-743746/70.

XX Predicting potential of oligonucleotides to hybridize to target
 PT nucleotide sequence comprises determining and evaluating for each
 PT oligonucleotide a parameter predictive of the oligonucleotides ability to
 PT hybridize with target.

XX Example 2; SEQ ID NO 602; 423bp; English.

XX The invention relates to a method of predicting the potential of
 CC oligonucleotides to hybridise to target nucleotide sequences. The method
 CC is useful for predicting the potential of an oligonucleotide to hybridise
 CC to a target nucleotide sequence, e.g. RNA or DNA or a sequence that
 CC contains chemically modified nucleotides. The method is also useful for
 CC predicting the potential of the oligonucleotides to hybridise to a
 CC complementary target nucleotide sequence. The method is useful to predict
 CC efficient hybridisation oligonucleotides for each of multiple target
 CC sequences therefore very large arrays may be constructed and tested with
 CC minimum synthesis of oligonucleotides. The present sequence represents a
 CC HIV PRT antisense derived probe.

XX Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

Query Match

Best Local Similarity 0.4%; Score 14.8; DB 1; Length 20;

Matches 16; Conservative 88.9%; Pred. No. 2.3e+02;

0; Mismatches 2; Indels 0; Gaps 0;

QY 1073 ACTCAAGGATTCTGGGAA 1090


```

RESULT 328
AAT77685/C
ID AAT77685 standard; DNA; 21 BP.
XX
XX AAT77685;
AC
XX
XX 15-SEP-1997 (first entry)
DT
XX
DE Wheat microsatellite WMS247 left primer.
XX
XX Microsatellite marker; hypervariable genomic fragment; Triticum aestivum;
KW wheat; Triticeae; sequence tagged site; STS; primer; PCR; amplify;
KW polymorphism; genetic analysis; hexaploid; tetraploid; mapping; ss.
XX
XX Synthetic.
OS
XX DE19525284-A1.
PN
XX
XX 02-JAN-1997.
PD
XX
XX 28-JUN-1995; 95DE-01025284.
PF
XX
XX 28-JUN-1995; 95DE-01025284.
PR
XX
XX (PFLA-) INST PFLANZENGENETIK & KULTURPFLANZENFOR.
PA
XX
XX Roeder M, Plaschke J, Ganai M;
PI
XX WPI; 1997-053731/06.
XX
XX Primers for STS microsatellite markers for wheat and related species -
PT useful for genetic mapping, analysis and labelling etc. of wheat.
XX
XX Claim 5; Page 8; 8pp; German.
XX
XX Microsatellite markers based on hypervariable genomic fragments, from
CC Triticum aestivum (wheat) or the tribe Triticeae, consist of a sequence
CC tagged site (STS), defined by 2 specific primers (of mean size 17-23
CC bases) that flank a microsatellite sequence at both ends, which can be
CC amplified to polymorphisms (PCR products of different sizes). The
CC microsatellites are n-fold tandem repeats (n = 10 or more) of di-, tri-
CC or tetra-nucleotide sequences, combination microsatellite sequences or an
CC imperfect sequence in which individual bases are mutated. The
CC microsatellite markers can be used for genetic analysis of hexaploid and
CC tetraploid forms of wheat and for genetic mapping or labelling of
CC monogenic and polygenic properties, and for their selection; for
CC analysing relationships and identifying varieties; and for evaluating
CC varietal purity, hybrid identification and plant growth. The markers can
CC differentiate between almost all European wheat lines and show a higher
CC degree of DNA polymorphism than known probes for the wheat genome. They
CC can be detected by PCR, so large numbers of samples can be analysed
CC easily (e.g. several hundred per day). Microsatellite marker-related
CC polymorphisms are stably inherited so can also serve as genetic markers.
CC AAT77003-22 and AAT77535-716 are primer pairs that define the
CC microsatellite markers. WMS247 has a GA type repeat
XX
XX Sequence 21 BP; 4 A; 6 C; 3 G; 8 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2633 TGTTCAGAAAAAATTG 2650
DB 19 TGGTCAGAAAAAAGATTG 2

RESULT 329
AAX09125
ID AAX09125 standard; DNA; 21 BP.
XX
XX AAX09125;
AC
XX
XX 24-MAR-1999 (first entry)
DT
XX
XX Human biallelic polymorphic marker upstream primer #5.
DE
XX
XX Polymorphism: biallelic; human; forensic; paternity testing; disease;
KW detection; phenotypic typing; characteristic; infection; hereditary;
KW autoimmune disease; cancer; inflammation; drug; therapy; medicament;
XX treatment; marker; primer; ss.
XX
XX Synthetic.
OS
XX WO9820165-A2.
PN
XX
XX 14-MAY-1998.
PD
XX
XX 05-NOV-1997; 97WO-US020313.
PF
XX
XX 06-NOV-1996; 96US-0030455P.
PR
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA
XX Lander ES, Wang D, Hudson T;
PI
XX WPI; 1998-286974/25.
XX
XX New isolated nucleic acid segments from the human genome - used for
PT determining polymorphic forms for use in e.g. forensics, paternity
XX testing or phenotypic typing for disease.
XX
XX Claim 15; Page 46; 310pp; English.
XX
XX AAX09121-X10268 are allele-specific oligonucleotide primers used in the
CC isolation of various biallelic polymorphic markers found in the human
CC genome (represented in AAX10269-X12937). These primers can be used in a
CC method for determining polymorphic forms in an individual for use in e.g.
CC forensics, paternity testing or for phenotypic typing for diseases such
CC as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial
CC hypercholesterolemia, polycystic kidney disease, hereditary
CC spherocytosis, von Willebrand's disease, tuberosus sclerosis, hereditary
CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,
CC autoimmune diseases, inflammation, cancer, diseases of the nervous
CC system, infection by pathogenic microorganisms, and characteristics such
CC as longevity, appearance (e.g. baldness, obesity), strength, speed,
CC endurance, fertility, and susceptibility or receptivity to particular
CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid
CC segments can also be used to produce medicaments for the treatment or
CC prophylaxis of such diseases
XX
XX Sequence 21 BP; 7 A; 2 C; 10 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3111 CAGGGAAACAGGTAGAGGA 3128
DB 3 CAGGGAGAGGTAGTGGGA 20

RESULT 330
AAX09125
ID AAX09125 standard; DNA; 21 BP.
XX
XX AAX09125;
AC
XX
XX 27-NOV-1998 (first entry)
DT
XX
XX Exon 2 of an ENAC subunit amplifying forward primer B-2.
XX

```

```

XX KW Epithelial sodium channel; ENaC; mutation; pathological condition;
KW ion transport; water retention; blood pressure; metabolic acidosis;
KW chronic respiratory disease; inflammation; human; PCR primer; ss.
XX
XX OS Synthetic.
OS Homo sapiens.
XX
XX PN WO9840516-A1.
XX
XX PD 17-SEP-1998.
XX
XX PF 11-MAR-1998; 98WO-US004681.
XX
XX PR 11-MAR-1997; 97US-0040171P.
XX
XX PA (UYUA ) UNIV YALE.
XX
XX PI Lifton RP, Chang SS, Rossier BC;
XX
XX DR WPI; 1998-506740/43.
XX
XX PT Determination of presence of mutation conferring pathological condition
PT mediated by altered ion transport - comprises analysing sample for
PT presence of mutation of potassium ion channel gene, ENaC, or in its
PT encoded protein.
XX
XX PS Example 1; Page 38; 56pp; English.
XX
XX CC Sequences shown in AAV57601 to AAV57686 represent primers used for the
CC PCR amplification of the exons of the different subunits of the human
CC epithelial sodium channel (ENaC) gene. This is used in the method of the
CC invention of determining the presence or absence of a mutation conferring
CC a pathological condition mediated by altered ion transport. The method
CC comprises analysing a nucleic acid sample, or protein sample, for the
CC presence of a mutation in the ENaC gene, or in its encoded protein. A
CC vector containing a nucleic acid encoding a human altered variant of the
CC ENaC protein can be used to transform host cells to produce an altered
CC variant of an ENaC protein. The protein can be used to identify agents
CC that effect ion transport. The agonists can be used to treat pathological
CC conditions resulting from abnormal ion transport, such as water
CC retention, increased blood pressure, chronic respiratory and metabolic
CC acidosis and inflammation
XX
XX SQ Sequence 21 BP; 3 A; 12 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2300 CCTCTAACCGCCCTCT 2317
Db 3 CCCCTAACCGCCCTCT 20

RESULT 331
AAZ26499
ID AAZ26499 standard; DNA; 21 BP.
XX
XX AC AAZ26499;
XX
XX DT 30-NOV-1999 (first entry)
XX
XX DE Human polymorphic region 688.
XX
XX KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9841648-A2.
XX
XX PD 24-SEP-1998.

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XX WO9841648-A2.
XX PN
XX 24-SEP-1998.
XX
XX PF 19-MAR-1998; 98WO-US005419.
XX
XX PR 20-MAR-1997; 97US-0041057P.
XX
XX PA (VARI-) VARIAGENICS INC.
XX
XX PI Housman D, Ledley FD, Stanton VP;
XX
XX DR WPI; 1998-521232/44.
XX
XX PT Identifying target genes for allele-specific drugs - used for diagnosis,
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT dysplastic lesions, endometriosis or graft versus host disease.
XX
XX PS Disclosure; Fig 7; 605pp; English.
XX
XX CC This invention describes a novel method for identifying an inhibitor
XX potentially useful for treatment of cancer, where the inhibitor is active
XX on a gene vital for cell growth or viability, and where the gene is
XX subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
XX used for preventing the development of cancer in a patient having a
XX precancerous condition, by administering to the patient a first allele
XX specific inhibitor (ASI) targeted to an allele of a first essential gene
XX present in cells of the precancerous condition, where the normal somatic
XX cells of the patient are heterozygous for the first gene, the inhibitor
XX is active on at least one but less than all allelic forms of the gene
XX present in a population and targets only one allelic form present in the
XX normal somatic cells, and the first gene. The products and methods can be
XX used in the diagnosis, prevention and treatment of LOH disorders, e.g.
XX cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
XX lesions, benign tumours, endometriosis, polycystic kidney disease, and
XX graft versus host disease. The method can also be used to remove
XX malignant cells from bone marrow transplants. AAZ25812-226825 represent
XX human polymorphic sites described in the method of the invention
XX
XX SQ Sequence 21 BP; 13 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3388 ACACCTCAAAAAAAAAA 3405
Db 4 ACCTTCAAAAAAAAAA 21

RESULT 332
AAZ26500
ID AAZ26500 standard; DNA; 21 BP.
XX
XX AC AAZ26500;
XX
XX DT 30-NOV-1999 (first entry)
XX
XX DE Human polymorphic region 689.
XX
XX KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9841648-A2.
XX
XX PD 24-SEP-1998.

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XX 19-MAR-1998; 98WO-US005419.
XX 20-MAR-1997; 97US-0041057P.
XX (VARI-) VARIAGENICS INC.
XX Houseman D, Ledley FD, Stanton VP;
XX WPI; 1998-521232/44.
XX Identifying target genes for allele-specific drugs - used for diagnosis,
XX prevention and treatment of, e.g. cancers, atherosclerotic plaque,
XX dysplastic lesions, endometriosis or graft versus host disease.
XX Disclosure; Fig 7; 605pp; English.
XX This invention describes a novel method for identifying an inhibitor
XX potentially useful for treatment of cancer, where the inhibitor is active
XX on a gene vital for cell growth or viability, and where the gene is
XX subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
XX used for preventing the development of cancer in a patient having a
XX precancerous condition, by administering to the patient a first allele
XX specific inhibitor (ASI) targeted to an allele of a first essential gene
XX present in cells of the precancerous condition, where the normal somatic
XX cells of the patient are heterozygous for the first gene, the inhibitor
XX is active on at least one but less than all allelic forms of the gene
XX present in a population and targets only one allelic form present in the
XX normal somatic cells, and the first gene. The products and methods can be
XX used in the diagnosis, prevention and treatment of LOH disorders, e.g.
XX cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
XX lesions, benign tumours, endometriosis, polycystic kidney disease, and
XX graft versus host disease. The method can also be used to remove
XX malignant cells from bone marrow transplants. AAZ25812-226825 represent
XX human polymorphic sites described in the method of the invention
XX
XX Sequence 21 BP; 15 A; 2 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3388 ACACACTCAAAAAA 3405
Db 2 ACTTCAAAAAA 19
RESULT 333
AAZ18494
ID AAZ18494 standard; DNA; 21 BP.
AC AAZ18494;
XX 19-OCT-1999 (first entry)
XX Polymorphic fragment in ASTH1J intronic region.
XX
XX ASTH1; asthma; human; chromosome 11p; ASTH1I; ASTH1J; genetic locus;
XX therapeutic; immunogen; polymorphism; ds.
XX Homo sapiens.
XX WO9937809-A1.
XX 29-JUL-1999.
XX
XX 21-JAN-1998; 98WO-US001260.
XX 21-JAN-1998; 98WO-US001260.
XX (AXYS-) AXYS PHARM INC.
XX Brooks-Wilson AR, Buckler A, Cardon L, Carey AH, Galvin M;

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PI Miller A, North M;
XX WPI; 1999-479058/40.
XX Mammalian asthma related genes, useful for diagnosis of a predisposition
XX to development of asthma.
XX Disclosure; Page 64; 195pp; English.
XX The invention identifies a genetic locus ASTH1, associated with asthma,
XX mapped to human chromosome 11p. ASTH1I and ASTH1J are genes present
XX within the locus, located close to each other on human chromosome 11p,
XX and have similar patterns of expression, and common sequence motifs. The
XX ASTH1 genes and fragments, encoded protein, genomic regulatory regions
XX and anti-ASTH1 antibodies are useful in the identification of individuals
XX predisposed to development of asthma, and for the modulation of gene
XX activity in vivo for prophylactic and therapeutic purposes. The ASTH1
XX protein is useful as an immunogen to raise specific antibodies, in drug
XX screening for compositions that mimic or modulate ASTH1 activity or
XX expression, including altered forms of ASTH1 protein, and as a
XX therapeutic. Sequences AAZ18366-218509 represent polymorphisms in the
XX ASTH1I and ASTH1J genes
XX
XX Sequence 21 BP; 9 A; 5 C; 3 G; 3 T; 0 U; 1 Other;
Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 3357 AAAGCAGACACTCAATAAAT 3376
Db 1 ACAGCAGGCAYTCAACAAAT 20
RESULT 334
AAZ75941/C
ID AAZ75941 standard; DNA; 21 BP.
XX AAZ75941;
XX 10-SEP-2001 (first entry)
XX Human biallelic marker downstream amplification primer SEQ ID NO:10297.
XX
XX Human genome; biallelic marker; high density disequilibrium map;
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX haplotyping; hybridisation; identification; characterisation;
XX amplification; single nucleotide polymorphism; SNP; PCR primer;
XX diagnosis; ss.
XX Homo sapiens.
XX WO9954500-A2.
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-IB0000822.
XX 21-APR-1998; 98US-0082614P.
XX 23-NOV-1998; 98US-0109732P.
XX (GEST ) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX WPI; 2000-013267/01.
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome.
XX Claim 9; Page 2426; 2745pp; English.
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
XX

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CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID Nos 2952, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention
 XX
 SQ Sequence 21 BP; 3 A; 4 C; 3 G; 11 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1961 GTCGAGGATAGCCTAAAA 1978
 Db 20 GTAAGGAAAGCCTAAAA 3

RESULT 335

AA80401
 ID AAA80401 standard; DNA; 21 BP.

XX
 AC AAA80401;

XX 22-NOV-2000 (first entry)

XX Human ASTH1J intron a polymorphic site, SEQ ID NO:144.

XX ASTH1 locus; ASTH1I; ASTH1J; human; chromosome 11p; asthma;
 KW bronchial hyperreactivity; ets family; transcription factor;
 KW splice variant; genetic predisposition; polymorphism; antibody;
 KW drug screening; prophylaxis; therapy; diagnosis;
 KW single nucleotide polymorphism; SNP; ss.

XX Homo sapiens.

XX US6087485-A.

XX 11-JUL-2000.

XX 21-JAN-1998; 98US-00009913.

XX 21-JAN-1997; 97US-0035663P.

XX 01-JUL-1997; 97US-0051432P.

XX (AXYS-) AXYS PHARM INC.

XX Galvin M, Miller A, North M, Cardon L, Buckler A;
 PI Brooks-Wilson AR, Carey AH;

XX WPI; 2000-505109/45.

XX New nucleic acids other than naturally occurring chromosomes encoding
 PT ASTH1 protein, for e.g. screening compositions that modulate expression
 PT or function of ASTH1 proteins or as diagnostics for genetic
 PT predisposition to asthma.

XX Example; Col 43-44; 131pp; English.

XX The invention relates to the ASTH1 locus on the short arm of human
 CC chromosome (11p). This locus comprises the ASTH1I and ASTH1J genes, which
 CC are associated with a genetic predisposition to asthma and bronchial
 CC hyperreactivity. The ASTH1I and ASTH1J genes are oriented in opposite
 CC directions with the ASTH1 locus, and have similar patterns of expression
 CC and common sequence motifs. They are both expressed in trachea, lung and

CC several other tissues. ASTH1I and ASTH1J are novel members of the ets
 CC family of transcription factors, which have been implicated in the
 CC activation of a variety of genes including the TCRA gene and cytokine
 CC genes known to be important in the aetiology of asthma. Both ASTH1I and
 CC ASTH1J mRNAs are alternatively spliced. Alternative splicing of
 CC transcripts has no effect on the open reading frame of ASTH1J, as the
 CC exons involved are all 5' to the start codon in exon b. In contrast,
 CC alternative splicing of ASTH1I transcripts results in 3 different ASTH1I
 CC isoforms. The invention also encompasses mouse asth1j protein. The ASTH1
 CC nucleic acids are useful as diagnostics to identify a hereditary
 CC predisposition to asthma, as probes for identifying ASTH1 related genes,
 CC for identifying expression of the gene in a biological specimen, and for
 CC generating genetically modified non-human animals or site specific gene
 CC modifications in cell lines. The encoded ASTH1 proteins are useful as
 CC immunogens to raise specific antibodies; in drug screening for
 CC compositions that mimic or modulate activity or expression of ASTH1
 CC and/or ASTH1J (including altered forms of these proteins); and as a
 CC therapeutic. The ASTH1 genes or fragments thereof, encoded proteins,
 CC ASTH1 genomic regulatory regions, and anti-ASTH1I and anti-ASTH1J
 CC antibodies are useful in the identification of individuals predisposed to
 CC development of asthma, and for modulation of gene activity in vivo for
 CC prophylactic and therapeutic purposes. The intact ASTH1I or ASTH1J
 CC proteins or active fragments thereof may be used to modulate or reduce
 CC bronchial hyperreactivity. Sequences AAA80260-A80261 and AAA80264-A80416
 CC represent polymorphic sites within the ASTH1J or ASTH1I genes
 XX
 SQ Sequence 21 BP; 9 A; 5 C; 3 G; 3 T; 0 U; 1 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 80.0%; Pred. No. 2.5e+02;
 Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3357 AAAGCAGACACTCAATAAAT 3376

Db 1 ACAGCAGGCAYTCAACAAT 20

RESULT 336

AAF60704

ID AAF60704 standard; DNA; 21 BP.

XX AAF60704;

XX 03-MAY-2001 (first entry)

XX Oligonucleotide #2.

XX Metal oxide support; probe-based assay; ss.

XX Unidentified.

XX WO200112846-A1.

XX 22-FEB-2001.

XX 09-AUG-2000; 2000WO-EP007736.

XX 16-AUG-1999; 99EP-00202649.

XX (PAMG-) PAMGENE BV.

XX Venema F;

XX WPI; 2001-226551/23.

XX Preparing metal oxide support loaded with biomolecules, useful in probe-
 based assays, comprises activating the support by a silylating agent
 PT comprising an amine group and attaching biomolecules to the activated
 PT surface.

XX Example; Page 10; 19pp; English.

XX The present invention relates to a method for preparing metal oxide

CC supports loaded with biomolecules. The method comprises activating the
 CC surface of the support with a silanating agent with an amine group and
 CC loading the support by attaching biomolecules to the activated surface.
 CC The loaded support is treated with an acidic solution provided that it is
 CC not used for preparing silica wafers which are aminated by silanation
 CC using (3-aminopropyl)monothoxymethylsilane and loaded with
 CC oligonucleotides. The metal oxide support is useful in performing a probe
 CC -based assay. Metal oxide supports are further useful for carrying
 CC biomolecules, e.g. for use as vaccines, and for separating other
 CC substances from mixtures by hybridising, binding or interacting otherwise
 CC with those other substances. The present sequence is an oligonucleotide
 CC used in the present invention

SQ Sequence 21 BP; 9 A; 2 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 480 TCTACAGTACTGGAAGAAG 497
 Db 2 TGTACAGAACTGGAAAAG 19

RESULT 337
 AAF60705/C
 ID AAF60705 standard; DNA; 21 BP.

XX AAF60705;
 XX
 XX 03-MAY-2001 (first entry)
 DT
 DE Oligonucleotide #3.
 XX

KW Metal oxide support; probe-based assay; ss.

OS Unidentified.

XX WO200112846-A1.

PN 22-FEB-2001.

PD 09-AUG-2000; 2000WO-BP007736.

PF 16-AUG-1999; 99EP-00202649.

PR (PAMG-) PAMGENE BV.

PA Venema F;

PI WPI; 2001-226551/23.

DR Preparing metal oxide support loaded with biomolecules, useful in probe-

XX based assays, comprises activating the support by a silanating agent
 PT comprising an amine group and attaching biomolecules to the activated
 PT surface.

PS Example; Page 10; 19pp; English.

XX The present invention relates to a method for preparing metal oxide
 CC supports loaded with biomolecules. The method comprises activating the
 CC surface of the support with a silanating agent with an amine group and
 CC loading the support by attaching biomolecules to the activated surface.
 CC The loaded support is treated with an acidic solution provided that it is
 CC not used for preparing silica wafers which are aminated by silanation
 CC using (3-aminopropyl)monothoxymethylsilane and loaded with
 CC oligonucleotides. The metal oxide support is useful in performing a probe
 CC -based assay. Metal oxide supports are further useful for carrying
 CC biomolecules, e.g. for use as vaccines, and for separating other
 CC substances from mixtures by hybridising, binding or interacting otherwise
 CC with those other substances. The present sequence is an oligonucleotide
 CC used in the present invention

SQ Sequence 21 BP; 4 A; 6 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 480 TCTACAGTACTGGAAGAAG 497
 Db 20 TGTACAGAACTGGAAAAG 3

RESULT 338
 AAF95858/C
 ID AAF95858 standard; DNA; 21 BP.

XX AAF95858;
 AC
 XX 06-JUN-2001 (first entry)
 DT

DE Human gene single nucleotide polymorphism #619.

XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
 KW polymorphism; vascular disease; coronary artery disease; forensics;
 KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
 KW pulmonary embolism; paternity test; ds.
 XX
 OS Homo sapiens.

XX
 XX Key Location/Qualifiers
 FH replace(11,G)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 FT
 XX

PN WO200118250-A2.

XX 15-MAR-2001.

XX 07-SEP-2000; 2000WO-US024503.

XX 10-SEP-1999; 99US-0153357P.

PR 26-JUL-2000; 2000US-0220947P.

PR 16-AUG-2000; 2000US-0225724P.

XX (WHEE) WHITEHEAD INST BIOMEDICAL RES.

PA (WHEE-) MILLENNIUM PHARM INC.

XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JU;

PI WPI; 2001-226749/23.

XX Nucleic acids comprising single nucleotide polymorphisms, useful in
 PT applications such as forensics, paternity testing, medicine, genetic
 PT analysis and phenotype correlations to diseases such as diabetes and
 PT atherosclerosis.

XX Example; Page 91; 242pp; English.

XX The present invention provides a method of diagnosing a vascular disease
 CC in an individual, involving determining the sequence at various
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
 CC genes. The sequences at a number of polymorphic sites are also provided
 CC in the specification. In particular, the method can be used in the
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
 CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
 CC useful in forensics, paternity testing, genetic analysis and phenotype
 CC correlations to diseases. The present sequence is an example of one of
 CC the human gene SNPs shown in the specification

SQ Sequence 21 BP; 7 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 2.5e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 78 GATGTGATCTGGCTCAC 95
 ||||| } |||||
 Db 20 GATGTGGTGTGGCTCAC 3

RESULT 339

ABAO3024
 ID ABA03024 standard; DNA; 21 BP.

XX AC ABA03024;

XX DT 04-FEB-2002 (first entry)

XX DE PCR primer Gus antisense.

XX KW PCR primer; cell death; toxic gene; tumour suppressor; ss.

XX OS Synthetic.

XX PN WO200172995-A2.

XX PD 04-OCT-2001.

XX PF 28-MAR-2001; 2001WO-US009953.

XX PR 28-MAR-2000; 2000US-0192586P.

XX PR 10-MAY-2000; 2000US-0203343P.

XX PR 23-JAN-2001; 2001US-0263226P.

XX PR 27-FEB-2001; 2001US-0271426P.

XX PA (UVRP) UNIV ROCHESTER.

XX PI Zauderer M, Smith ES;

XX DR WPI; 2001-570897/64.

XX PT Selecting target polynucleotides, particularly toxic genes, involves

XX PT introducing a library of insert polynucleotides into a host cell

XX PT population, where the target polynucleotide promotes cell death.

XX PS Example 19; Page 235; 359pp; English.

XX CC The present invention relates to a method for selecting a target

XX CC polynucleotide. The method comprises introducing into a host cell

XX CC a population a library of insert polynucleotides, where expression of the

XX CC target polynucleotide directly or indirectly promotes host cell death.

XX CC The cells are cultured and the insert polynucleotides are collected from

XX CC the cells which die. The method is useful for selecting target

XX CC polynucleotides, particularly polynucleotides which alter cell phenotypes

XX CC of induce or inhibit cell death. The method can be used to isolate toxic

XX CC genes such as tumour suppressors. The present sequence is a PCR primer,

XX CC which was used in an example from the present invention

XX SQ Sequence 21 BP; 1 A; 7 C; 4 G; 9 T; 0 U; 0 Other;

Query Match

Best Local Similarity 0.4%; Score 14.8; DB 1; Length 21;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 878 ATTGGATGCTCCCTGCT 895
 ||||| } |||||
 Db 3 ATTGGTGGCTCCCTGCT 20

RESULT 340

AAH62233/c

ID AAH62233 standard; DNA; 21 BP.

XX AC AAH62233;

XX DT 12-SEP-2001 (first entry)

XX

DE

XX

KW

KW

XX

OS

XX

PH

FT

FT

XX

XX

PN

XX

XX

PD

XX

XX

PF

XX

XX

PR

XX

XX

PA

XX

PI

XX

XX

DR

XX

XX

PT

XX

PT

XX

PT

XX

XX

PS

XX

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

Zinc finger protein KUP polymorphism containing DNA fragment #134.

Single nucleotide polymorphism; SNP; human; cancer; inflammation;
 heart disease; paternity testing; forensic science; ds.

Homo sapiens.

Key Location/Qualifiers

Variation replace(11,A)

FT /*tag= a

FT /standard_name= "single nucleotide polymorphism"

XX WO200138576-A2.

XX 31-MAY-2001.

XX 17-NOV-2000; 2000WO-US031639.

XX 24-NOV-1999; 99US-0167334P.

XX (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX Cargill M, Ireland JS, Lander ES;

XX WPI; 2001-367705/38.

New nucleic acid segments of the human genome, particularly from genes
 including polymorphic sites, for phenotype correlation, forensics,
 paternity testing, medicine and genetic analysis.

Claim 1; Page 40; 80pp; English.

DNA sequences AAH62100 - AAH62688 represent segments of human genes which
 contain single nucleotide polymorphisms (SNPs). A method is included in
 the invention for analysing a nucleic acid sample, which consists of
 determining the base occupying any one of the polymorphic sites given in
 the SNP containing sequences. The nucleotide sequences can be used in the
 diagnosis or monitoring of diseases, such as cancer, inflammation, heart
 diseases, diseases of the cardiovascular system, and infection by
 microorganisms. The oligonucleotides are also useful in the manufacture
 of a medicament for the treatment or prophylaxis of the diseases, and as
 a pharmaceutical. SNP containing oligonucleotides are useful in
 applications such as phenotype correlation, forensics, paternity testing,
 medicine and genetic analysis

Sequence 21 BP; 10 A; 3 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 2.5e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2687 TTGACATTGCTTTCAGTA 2704

||||| } |||||

Db 19 TTGACACTGTTTCAGTA 2

RESULT 341

AAH27174/c

ID AAH27174 standard; DNA; 21 BP.

XX AAH27174;

XX AC

XX DT 08-AUG-2001 (first entry)

XX DE Drug-resistance gene related PCR primer R4.

XX KW Drug-resistance; succinate dehydrogenase Ip subunit; fungus; PCR primer;

XX KW ss.

XX OS Unidentified.

XX JP2001069987-A.

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XX PD 21-MAR-2001.
XX PF 03-SEP-1999; 99JP-00250692.
XX PR 03-SEP-1999; 99JP-00250692.
XX PA (KANS-) KANSAI TLO KK.
XX DR WPI; 2001-297393/31.
XX PT A drug-resistant gene.
XX PS Disclosure; Page 10; 17pp; Japanese.
XX CC This invention relates to a drug resistance gene derived from a fungus
XX CC forming fruit body. Included in the invention are a vector containing the
XX CC drug-resistance gene, and a fungus forming fruit body into which the
XX CC vector is introduced. The vector can be used for improving grades of
XX CC fungi. The present sequence represents PCR primer used in the course of
XX CC the invention for the identification of the drug resistance gene
XX CC
XX CC Sequence 21 BP; 6 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
XX CC
Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2363 GTGGTTGGCATTGTCATC 2380
DB 21 GTCGTTGGCAGTGTATC 4
RESULT 342
AAH62012/c
ID AAH62012 standard; DNA; 21 BP.
XX AC AAH62012;
XX DT 10-SEP-2001 (first entry)
XX DE IL6 hairpin/hammerhead ribozyme recognition site SEQ ID NO:4436.
XX KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
XX KW recognition site; target; ribozyme binding site; eye disease; vulnery;
XX KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
XX KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
XX KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
XX KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
XX KW antiscaling; ophthalmological; keratolytic; gene therapy; viral wart;
XX KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
XX KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
XX KW sickle cell retinopathy; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200130362-A2.
XX PD 03-MAY-2001.
XX PF 26-OCT-2000; 2000WO-US029500.
XX PR 26-OCT-1999; 99US-0161532P.
XX PA (IMMU-) IMMUSOL INC.
XX PI Robbins JM, Tritz R;
XX DR WPI; 2001-300427/31.
XX PT Treating proliferative skin or eye diseases and scarring, using ribozymes
XX PT that cleave RNA encoding cytokines involved in inflammation, matrix
XX PT

PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX Example 1; Page 22; 408pp; English.
XX The present invention describes a method for treating a proliferative
XX CC skin or eye disease and scarring. The method involves administering a
XX CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
XX CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
XX CC dependent kinase, growth factor or a reductase, or administering a
XX CC nucleic acid molecule (II) comprising a promoter operably linked to a
XX CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
XX CC dermatological, cytostatic, antiseborrheic, antidiabetic, antiscaling,
XX CC ophthalmological, vulnery, keratolytic and virucide activities, and
XX CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
XX CC in gene therapy. (I) and (II) are useful for treating proliferative skin
XX CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
XX CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
XX CC also be used for treating proliferative eye diseases such as diabetic
XX CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
XX CC prematurity and retinal detachment, and for treating and preventing
XX CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
XX CC scar. AAH57577 to AAH62099 represent sequences used in the
XX CC exemplification of the present invention
XX CC
XX CC Sequence 21 BP; 3 A; 4 C; 5 G; 9 T; 0 U; 0 Other;
XX CC
Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1504 AATCCCAAGACAGTG 1521
DB 21 AACTCCAAAGACAGTG 4
RESULT 343
AAF89051/c
ID AAF89051 standard; DNA; 21 BP.
XX AC AAF89051;
XX DT 06-JUL-2001 (first entry)
XX DE GC box assay FATP5 sequence SEQ ID NO: 112.
XX KW Fatty acid transport protein; FATP; human; mouse; rat; rice blast fungus;
XX KW yeast; fat absorption; obesity; diabetes; heart disease; hyperlipidaemia;
XX KW weight control; tuberculosis; TB; anti-fungal; ds.
XX OS Unidentified.
XX PN WO200121795-A2.
XX PD 29-MAR-2001.
XX PF 21-SEP-2000; 2000WO-US025891.
XX PR 23-SEP-1999; 99US-00405504.
XX PR 23-SEP-1999; 99US-00405505.
XX PR 16-DEC-1999; 99US-00465280.
XX PR 17-FEB-2000; 2000US-00506252.
XX PR 06-JUL-2000; 2000US-00611197.
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Stahl A, Hirsch DJ, Lodish HF, Gimeno RE, Tartaglia LA;
XX DR WPI; 2001-354783/37.
XX PT New fatty acid transport proteins (FATPs) useful for the manufacture of
XX PT medicament for treating obesity, diabetes and heart disease.

```

PS Disclosure; Fig 104; 287pp; English.

XX The present invention provides the protein and coding sequences of fatty acid transport proteins (FATPs) from a number of species, including FATP1, FATP2, FATP3, FATP4, FATP5 and FATP6 from the human, FATP1-FATP5 from the mouse, FATP4 and b from *C. elegans*, and FATP from *Aspergillus nidulans*, *Drosophila*, zebrafish, *Magnaporthe grisea*, *Mycobacterium tuberculosis* and *Cochliobolus heterostrophus*. The FATP from *M. tuberculosis* can be used to identify inhibitors which can then be used to treat TB. That from *M. grisea* (also known as rice blast fungus) can be used to develop anti-fungal agents capable of preventing infection of rice. Those from the human can be used to develop treatments for diabetes, heart disease, obesity, hyperlipidaemia and weight control. The present sequence is one of the sequences described in the exemplification of the invention

XX Sequence 21 BP; 2 A; 12 C; 4 G; 3 T; 0 U; 0 Other;

XX Query Match 0.4%; Score 14.8; DB 1; Length 21;

XX Best Local Similarity 88.9%; Pred. No. 2.5e+02;

XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1559 GGGGTGTCGGAACCTGTG 1576

DB 18 GGGCGGGGGAACCTGTG 1

RESULT 344

ABS97282

ID ABS97282 standard; DNA; 21 BP.

XX ABS97282;

XX 23-DEC-2002 (first entry)

XX Human aryl hydrocarbon receptor B1 (AHR) polymorphic sequence #16.

XX Human; BS; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; PCR; cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF; adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR1I2; aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS; cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological; epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP; glutathione-S-transferase 12; GSTI2; histamine-N-methyl transferase; HMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT; NADPH quinone oxidoreductase 2; NQO2; sulfoxidoreductase 2B7; STM; UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7; UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA; multidrug resistance 1; lactotransferrin; orphan nuclear receptor; multidrug resistance associated protein 3; cancer; prostate; acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5; altered drug metabolism; cardiovascular function; colorectal tumour; central nervous system; pulmonary; immunological.

XX Homo sapiens.

XX WO200257410-A2.

XX 25-JUL-2002.

XX 28-NOV-2001; 2001WO-US044838.

XX 28-NOV-2000; 2000US-00724389.

XX (DNAS-) DNA SCI LAB INC.

XX Guida M, Hall J;

XX WPI; 2002-698522/75.

XX Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for

PT disorder-related traits.

XX Example 5; Page 107; 714pp; English.

XX This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2), cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1), aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating protein (FLAP), glutathione-S-transferase 12 (GSTI2), histamine-N-methyl transferase (NNMT), (kallikrein 2) KLK2, nicotinamide-N-methyl transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2), sulfoxidoreductase 2B4 (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1 (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3 (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence. The polymorphisms in the human genes cited in the invention are useful as genetic linkage markers for locating and characterizing the genes that are responsible for specific traits within the genome and eventually identifying the genes responsible for a variety of disorder-related traits as a result of their e.g., overexpression, constitutive expression, mutation or underexpression, which may be used in diagnosing and/or treating the disorders. The nucleic acid molecules comprising the polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502E1, AHR, EPHX2, GSTI2, NNMT, NQO2, STM, UGT2B4, UGT2B7, UGT2B15, AHR, MDR1 and/or MDR3 are useful for screening individuals for altered drug metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2, AHR, MDR1 and/or MDR3 may also be used to screen individuals for susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are used to screen for altered cardiovascular function, in COX2 for altered susceptibility to colorectal tumours, in DBI or CHMR1 for altered central nervous system function, in FLAP and NNMT for altered pulmonary, immunological or haematological function, in KLK2 for altered serine protease activity in the prostate, in LTF for altered immunological or haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and peripheral nervous system function. The present sequence represents a PCR primer used to amplify the sequences of the invention

XX Sequence 21 BP; 6 A; 1 C; 2 G; 12 T; 0 U; 0 Other;

XX Query Match 0.4%; Score 14.8; DB 1; Length 21;

XX Best Local Similarity 88.9%; Pred. No. 2.5e+02;

XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2550 ATTTTGTGTGATGTAAT 2567

DB 2 ATTTTATTGATGTACAT 19

RESULT 345

ABT04600/C

ID ABT04600 standard; DNA; 21 BP.

XX ABT04600;

XX 25-SEP-2002 (first entry)

XX Human PTGS1 gene probe SEQ ID NO: 66.

XX Human; drug metabolism; enzyme; probe; ss.

XX Homo sapiens.

XX JP2002142780-A.

XX 21-MAY-2002.

XX 28-AUG-2001; 2001JP-00257338.


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PR 04-SEP-2000; 2000JP-00267163.
XX (SAKA ) OTSUKA SEIYAKU KOGYO KK.
XX WPI; 2002-552472/59.
XX Measurement of an enzyme participating to the first phase reaction of
PT drug metabolism, a probe and a kit for it.
XX Claim 8; Page 24; 36pp; Japanese.
XX The present invention relates to probes which can be used for the
CC measurement of an enzyme. The probes can be used for the measurement of
CC an enzyme participating to the first phase reaction of drug metabolism.
CC The present sequence is a probe shown in the invention
XX
SQ Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
      Query Match      0.4%; Score 14.8; DB 1; Length 21;
      Best Local Similarity 88.9%; Pred. No. 2.5e+02;
      Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 380 GTCAAGCTTCAGCTGCAG 397
DB 18 GTCAAAATTCAGCTGCAG 1
      ||||| ||||| ||||| |||||
RESULT 346
ABS68816
ID ABS68816 standard; DNA; 21 BP.
AC ABS68816;
XX
XX 20-NOV-2002 (first entry)
XX PCR primer, #2, used to amplify E. coli gus A gene.
XX
XX Regulator; transcription; cell death; phenotype; molecular scaffold;
KW gene therapy; cancer; cardiovascular disease; arrhythmia; heart failure;
KW ischaemia; obesity; neurodegenerative disease; Alzheimer's disease;
KW bone pathology; dermatologic disease; psoriasis; infection; AIDS;
KW acquired immunodeficiency syndrome; cosmetic; wound healing; primer;
KW antibiotic transport; drug toxicity; drug resistance; immunobiology;
KW inflammation; allergic response; human immunodeficiency virus; ss; PCR.
XX
XX Escherichia coli.
OS
XX WO200262822-A2.
PN
XX 15-AUG-2002.
PD
XX 04-FEB-2002; 2002WO-US002814.
PF
XX 02-FEB-2001; 2001US-0265589P.
XX 05-FEB-2001; 2001US-0265880P.
PR 27-FEB-2001; 2001US-0271423P.
XX (UYRP ) UNIV ROCHESTER.
PA
XX Zauderer M, Smith ES;
PI
XX WPI; 2002-643398/69.
DR
XX Identifying regulator polypeptides which influence target transcriptional
PT regulatory regions, useful for treating cancer, comprises introducing
PT host cells expressing the polypeptide into a library of polynucleotides.
XX
XX Example 5; Page 112; 224pp; English.
PS
XX The invention discloses a method for identifying polynucleotides encoding
CC a regulator polypeptide, whose expression induces activation of a target
CC transcriptional regulatory region in a host cell. The method comprises
CC providing a population of eukaryotic host cells capable of expressing the

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CC polypeptide, introducing into the host cell a library of polynucleotides
CC encoding the polypeptides, permitting expression of the polypeptides and
CC then recovering them from the host cells. The target transcriptional
CC regulatory region is operably associated with a polynucleotide encoding a
CC gene product, the expression of which results in host cell death or cause
CC the host cells to exhibit a pre-determined modified phenotype and where
CC the gene product is expressed upon activation of target transcriptional
CC regulatory region. Each candidate regulator polypeptide comprises a
CC candidate peptide and a molecular scaffold fused to the peptide so that
CC the peptide is displayed on the surface of the candidate regulator
CC polypeptide. The methods are useful in selecting and/or screening
CC regulator molecules, such as polypeptides, which directly or indirectly
CC induce or suppress the transcriptional activation of a target
CC transcriptional regulatory region in a eukaryotic host cell. These
CC regulator molecules may be used (e.g. in gene therapy) for preventing or
CC treating cancers (e.g. breast or ovarian cancer), cardiovascular diseases
CC (e.g. arrhythmia, heart failure, ischaemia), obesity, neurodegenerative
CC diseases (e.g. Alzheimer's disease), bone pathologies, dermatologic
CC diseases (e.g. psoriasis), infections (e.g. viral, bacterial), acquired
CC immunodeficiency syndrome (AIDS), in cosmetic applications and in wound
CC healing. The method is also useful in screening regulator molecules that
CC block antibiotic transport mechanisms, in drug toxicities and drug
CC resistance applications and in improving the performance of existing or
CC developmental drugs. It may also be used in immunobiology, inflammation,
CC allergic response and in biotechnology applications. The sequences
CC presented in ABS68815-ABS68832 are the PCR primers used to amplify the
CC reporter genes and gene regions required in the creation of vectors to
CC express the regulator polypeptides
XX
XX Sequence 21 BP; 1 A; 7 C; 4 G; 9 T; 0 U; 0 Other;
      Query Match      0.4%; Score 14.8; DB 1; Length 21;
      Best Local Similarity 88.9%; Pred. No. 2.5e+02;
      Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 878 ATTGGATGCTCCCTGCT 895
DB 3 ATTGGTGGCTCCCTGCT 20
      ||||| ||||| ||||| |||||
RESULT 347
ABX17461
ID ABX17461 standard; DNA; 21 BP.
XX ABX17461;
AC
XX
XX 04-FEB-2003 (first entry)
XX
XX GUS reporter gene for MVA trimolecular recombination vector primer #2.
XX ss; PCR; antigen-specific immunoglobulin; Ig; early/late promoter;
KW heavy chain constant region; light chain constant region; primer;
KW variable region; camelised Ig heavy chain variable region.
XX
XX Escherichia coli.
OS
XX US2002123057-A1.
PN
XX 05-SEP-2002.
PD
XX 14-NOV-2001; 2001US-00987456.
PF
XX 17-NOV-2000; 2000US-0249268P.
PR 18-JAN-2001; 2001US-0262067P.
PR 27-FEB-2001; 2001US-0271424P.
PR 15-JUN-2001; 2001US-0298087P.
XX
XX (UYRP ) UNIV ROCHESTER.
PA
XX Zauderer M, Smith ES;
PI
XX WPI; 2003-066785/06.
DR
XX

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PT Selecting polynucleotides which encode antigen-specific immunoglobulin
PT molecules, by introducing the library of polynucleotides into the host
XX cells, and recovering the polynucleotides of the library for the antigen.
PS Example 9; Page 48; 108pp; English.
XX
CC The invention relates to selecting polynucleotides which encode antigen -
CC specific immunoglobulins (Ig) (or fragments) comprising introducing into
CC a population of host cells, a 1st and 2nd library of polynucleotides
CC encoding, several 1st and 2nd Ig subunit polypeptides, permitting
CC expression of Ig molecules (via control element e.g. an early/late
CC promoter), contacting Ig molecules with an antigen, and recovering
CC polynucleotides of the 1st library for the antigen. The Ig molecules are
CC heavy and light chain constant regions and variable regions linked via
CC peptide linkers and optionally directed via signal peptides or
CC transmembrane domains to different cell compartments. Also included is a
CC method of selecting polynucleotides which encode a single-domain antigen-
CC specific Ig molecule (its anti-specific fragment), by: (a) introducing
CC into a population of eukaryotic host cells capable of expressing the Ig
CC molecule a library of polynucleotides encoding (through operable
CC association with a transcriptional control region) several single-domain
CC Ig polypeptides (each comprising a Ig heavy chain constant region, a
CC camouflaged Ig heavy chain variable region, and a signal peptide capable of
CC directing cell surface expression or secretion of Ig subunit polypeptide)
CC ; (b) permitting expression of Ig molecules (or antigen-specific
CC fragments) from the host cells; (c) contacting the Ig molecules with an
CC antigen; and (d) recovering polynucleotides of the library from those
CC host cells expressing Ig molecules which bind the antigens. The methods
CC are useful for selecting polynucleotides which encode an antigen-specific
CC Ig molecule, or its fragment. The present sequence is a PCR primer used
CC to construct the Ig expression constructs used in the method of the
CC invention
XX
SQ Sequence 21 BP; 1 A; 7 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 878 ATTGATGCTCCCTGCT 895
||||| |||||||||
Db 3 ATTGTTGCTCCCTGCT 20

RESULT 348
ABZ69340/c
ID ABZ69340 standard; DNA; 21 BP.
XX
AC ABZ69340;
XX
XX 11-AUG-2003 (first entry)
XX
DE Human SLC11A3 coding sequence PCR primer #18.
XX
XX Human; hereditary haemochromatosis; HH; ferroportin 1 gene; SLC11A3;
KW mutation; iron transport; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX WO2003002589-A1.
XX
XX 09-JAN-2003.
XX
XX 01-JUL-2002; 2002WO-US020771.
XX
XX 29-JUN-2001; 2001US-0301429P.
PR 10-OCT-2001; 2001US-00973180.
XX
XX (UYRO-) UNIV ROTTERDAM ERASMUS.
PA (DEAN/) DEAN D D.
XX
XX Dean DD, Van Duijn CM, Heutink P, Oostra BA;
PI
XX

DR WPI; 2003-201489/19.
XX
XX New isolated DNA sequence and polypeptide, useful for diagnosing a
PT patient as having an increased risk of developing hereditary
PT hemochromatosis disease or anemia, or screening potential therapeutic
PT agents for treating the disease.
XX
XX Disclosure; Page 28; 66pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC ferroportin 1 (SLC11A3) gene, and describes the A734C base change present
CC in the gene which causes hereditary haemochromatosis (HH). This affects
CC SLC11A3 mediated iron transport. The sequences can be used in the
CC diagnosis and treatment of hereditary haemochromatosis and anaemia. The
CC present sequence is a PCR primer used to isolate the sequences in the
CC exemplification of the invention
XX
SQ Sequence 21 BP; 6 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1771 TATGCTGAGGCTTGAAA 1788
||||| |||||||
Db 18 TATGTTGAGGCTGAAA 1

RESULT 349
ABZ22424
ID ABZ22424 standard; DNA; 21 BP.
XX
AC ABZ22424;
XX
XX 24-MAR-2003 (first entry)
XX
DE Gus gene PCR primer SEQ ID NO:127.
XX
XX Identification; intrabody; eukaryotic cell; immunoglobulin; selection;
KW cardiovascular; diminished arrhythmia potential; cardiomyocyte; stroke;
KW enhanced contractile property; heart failure; arrhythmia; embolic;
KW sarcolemmal calcium cycling; artery; arteriole; angina; atherosclerosis;
KW LDL metabolism; HDL metabolism; skin biology; keloid formation;
KW PCR primer; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200286096-A2.
XX
XX 31-OCT-2002.
XX
XX 23-JAN-2002; 2002WO-US001677.
XX
XX 23-JAN-2001; 2001US-0263225P.
PR 24-JAN-2001; 2001US-0263200P.
XX
XX 27-FEB-2001; 2001US-0271422P.
PR 15-JUN-2001; 2001US-0298095P.
XX
XX (UYRP) UNIV ROCHESTER MEDICAL CENT.
PA
XX
XX Zauderer M, Wei C, Smith ES;
PI
XX WPI; 2003-103408/09.
XX
XX Selecting polynucleotides encoding an intracellular immunoglobulin which
PT induces a modified phenotype in a eukaryotic host cell, by introducing
PT library of polynucleotides encoding immunoglobulin subunit polypeptides.
XX
XX Example 8; Page 146; 257pp; English.
XX
XX The present invention describes a method for selecting polynucleotides
CC (PNs) encoding an intracellular immunoglobulin molecule or its fragment

CC whose expression induces a modified phenotype in a eukaryotic host cell
 CC (I). The method comprises introducing into (I) a first and second library
 CC of PNs encoding, through operable association with a transcriptional
 CC control region, first and second intracellular immunoglobulin subunit
 CC polypeptides, respectively. The method is useful for selecting
 CC polynucleotides which encode an intracellular immunoglobulin molecule, or
 CC fragment. The method is useful e.g. for identifying polynucleotides which
 CC singly or collectively encode intracellular immunoglobulin molecules, or
 CC which sensitise host cells to killing by an agent. The method may also be
 CC used in cardiovascular applications; for screening for diminished
 CC arrhythmia potential in cardiomyocytes and for enhanced contractile
 CC properties of cardiomyocytes and diminish heart failure potential; for
 CC identifying intracellular immunoglobulin molecules that will regulate
 CC intracellular and sarcolemmal calcium cycling in cardiomyocytes to
 CC prevent arrhythmias or that will diminish embolic phenomena in arteries
 CC and arterioles leading to strokes and angina; in screening for decreases
 CC in atherosclerosis-producing mechanisms to find intracellular
 CC immunoglobulin molecules that regulate LDL and HDL metabolism; in skin
 CC biology applications; and in regulating or inhibiting keloid formation.
 CC AB222379 to AB222449 and ABP56536 to ABP56618 represent sequences used in
 CC the exemplification of the present invention
 XX
 SQ Sequence 21 BP; 1 A; 7 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 878 ATTGATGCTCCCTGCT 895
 |||||
 Db 3 ATTGTTGCTCCCTGCT 20
 |||||
 RESULT 350
 ABA00728/c
 ID ABA00728 standard; DNA; 21 BP.
 AC ABA00728;
 XX
 XX 18-MAR-2003 (first entry)
 DE IL-12 p40 sense primer.
 XX
 XX Primer; PCR; RT-PCR; dendritic cell; dendrite; interferon; IFN;
 KW granulocyte/macrophage-colony stimulating factor; GM-CSF; cytokine;
 KW interleukin-4; IL-4; mononuclear cell; lymphoma; Epstein-Barr virus;
 KW peripheral blood mononuclear cell; PBMC; vaccine; viral infection; HIV;
 KW HBV; HCV; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200288328-A2.
 PN
 XX 07-NOV-2002.
 PD
 XX 29-APR-2002; 2002WO-EP004709.
 PF
 XX 27-APR-2001; 2001US-00845042.
 PR
 XX (SUPE-) INST SUPERIORE DI SANITA.
 PA
 XX Belardelli F, Santini SM, Parlato S, Di Pucchio T, Logozzi M;
 PI Lapenta C, Ferrantini M, Santodonato L, D'agostino G;
 PI
 XX WPI; 2003-120470/11.
 DR
 XX Preparation of dendritic cells, useful in a vaccine or a pharmaceutical
 PT composition for the prevention and/or treatment of infectious or
 PT neoplastic disease, comprises culturing mononuclear cells in a medium
 PT with type I interferon.
 PS
 XX Example 2; Page 37; 91pp; English.

CC The sequences given in ABA00724-33 are primers which were used in RT-PCR
 CC to determine whether dendritic cells treated with interferon (IFN)/
 CC granulocyte/macrophage-colony stimulating factor (GM-CSF) exhibited any
 CC specific pattern of cytokine expression as compared to cells cultured in
 CC the presence of interleukin-4 (IL-4)/GM-CSF. The dendritic cells used
 CC were the cells of the invention which were prepared by culturing
 CC mononuclear cells in a culture medium containing type I IFN, where the
 CC adherent PBMCs and highly purified CD14⁺ monocytes isolated from PBMCs.
 CC The dendritic cells are useful for the preparation of a vaccine or a
 CC pharmaceutical composition for the prevention or the treatment of a
 CC pathology associated with the presence of an antigen in the human body.
 CC The pathology is an infectious or neoplastic disease. The infectious
 CC disease is a viral infection, preferably HIV, HBV or HCV infection. The
 CC neoplastic disease is lymphoma, and virally induced, preferably by an
 CC Epstein-Barr virus
 XX
 SQ Sequence 21 BP; 8 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 386 CTTGAGCTGCGAGCTCTT 403
 |||||
 Db 20 CTTGAGCTGCGAAGTCTT 3
 |||||
 RESULT 351
 ACC00603
 ID ACC00603 standard; DNA; 21 BP.
 AC ACC00603;
 XX
 XX 23-JUN-2003 (first entry)
 DT
 XX Human CAP2 gene exon 3 specific forward primer.
 DE
 XX CAP2; bipolar disorder; BP; single nucleotide polymorphism; SNP;
 KW cytoplasmic antiprotease 2; human; PCR; primer; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO2003025222-A1.
 PN
 XX 27-MAR-2003.
 PD
 XX 17-SEP-2002; 2002WO-EP010667.
 PF
 XX 17-SEP-2001; 2001EP-00203558.
 PR
 XX (JANC) JANSSEN PHARM NV.
 PA
 XX Del-Favero JPL, Van Broeckhoven C;
 PI
 XX WPI; 2003-354610/33.
 DR
 XX Diagnosing bipolar disorder (BP) or susceptibility to BP in an individual
 PT comprises determining and analyzing single nucleotide polymorphisms in
 PT the cytoplasmic antiprotease 2 gene of the individual.
 PS
 XX Example 1; Page 24; 46pp; English.

CC The invention relates to diagnosing bipolar disorder (BP) or
 CC susceptibility to BP in an individual. The method involves determining,
 CC in a sample from the individual, the single nucleotide polymorphism (SNP)
 CC in the cytoplasmic antiprotease 2 (CAP2) gene of the individual and
 CC determining the status of the individual by reference to polymorphism in
 CC the CAP2 gene. The method is useful in diagnosing bipolar disorder, or
 CC susceptibility to this disorder, in an individual. Sequences ACC00603-10
 CC represent PCR primers for sequencing the human CAP2 cDNA
 XX
 XX Sequence 21 BP; 4 A; 5 C; 1 G; 11 T; 0 U; 0 Other;

```

Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2142 CCTTTAATTCCTTGTC 2159
    |||||
Db 2 CTTTCAATTCCTTGTC 19

RESULT 352
ACC84380/C
ID ACC84380 standard; DNA; 21 BP.
XX
AC ACC84380;
XX
DT 03-OCT-2003 (first entry)
XX
DE Fluorescein labelled target sequence F2.
XX
KW PLRV; reporter; probe; microarray; ss.
XX
OS Unidentified.
XX
PH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /*mod_base= OTHER
FT /*note= "OTHER= 5' fluorescein label"
XX
PN WO2003054551-A1.
XX
PD 03-JUL-2003.
XX
PF 17-DEC-2002; 2002WO-EP014426.
XX
PR 21-DEC-2001; 2001EP-00870295.
PR 28-MAY-2002; 2002US-0383666P.
XX
PA (PAMG-) PAMGENE BV.
XX
PI Van Beuningen MGJ;
XX
DR WPI; 2003-569292/53.
XX

Identification of analyte in biological sample, involves determining
signal of reporter molecule binding to internal reference, determining
signal of analyte binding to receptor, and normalizing signals.

Example 1; Page 38; 61pp; English.
XX
The present sequence is that of F2, a 5' fluorescein labelled target
sequence used in an example of the invention. The invention relates to
methods and arrays suited to correct for signal errors due to variation
in sample preparation. Methods and compositions for performing
quantitative array-based assays are provided. A reporter and an analyte
are used, where the reporter binds selectively to an internal reference
present on the array, i.e. at least a subset, if not all, of the spots
present on the array used in the method contain an internal reference
which can be bound by the reporter. The method is useful for the
identification of an analyte in a biological sample, particularly for use
in expression profiling assay, genotyping, sequence determination by
hybridisation, gene quantitation, gene abnormality analysis (MAPH), PCR,
NASBA or TYRAS (claimed)
XX
Sequence 21 BP; 4 A; 6 C; 2 G; 9 T; 0 U; 0 Other;

Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 480 TCTACAGTACTGGAAG 497
    |||||
Db 2 TCTACAGTACTGGAAG 3

RESULT 354
ACC84383
ID ACC84383 standard; DNA; 21 BP.

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Db 20 TGTACAGAACTGGAAG 3

RESULT 353
ACC84393/C
ID ACC84393 standard; DNA; 21 BP.
XX
AC ACC84393;
XX
DT 03-OCT-2003 (first entry)
XX
DE HIVpol7p41 target sequence, for normalization of PamChip assay.
XX
KW HIV; microarray; ss.
XX
OS Human immunodeficiency virus.
XX
PH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /*mod_base= OTHER
FT /*note= "OTHER= fluorescent label"
XX
PN WO2003054551-A1.
XX
PD 03-JUL-2003.
XX
PF 17-DEC-2002; 2002WO-EP014426.
XX
PR 21-DEC-2001; 2001EP-00870295.
PR 28-MAY-2002; 2002US-0383666P.
XX
PA (PAMG-) PAMGENE BV.
XX
PI Van Beuningen MGJ;
XX
DR WPI; 2003-569292/53.
XX

Identification of analyte in biological sample, involves determining
signal of reporter molecule binding to internal reference, determining
signal of analyte binding to receptor, and normalizing signals.

Example 4; Page 41; 61pp; English.
XX
The present sequence is that of an HIVpol7p41 target sequence for a set
of 11 specific receptors (probes) (see ACC84382-92) that were spotted on
an array and used in normalization of a PamChip assay in an example of
the method of the invention. The invention relates to methods and arrays
suited to correct for signal errors due to variation in sample
preparation. Methods and compositions for performing quantitative array-
based assays are provided. A reporter and an analyte are used, where the
reporter binds selectively to an internal reference present on the array;
at least a subset, if not all, of the spots present on the array used in
the method contain an internal reference which can be bound by the
reporter. The method is useful for the identification of an analyte in a
biological sample, particularly for use in expression profiling assay,
genotyping, sequence determination by hybridisation, gene quantitation,
gene abnormality analysis (MAPH), PCR, NASBA or TYRAS (claimed)
XX
Sequence 21 BP; 4 A; 6 C; 2 G; 9 T; 0 U; 0 Other;

Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 480 TCTACAGTACTGGAAG 497
    |||||
Db 2 TGTACAGAACTGGAAG 3

RESULT 354
ACC84383
ID ACC84383 standard; DNA; 21 BP.

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XX AC ACC84383;
XX DT 03-OCT-2003 (first entry)
XX DE Probe HIVpol7p41-4 used in normalization of PamChip assay.
XX KW HIV; probe; microarray; ss.
XX OS Human immunodeficiency virus.
XX PN WO2003054551-A1.
XX PD 03-JUL-2003.
XX PF 17-DEC-2002; 2002WO-EP014426.
XX PR 21-DEC-2001; 2001EP-00870295.
XX PR 28-MAY-2002; 2002US-0383666P.
XX PA (PAMG-) PAMGENE BV.
XX PI Van Beuningen MGJ;
XX DR WPI; 2003-569292/53.
XX PT Identification of analyte in biological sample, involves determining
PT signal of reporter molecule binding to internal reference, determining
PT signal of analyte binding to receptor, and normalizing signals.
XX PS Example 4; Page 41; 61pp; English.
XX CC The present sequence is that of HIVpol7p41-4, a specific receptor (probe)
CC used in an array system to detect a target sequence (see ACC84393). This
CC sequence has 0 mismatches with the target. It is one of a set of 11
CC specific receptors (see ACC84382-92) used in normalization of a PamChip
CC assay as an example of the method of the invention. The invention relates
CC to methods and arrays suited to correct for signal errors due to
CC variation in sample preparation. Methods and compositions for performing
CC quantitative array-based assays are provided. A reporter and an analyte
CC are used, where the reporter binds selectively to an internal reference
CC present on the array; at least a subset, if not all, of the spots present
CC on the array used in the method contain an internal reference which can
CC be bound by the reporter. The method is useful for the identification of
CC an analyte in a biological sample, particularly for use in expression
CC profiling assay, genotyping, sequence determination by hybridisation,
CC gene quantitation, gene abnormality analysis (MAPH), PCR, NASBA or TYRAS
CC (claimed)
XX SQ Sequence 21 BP; 9 A; 2 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 480 TCTACAGTACTGGAAAG 497
Db | | | | | | | | | | | | | | | | | | | |
2 TGTACGAACTGGAAAG 19

RESULT 355
ACF04439
TID ACF04439 standard; RNA; 21 BP.
XX AC ACF04439;
XX DT 04-DEC-2003 (first entry)
XX DE Bcr-abl fusion gene RNA interference sequence S2.
XX KW Tyrosine kinase inhibitor; mutant tyrosine kinase; RNA interference;
KW bcr-abl fusion gene; antisense; cytosstatic; myeloid leukaemia;
KW lymphatic leukaemia; myeloblastic leukaemia; ds.

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XX OS Unidentified.
XX PN WO2003062432-A1.
XX PD 31-JUL-2003.
XX PF 22-JAN-2003; 2003WO-EP000604.
XX PR 22-JAN-2002; 2002DE-01002419.
XX PA (RIBO-) RIBOPHARMA AG.
XX PI Vornlocher H, Limmer S, Kreutzer R, Van Der Kuip H, Aulitzky W;
XX DR WPI; 2003-587412/55.
XX PT Increasing activity of inhibitor of a tyrosine kinase, useful in
PT treatment of leukemia, by RNA interference inhibition of gene expression.
XX PS Disclosure; Page 17; 48pp; German.
XX CC The present invention relates to a method of increasing the activity of
CC an inhibitor of the activity of a tyrosine kinase, the product of a
CC mutant gene, comprising inhibiting expression of the mutant gene by RNA
CC interference. The method is used to treat chronic myeloid, acute
CC lymphatic and acute myeloblastic leukaemias. The present sequence is an
CC RNA used in the inhibition of a bcr-abl fusion gene in the
CC exemplification of the invention
XX SQ Sequence 21 BP; 7 A; 5 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 72.2%; Pred. No. 2.5e+02;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2200 AGTTGAAAGGCCATCAG 2217
Db | | | | | | | | | | | | | | | | | | | |
4 AGUUGAAAGCCCUUCAG 21

Search completed: September 28, 2004, 08:34:54
Job time : 17 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 28, 2004, 08:37:08 ; Search time 13 Seconds
(without alignments)
3.807 Million cell updates/sec

Title: US-10-798-923A-4

Perfect score: 3405

Sequence: 1 cgcacacccaagtccaag.....acacactcaaaaaaaaaa 3405

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 385 seqs, 7268 residues

Total number of hits satisfying chosen parameters: 770

Minimum DB seq length: 8

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 386 summaries

Database : rni4.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	27	0.8	27	1	US-08-989-299-13
C 3	27	0.8	27	1	US-09-407-427-13
C 4	20.2	0.6	25	1	US-09-866-108A-13747
C 5	19.2	0.6	25	1	US-09-866-108A-13746
C 6	19.2	0.6	25	1	US-09-866-108A-13748
C 7	18.2	0.5	25	1	US-09-866-108A-13745
C 8	18.2	0.5	25	1	US-09-866-108A-13749
C 9	17.6	0.5	24	1	US-09-304-452-1
C 10	17.6	0.5	25	1	US-09-866-108A-15237
C 11	17.6	0.5	25	1	US-09-866-108A-15238
C 12	17.2	0.5	23	1	US-09-472-035A-1
C 13	16.8	0.5	22	1	US-09-268-992-14
C 14	16.8	0.5	22	1	US-09-657-474-14
C 15	16.4	0.5	21	1	US-08-808-550-13
C 16	16.2	0.5	21	1	US-08-076-090-3
C 17	16.2	0.5	21	1	US-08-173-489C-117
C 18	16.2	0.5	21	1	PCT-US94-06661-3
C 19	16.2	0.5	21	1	PCT-US96-09430-9
C 20	16	0.5	19	1	US-09-422-978-4843
C 21	15.8	0.5	20	1	US-08-952-967-5
C 22	15.8	0.5	20	1	US-09-657-452A-54
C 23	15.8	0.5	22	1	US-09-216-393B-193
C 24	15.6	0.5	21	1	US-07-998-289B-14
C 25	15.6	0.5	22	1	US-08-265-310-19
C 26	15.6	0.5	22	1	US-08-721-260-13
C 27	15.6	0.5	22	1	US-08-951-742-19
C 28	15.4	0.5	18	1	US-08-716-459-2
C 29	15.4	0.5	18	1	US-09-422-978-6432
C 30	15.4	0.5	20	1	US-09-280-805-245
C 31	15.4	0.5	21	1	US-08-263-911-13
C 32	15.4	0.5	21	1	US-09-035-593-3
C 33	15.2	0.4	20	1	US-09-429-323-67

Sequence 19, Appl	1	US-09-444-053-19	20	1	US-09-444-053-19	0.4	15.2	C 34
Sequence 60, Appl	20	US-09-918-686-60	20	1	US-09-918-686-60	0.4	15.2	C 35
Sequence 6588, Ap	20	US-09-422-978-6588	20	1	US-09-422-978-6588	0.4	15.2	C 36
Sequence 1301, Ap	20	US-09-198-452A-1301	20	1	US-09-198-452A-1301	0.4	15.2	C 37
Sequence 3147, Ap	20	US-09-198-452A-3147	20	1	US-09-198-452A-3147	0.4	15.2	C 38
Sequence 24, Appl	21	US-08-890-719-24	21	1	US-08-890-719-24	0.4	15.2	C 39
Sequence 26, Appl	21	US-08-890-719-26	21	1	US-08-890-719-26	0.4	15.2	C 40
Sequence 243, App	21	US-08-943-731-243	21	1	US-08-943-731-243	0.4	15.2	C 41
Sequence 6151, Ap	21	US-09-422-978-6151	21	1	US-09-422-978-6151	0.4	15.2	C 42
Sequence 10328, Ap	21	US-09-422-978-10328	21	1	US-09-422-978-10328	0.4	15.2	C 43
Sequence 10352, A	21	US-09-422-978-10352	21	1	US-09-422-978-10352	0.4	15.2	C 44
Sequence 10665, A	21	US-09-422-978-10665	21	1	US-09-422-978-10665	0.4	15.2	C 45
Sequence 27, Appl	15	US-08-832-021-27	15	1	US-08-832-021-27	0.4	15	C 46
Sequence 116, App	20	US-09-280-799-116	20	1	US-09-280-799-116	0.4	15	C 47
Sequence 14, Appl	20	US-09-042-785A-14	20	1	US-09-042-785A-14	0.4	15	C 48
Sequence 30, Appl	18	US-08-505-509-30	18	1	US-08-505-509-30	0.4	14.8	C 49
Sequence 30, Appl	18	US-08-491-690A-30	18	1	US-08-491-690A-30	0.4	14.8	C 50
Sequence 73, Appl	18	US-09-280-409-73	18	1	US-09-280-409-73	0.4	14.8	C 51
Sequence 45, Appl	18	US-09-474-922A-45	18	1	US-09-474-922A-45	0.4	14.8	C 52
Sequence 26, Appl	18	US-09-071-433-26	18	1	US-09-071-433-26	0.4	14.8	C 53
Sequence 545, App	18	US-08-679-645-545	18	1	US-08-679-645-545	0.4	14.8	C 54
Sequence 6, Appl	18	US-09-287-599A-6	18	1	US-09-287-599A-6	0.4	14.8	C 55
Sequence 22, Appl	19	US-08-938-669A-22	19	1	US-08-938-669A-22	0.4	14.8	C 56
Sequence 12, Appl	19	US-09-475-947A-12	19	1	US-09-475-947A-12	0.4	14.8	C 57
Sequence 22, Appl	19	US-09-306-828-22	19	1	US-09-306-828-22	0.4	14.8	C 58
Sequence 25, Appl	20	US-08-078-683A-25	20	1	US-08-078-683A-25	0.4	14.8	C 59
Sequence 11, Appl	20	US-08-094-079-11	20	1	US-08-094-079-11	0.4	14.8	C 60
Sequence 10, Appl	20	US-08-184-422-10	20	1	US-08-184-422-10	0.4	14.8	C 61
Sequence 3, Appl	20	US-09-226-56B-3	20	1	US-09-226-56B-3	0.4	14.8	C 62
Sequence 34, Appl	20	US-09-359-757-34	20	1	US-09-359-757-34	0.4	14.8	C 63
Sequence 10, Appl	20	US-08-589-771B-10	20	1	US-08-589-771B-10	0.4	14.8	C 64
Sequence 193, App	20	US-09-249-730-193	20	1	US-09-249-730-193	0.4	14.8	C 65
Sequence 38, Appl	20	US-09-428-584-38	20	1	US-09-428-584-38	0.4	14.8	C 66
Sequence 82, Appl	20	US-08-765-340-82	20	1	US-08-765-340-82	0.4	14.8	C 67
Sequence 135, App	20	US-09-490-692-135	20	1	US-09-490-692-135	0.4	14.8	C 68
Sequence 87, Appl	20	US-09-280-805-87	20	1	US-09-280-805-87	0.4	14.8	C 69
Sequence 500, App	20	US-09-313-932-500	20	1	US-09-313-932-500	0.4	14.8	C 70
Sequence 601, App	20	US-09-021-701-601	20	1	US-09-021-701-601	0.4	14.8	C 71
Sequence 602, App	20	US-09-021-701-602	20	1	US-09-021-701-602	0.4	14.8	C 72
Sequence 603, App	20	US-09-021-701-603	20	1	US-09-021-701-603	0.4	14.8	C 73
Sequence 4, Appl	20	US-09-207-857-4	20	1	US-09-207-857-4	0.4	14.8	C 74
Sequence 17, Appl	20	US-09-373-845-17	20	1	US-09-373-845-17	0.4	14.8	C 75
Sequence 46, Appl	20	US-09-488-856A-46	20	1	US-09-488-856A-46	0.4	14.8	C 76
Sequence 26, Appl	20	US-08-618-957A-26	20	1	US-08-618-957A-26	0.4	14.8	C 77
Sequence 15, Appl	20	US-09-702-246-15	20	1	US-09-702-246-15	0.4	14.8	C 78
Sequence 157, App	20	US-09-517-467B-157	20	1	US-09-517-467B-157	0.4	14.8	C 79
Sequence 69, Appl	20	US-09-375-318-69	20	1	US-09-375-318-69	0.4	14.8	C 80
Sequence 25, Appl	20	US-08-471-970A-25	20	1	US-08-471-970A-25	0.4	14.8	C 81
Sequence 4789, Ap	20	US-09-198-452A-4789	20	1	US-09-198-452A-4789	0.4	14.8	C 82
Sequence 193, App	20	US-09-249-247-193	20	1	US-09-249-247-193	0.4	14.8	C 83
Sequence 33, Appl	20	US-09-081-385-33	20	1	US-09-081-385-33	0.4	14.8	C 84
Sequence 4, Appl	20	US-09-909-280A-4	20	1	US-09-909-280A-4	0.4	14.8	C 85
Sequence 144, App	21	US-09-009-913-144	21	1	US-09-009-913-144	0.4	14.8	C 86
Sequence 10297, A	21	US-09-422-978-10297	21	1	US-09-422-978-10297	0.4	14.8	C 87
Sequence 54, Appl	21	US-09-380-836-54	21	1	US-09-380-836-54	0.4	14.8	C 88
Sequence 76, Appl	16	US-09-829-855-76	16	1	US-09-829-855-76	0.4	14.4	C 89
Sequence 2015, Ap	17	US-08-373-124A-2015	17	1	US-08-373-124A-2015	0.4	14.4	C 90
Sequence 2015, Ap	17	US-08-435-628-2015	17	1	US-08-435-628-2015	0.4	14.4	C 91
Sequence 40, Appl	17	US-08-985-162-40	17	1	US-08-985-162-40	0.4	14.4	C 92
Sequence 4306, Ap	17	US-09-371-772B-4306	17	1	US-09-371-772B-4306	0.4	14.4	C 93
Sequence 40, Appl	17	US-09-401-063-40	17	1	US-09-401-063-40	0.4	14.4	C 94
Sequence 32, Appl	18	US-08-078-683A-32	18	1	US-08-078-683A-32	0.4	14.4	C 95
Sequence 27, Appl	18	US-09-270-140A-27	18	1	US-09-270-140A-27	0.4	14.4	C 96
Sequence 65, Appl	18	US-09-270-140A-65	18	1	US-09-270-140A-65	0.4	14.4	C 97
Sequence 32, Appl	18	US-08-471-970A-32	18	1	US-08-471-970A-32	0.4	14.4	C 98
Sequence 5818, Ap	18	US-09-422-978-5818	18	1	US-09-422-978-5818	0.4	14.4	C 99
Sequence 8906, Ap	19	US-09-422-978-8906	19	1	US-09-422-978-8906	0.4	14.4	C 100
Sequence 359, App	20	US-08-117-952-359	20	1	US-08-117-952-359	0.4	14.4	C 101
Sequence 31, Appl	20	US-09-357-070-31	20	1	US-09-357-070-31	0.4	14.4	C 102
Sequence 38, Appl	20	US-09-428-219-38	20	1	US-09-428-219-38	0.4	14.4	C 103
Sequence 59, Appl	20	US-09-657-481A-59	20	1	US-09-657-481A-59	0.4	14.4	C 104
Sequence 19, Appl	20	US-09-360-197-19	20	1	US-09-360-197-19	0.4	14.4	C 105
Sequence 119, App	20	US-09-676-610B-119	20	1	US-09-676-610B-119	0.4	14.4	C 106

107	14.4	0.4	20	1	US-09-422-978-7273	Sequence 7273, Ap	180	14.2	0.4	20	1	US-09-649-728-10	Sequence 10, Appl
c 108	14.4	0.4	20	1	US-09-198-452A-2103	Sequence 2103, Ap	c 181	14.2	0.4	20	1	US-09-909-595-24	Sequence 24, Appl
c 109	14.4	0.4	20	1	US-08-664-596B-33	Sequence 33, Appl	c 182	14.2	0.4	20	1	US-09-389-956-87	Sequence 87, Appl
c 110	14.2	0.4	19	1	US-08-233-130A-2	Sequence 2, Appl	c 183	14.2	0.4	20	1	US-09-823-634A-14	Sequence 14, Appl
c 111	14.2	0.4	19	1	US-08-913-833-35	Sequence 35, Appl	c 184	14.2	0.4	20	1	US-09-823-647B-14	Sequence 14, Appl
c 112	14.2	0.4	19	1	US-09-289-380-10	Sequence 10, Appl	c 185	14.2	0.4	20	1	US-09-825-497A-8	Sequence 8, Appl
c 113	14.2	0.4	19	1	US-09-041-185-3	Sequence 3, Appl	c 186	14.2	0.4	20	1	US-09-112-580-207	Sequence 207, Appl
c 114	14.2	0.4	19	1	US-09-580-794C-35	Sequence 35, Appl	c 187	14.2	0.4	20	1	US-09-628-129-2	Sequence 2, Appl
c 115	14.2	0.4	19	1	US-09-091-952A-122	Sequence 122, App	c 188	14.2	0.4	20	1	US-09-495-714C-130	Sequence 130, Appl
c 116	14.2	0.4	19	1	US-09-422-978-90679	Sequence 90679, Ap	c 189	14.2	0.4	20	1	US-09-435-714C-131	Sequence 131, Appl
c 117	14.2	0.4	19	1	US-09-422-978-9062	Sequence 9062, Ap	c 190	14.2	0.4	20	1	PCT-US93-02213-33	Sequence 33, Appl
c 118	14.2	0.4	20	1	US-07-807-529A-34	Sequence 34, Appl	c 191	14.2	0.4	20	1	PCT-US94-07770-33	Sequence 33, Appl
c 119	14.2	0.4	20	1	US-08-089-996-33	Sequence 33, Appl	c 192	14.2	0.4	20	1	5171843-3	Patent No. 5171843
c 120	14.2	0.4	20	1	US-08-478-178A-33	Sequence 33, Appl	c 193	14	0.4	14	1	US-08-832-021-13	Sequence 13, Appl
c 121	14.2	0.4	20	1	US-08-488-177-33	Sequence 33, Appl	c 194	14	0.4	14	1	US-08-832-021-13	Sequence 13, Appl
c 122	14.2	0.4	20	1	US-08-481-072A-33	Sequence 33, Appl	c 195	14	0.4	14	1	US-08-832-021-13	Sequence 13, Appl
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c 134	14.2	0.4	20	1	US-08-430-944D-83	Sequence 83, Appl	c 207	14	0.4	20	1	US-09-968-445-7	Sequence 7, Appl
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ALIGNMENTS

RESULT 1

US-08-664-596B-33/c
 ; Sequence 33, Application US/08664596B
 ; Patent No. 5807703
 ; GENERAL INFORMATION:
 ; APPLICANT: Jacobs, Kenneth
 ; APPLICANT: McCoy, John

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/ APPLICANT: LaVallie, Edward
/ APPLICANT: Racie, Lisa
/ APPLICANT: Merberg, David
/ APPLICANT: Treacy, Maurice
/ APPLICANT: Evans, Cheryl
/ APPLICANT: Spaulding, Vikki
/ APPLICANT: Bowman, Michael
/ TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
/ TITLE OF INVENTION: ENCODING THEM
/ NUMBER OF SEQUENCES: 37
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genetics Institute, Inc.
/ STREET: 87 CambridgePark Drive
/ CITY: Cambridge
/ STATE: Massachusetts
/ COUNTRY: U.S.A.
/ ZIP: 02140
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA: US/08/664,596B
/ FILING DATE:
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Brown, Scott A. 32,724
/ REGISTRATION NUMBER: 32,724
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 498-8224
/ TELEFAX: (617) 876-5851
/ INFORMATION FOR SEQ ID NO: 33:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 29 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "Oligonucleotide"
US-08-664-596B-33

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Best Local Similarity 96.6%; Pred. No. 0.18;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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/ Patent No. 6194556
/ GENERAL INFORMATION:
/ APPLICANT: Acton, Susan L.
/ APPLICANT: Robinson, Keith E.
/ TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
/ TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: FOLEY, HOAG & ELIOT LLP
/ STREET: One Post Office Square
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02109-2170
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/989,299
/ FILING DATE: 11-DEC-1997
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Arnold E., Beth
/ REGISTRATION NUMBER: 35,430
/ REFERENCE/DOCKET NUMBER: MIA-025.01
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-832-1000
/ TELEFAX: 617-832-7000
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 27 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
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US-08-989-299-13

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RESULT 3
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/ Sequence 13, Application US/09407427
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/ GENERAL INFORMATION:
/ APPLICANT: Acton, Susan L.
/ APPLICANT: Robinson, Keith E.
/ TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
/ MOLECULE TYPE: AND DIAGNOSTIC USES THEREFOR
/ FILE REFERENCE: MNI-132CP2
/ CURRENT APPLICATION NUMBER: US/09/407,427
/ CURRENT FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 09/163,648
/ PRIOR FILING DATE: 1998-09-30
/ PRIOR APPLICATION NUMBER: 08/989,299
/ PRIOR FILING DATE: 1997-12-11
/ NUMBER OF SEQ ID NOS: 14
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US-09-407-427-13

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Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1550 GAGATAGTTGGGCTGGTGGAACTCTGTG 1576
Db 27 GAGATAGTTGGGCTGGTGGAACTCTGTG 1

RESULT 4
US-09-866-108A-13747/c
/ Sequence 13747, Application US/09866108A
/ Patent No. 6686188
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharron G.
```

```
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13747
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13747

Query Match      0.6%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 8.1;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2213 ATCAGGATGTCGCGAGCGGTATCA 2237
      ||||| ||||| ||||| ||||| |||||
Db 25 ATCAGGCTGTCCGAGCGCGATCA 1

RESULT 5
US-09-866-108A-13746/c
; Sequence 13746, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOICA-7
; CURRENT APPLICATION NUMBER: US 60/207,456
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13747
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13747
```

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; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13746
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13746

Query Match      0.6%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2214 TCAGGATGTCGCGAGCGGTATCA 2237
      ||||| ||||| ||||| ||||| |||||
Db 25 TCAGGCTGTCCGAGCGCGATCA 2

RESULT 6
US-09-866-108A-13748/c
; Sequence 13748, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13748
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
```

US-09-866-108A-13748

Query Match 0.5%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2213 ATCAGGATGTCGCGAGCCGATC 2236
||||| ||||| ||||| ||||| |||||
Db 24 ATCAGGCTGTCCGAGCCGATC 1

RESULT 7

US-09-866-108A-13745/c
; Sequence 13745, Application US/09866108A
; Patent No. 6686188

; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: A6OMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-05-26

US-09-304-452-1

Query Match 0.5%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1466 ATGTTAGTAGAGTGAGTGATG 1489
||||| ||||| ||||| ||||| |||||
Db 1 ATGTTAGTAGAGAGAGGAGGATG 24

RESULT 10

US-09-866-108A-15237/c

; Sequence 15237, Application US/09866108A
; Patent No. 6686188

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: ACOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; SOFTWARE: Acomica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 15237

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-15237

Query Match 0.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 391 GCTGCAGGCTCTTCAGCAAAATGG 414
||||| ||||| ||||| ||||| |||||
Db 25 GCTCCGGGCTCTTCACAAATGG 2

RESULT 11

US-09-866-108A-15238/c

; Sequence 15238, Application US/09866108A

; Patent No. 6686188

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Acomica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 15238

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-15238

Query Match 0.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 391 GCTGCAGGCTCTTCAGCAAAATGG 414
||||| ||||| ||||| ||||| |||||
Db 24 GCTCCGGGCTCTTCACAAATGG 1

RESULT 12

US-09-472-035A-1

; Sequence 1, Application US/09472035A

; Patent No. 6322985

; GENERAL INFORMATION:

; APPLICANT: Yechezkel Kashi et al.

; TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND

; TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS

; TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR

; TITLE OF INVENTION: PROKARYOTE CLASSIFICATION AND TYPING

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina

; STREET: 2001 Jefferson Davis Highway, Suite 207

; CITY: Arlington

; STATE: Virginia

; COUNTRY: United States of America

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

; COMPUTER: Twinhead* Slimnote-890TX

; OPERATING SYSTEM: MS DOS version 6.2,

; OPERATING SYSTEM: Windows version 3.11

; SOFTWARE: Word for Windows version 2.0 converted to

; SOFTWARE: an ASCII file

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/472,035A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 74/77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-5625553
; TELEFAX: 972-3-5625554
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-472-035A-1

Query Match 0.5%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2751 GATTTTGTATTAGATATATTA 2772
DB 1 GATTTTCATATGAGTATATTA 22

RESULT 13
US-09-268-992-14/c
; Sequence 14, Application US/09268992
; Patent No. 6342351
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/09/268,992
; EARLIER FILING DATE: 1999-03-16
; EARLIER APPLICATION NUMBER: 09/236,134
; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: 60/106,056
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 60/088,312
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/078,044
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; US-09-268-992-14

Query Match 0.5%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3356 CAAAGCAGACACTCAATAAA 3375
DB 22 CACAGCAGACACACAATAAA 3

RESULT 14
US-09-657-474-14/c

; Sequence 14, Application US/09657474
; Patent No. 6399762
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; APPLICANT: Freimer, N.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/09/657,474
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 09/268,992
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/236,134
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/106,056
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/088,312
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/078,044
; PRIOR FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; US-09-657-474-14

Query Match 0.5%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3356 CAAAGCAGACACTCAATAAA 3375
DB 22 CACAGCAGACACACAATAAA 3

RESULT 15
US-08-808-550-13/c
; Sequence 13, Application US/08808550
; Patent No. 5871992
; GENERAL INFORMATION:
; APPLICANT: Teebor, George W.
; APPLICANT: Hilbert, Timothy P.
; TITLE OF INVENTION: MAMMALIAN ENDONUCLEASE III AND
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,550
; FILING DATE: 26-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-001 N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Primer P6"
HYPOTHETICAL: NO
US-08-808-550-13

Query Match 0.5%; Score 16.4; DB 1; Length 21;
Best Local Similarity 94.4%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 385 GCTTCAGTCGAGGCTCT 402
DB 21 GCTTCGTCGAGGCTCT 4

RESULT 16

US-08-076-090-3
Sequence 3, Application US/08076090
Patent No. 5631162
GENERAL INFORMATION:
APPLICANT: LeBoulch, Philippe
APPLICANT: London, Irving M.
APPLICANT: Tuan, Dorothy
TITLE OF INVENTION: Retroviral Vectors for Transducing
TITLE OF INVENTION: Beta-Globulin Gene and Beta-Locus Control Region
TITLE OF INVENTION: Derivatives
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/076,090
FILING DATE: 19930611
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT 6128
TELEPHONE: (404) 815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Beta-globin gene
US-08-076-090-3

Query Match 0.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2407 GAAGAAGAAAAATAAGCAAG 2427
DB 1 GGAGAGAGAAAAAAGAAAG 21

RESULT 17

US-08-173-489C-117/c
Sequence 117, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: beta-globin gene (accession # V00499)
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Lawn, R M, Efstratiadis, A, O'Connell,
AUTHORS: C, Maniatis, T.
TITLE: The nucleotide sequence of
JOURNAL: Cell
VOLUME: 21
PAGES: 647-651
DATE: 1980
RELEVANT RESIDUES IN SEQ ID NO: 117 :FROM 1 TO 21
US-08-173-489C-117

Query Match 0.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2407 GAAGAAGAAAAATAAGCAAG 2427
DB 21 GGAGAGAGAAAAAAGAAAG 1

```
RESULT 18
PCT-US94-06661-3
; Sequence 3, Application PC/TUS9406661
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Retroviral Vectors for Transducing
; TITLE OF INVENTION: Beta-Globulin Gene and Beta-Locus Control Region
; TITLE OF INVENTION: Derivatives
; NUMBER OF SEQUENCES: 5
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 10-JUN-1994
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: Beta-globin gene
PCT-US94-06661-3

Query Match          0.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2407 GAAGAAGAAAAATAAAGCAAG 2427
      1  GGAGAGAGAAAAAAGAAAG 21
Db

RESULT 19
PCT-US96-09430-9/c
; Sequence 9, Application PC/TUS9609430
; GENERAL INFORMATION:
; APPLICANT: Glazer, Peter M.
; TITLE OF INVENTION: TREATMENT OF HEMOGLOBINOPATHIES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OncorPharm, Inc.
; STREET: 200 Perry Parkway
; CITY: Gaithersburg
; STATE: Maryland
; COUNTRY: US
; ZIP: 20877
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09430
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/473,845
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Karta, Glenn E.
; REGISTRATION NUMBER: 30,649
; REFERENCE/DOCKET NUMBER: PA-0040
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-527-2058
; TELEFAX: 301-208-6997
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US96-09430-9

Query Match          0.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2407 GAAGAAGAAAAATAAAGCAAG 2427
      1  GGAGAGAGAAAAAAGAAAG 21
Db

RESULT 20
US-09-422-978-4843/c
; Sequence 4843, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET 020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4843
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-1814 for SEQ 909,
US-09-422-978-4843

Query Match          0.5%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709 TTCTGTCCTCTGGATT 2724
      17 TTCTGTCCTCTGGATT 2
Db

RESULT 21
US-08-952-967-5
; Sequence 5, Application US/08952967
; Patent No. 6086871
; GENERAL INFORMATION:
; APPLICANT: Fischer, Bernhard
; APPLICANT: Schlokot, Uwe
; APPLICANT: Mitterer, Artur
; APPLICANT: Falkner, Falko-Guenther
; APPLICANT: Eibl, Johann
; TITLE OF INVENTION: PROTHROMBIN DERIVATIVES
; NUMBER OF SEQUENCES: 22
```



```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Versi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,967
FILING DATE: 26-JAN-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AT96/00105
FILING DATE: 12-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AT A 1006/95
FILING DATE: 13-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,715
REFERENCE/DOCKET NUMBER: 065691/0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer 2197"
US-08-952-967-5

```

US-08-952-967-5

Query Match 0.5%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 56;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1967	ATAAGCCTAAATCAGCTC	1985
D _b	2	ATAAGCCTGAAATCAACTC	20

```

RESULT 22
US-09-657-452A-54
; Sequence 54, Application US/09657452A
; Patent NO. 6426188
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHORYLASE KINASE ALPHA 1 EXPRESSION
; FILE REFERENCE: RYS-0125
; CURRENT APPLICATION NUMBER: US/09/657,452A
; CURRENT FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 54
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-657-452A-54

```

Query Match 0.5%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 56;
Matches 17; Conservative 0; Mismatches 2; Indels

QY 3249 AACTGTGGAGTGAATGGAA 3267
Db 2 AACTGTGGAGTGAAGTAA 20

RESULT 23

```

US-09-216-393B-193/c
; Sequence 193, Application US/09216393B
; Patent No. 6514694
; GENERAL INFORMATION:
; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDII
; FILE REFERENCE: TX-1-C2
; CURRENT APPLICATION NUMBER: US/09/216
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,825
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 193
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-216-393B-193

```

```
Query Match          0.5%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 64;
Matches 17: Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 3132 TGCTTTTTCACCTTCCAAGG 3150
Db 21 TGCTTCTGCACCTTCCAAGG 3

RESULT 24

RES001 24
 US-07-998-289B-14/c
 ; Sequence 14, Application US/07998289B
 ; Patent No. 6027876
 ;
 ; GENERAL INFORMATION:
 ; APPLICANT: Black, Bruce C
 ; APPLICANT: Taylor, Martin
 ; APPLICANT: Heckel, David G
 ; TITLE OF INVENTION: Method for Monitoring Pesticide
 ; TITLE OF INVENTION: Resistance
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Darby & Darby PC
 ; STREET: 805 Third Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: US
 ; ZIP: 10022
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/998,289B
 ; FILING DATE: 30-DEC-1992
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Robinson, Joseph R
 ; REGISTRATION NUMBER: 33,448
 ; REFERENCE/DOCKET NUMBER: 0646/OA939
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-527-7700
 ; TELEFAX: 212-753-6237
 ; TELEX: 236687
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:

; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORGANISM: Heliothis virescens
; IMMEDIATE SOURCE:
; CLONE: D&K-
US-07-998-289B-14

Query Match 0.5%; Score 15.6; DB 1; Length 21;
Best Local Similarity 71.4%; Pred. No. 66;
Matches 15; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1070 ATGACTCAAGATCTCTGGAA 1090
||||| ||| ||| ||| ||| |||
Db 21 ATGACNCARGATTTTGGGAR 1

RESULT 25
US-08-265-310-19
; Sequence 19, Application US/08265310
; Patent No. 5856166
; GENERAL INFORMATION:
; APPLICANT: Bartfeld, Daniel
; APPLICANT: Butler, Michael J.
; APPLICANT: Hadary, Dany
; APPLICANT: Jenish, David
; APPLICANT: Krieger, Timothy
; APPLICANT: Malek, Lawrence T.
; APPLICANT: Soostmeyer, Gisela
; APPLICANT: Walczyk, Eva
; APPLICANT: Krygsman, Phyllis
; APPLICANT: Garven, Shella
; TITLE OF INVENTION: STREPTOMYCES PROTEASES AND IMPROVED
; TITLE OF INVENTION: STREPTOMYCES STRAINS FOR EXPRESSION OF PEPTIDES AND
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,310
; FILING DATE: 24-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,508
; FILING DATE: 23-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 18740/133/CACO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 672 5300
; TELEFAX: 202 672 5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-265-310-19

Query Match 0.5%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 384 AGCTTCAGCTGCAGGCTCTTCA 405
||||| ||| ||| ||| ||| |||
Db 1 AGCTTAGGCTGCAGGCGCTGCA 22

RESULT 26
US-08-721-260-13/c
; Sequence 13, Application US/08721260
; Patent No. 5968755
; GENERAL INFORMATION:
; APPLICANT: Roederer, Mario
; APPLICANT: Rabin, Ronald
; APPLICANT: Herzenberg, Leonard A.
; TITLE OF INVENTION: Methods for Determining T-cell Profiles
; TITLE OF INVENTION: of Immunocompromised Subjects
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/721,260
; FILING DATE: 26-SEP-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/004,364
; FILING DATE: 27-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8600-0161.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: GM-CSF primer A
US-08-721-260-13

Query Match 0.5%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 391 GCTGCAGGCTCTTCAGCAAAAT 412
||||| ||| ||| ||| ||| |||
Db 22 GCAGCAGGCTCTGCAGCCACAT 1

RESULT 27
US-08-951-742-19
; Sequence 19, Application US/08951742
; Patent No. 6127144

```

; GENERAL INFORMATION:
; APPLICANT: Bartfeld, Daniel
; APPLICANT: Michael J. Butler
; APPLICANT: Dany Hadary
; APPLICANT: David Jenish
; APPLICANT: Tim Krieger
; APPLICANT: Lawrence T. Malek
; APPLICANT: Gisela Soostmeyer
; APPLICANT: Eva Walczyk
; APPLICANT: Phyllis Krygsman
; APPLICANT: Sheila Garven
; TITLE OF INVENTION: METHOD FOR EXPRESSION OF PROTEINS IN
; TITLE OF INVENTION: BACTERIAL HOST CELLS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,742
; FILING DATE: 16-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 0189740/0140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-951-742-19

Query Match 0.5%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 384 AGCTTCAGCTGCAGGCTCTTCA 405
Db 1 AGCTTAGGCTGCAGGCGCTGCA 22

RESULT 28
US-08-716-459-2/c
; Sequence 2, Application US/08716459
; Patent No. 5821062
; GENERAL INFORMATION:
; APPLICANT: KOMAI, Koichiro
; APPLICANT: KANEKO, Hideo
; APPLICANT: NAKATSUKA, Iwao
; TITLE OF INVENTION: OLIGONUCLEOTIDE FOR USE IN CHECKING
; TITLE OF INVENTION: PRESENCE OR ABSENCE OF MUTATION IN
; TITLE OF INVENTION: HUMAN-DERIVED CYTOCHROME P450IIC18 GENE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
```

```

; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM PC
; OPERATING SYSTEM: IBM DOS Version 5.00
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,459
; FILING DATE: 27 SEPTEMBER 1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP-059385/1994
; APPLICATION NUMBER: JP-059386/1994
; FILING DATE: 29-03-1994
; FILING DATE: 29-03-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 20-4081PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid synthetic DNA
; US-08-716-459-2

Query Match 0.5%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1516 CCAGTGGCTGAAAAAGT 1532
Db 18 CCAGTGGCTGAAAAAGT 2

RESULT 29
US-09-422-978-6432
; Sequence 6432, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6432
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-1143 for SEQ 2498,
; US-09-422-978-6432

Query Match 0.5%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 598 GGAAGCTGGAGATCTG 614
|||||
Db 2 GGAAGCTGGAGTCTG 18

RESULT 30

US-09-280-805-245/C
; Sequence 245, Application US/09280805
; Patent No. 6184212
; GENERAL INFORMATION:
; APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
; APPLICANT: Graham, Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 271
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PC
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/280,805
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/048,810
; FILING DATE: March 26, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Licata, Jane Massey
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0346
; TELEPHONE: 609-810-1515
; TELEFAX: 609-810-1454
; INFORMATION FOR SEQ ID NO: 245:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-09-280-805-245

Query Match 0.5%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 81 GTGATCTGGCTCACAG 97
|||||
Db 18 GTGATCTGGCTCACTG 2

RESULT 31

US-08-263-911-13
; Sequence 13, Application US/08263911
; Patent No. 5877291
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S
; APPLICANT: Gourlie, Brian B
; TITLE OF INVENTION: MULTIVALENT SINGLE CHAIN ANTIBODIES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland

; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/263,911
; FILING DATE: 21-JUN-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,263
; FILING DATE: 11-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ulmer, Duane C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-41,014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-263-911-13

Query Match 0.5%; Score 15.4; DB 1; Length 21;
Best Local Similarity 94.1%; Pred. No. 73;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 458 ATTCTAATACATGAG 474
|||||
Db 5 ATTTAAATACATGAG 21

RESULT 32

US-09-035-593-3
; Sequence 3, Application US/09035593
; Patent No. 5985264
; GENERAL INFORMATION:
; APPLICANT: Metzger, Dennis W.
; APPLICANT: Arulanandam, Bernard P.
; TITLE OF INVENTION: IL-12 STIMULATION OF NEONATAL IMMUNITY
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: TWO MILITIA DRIVE
; CITY: LEXINGTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,593
; FILING DATE: 05-MAR-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MCO97-02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-09-035-593-3

Query Match 0.4%; Score 15.4; DB 1; Length 21;
Best Local Similarity 94.1%; Pred. No. 73;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2373 TTGTCATCCTGATCTTC 2389
Db 2 TTGTCATCCTGCTCTTC 18
|||||

RESULT 33
US-09-429-323-67
; Sequence 67, Application US/09429323A
; Patent No. 6140126
; Patent No. 6140126 6140123
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF Y-BOX BINDING PROTEIN 1 EXPRESSION
; FILE REFERENCE: RTS-0092
; CURRENT APPLICATION NUMBER: US/09/429,323A
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-429-323-67

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 75;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2139 TCTCCTTTAATTCCTTGTC 2158
Db 1 TCTCCTTGATTCCTTTATC 20
|||||

RESULT 34
US-09-444-053-19/c
; Sequence 19, Application US/09444053A
; Patent No. 6165728
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF NCK-2 EXPRESSION
; FILE REFERENCE: RTS-0122
; CURRENT APPLICATION NUMBER: US/09/444,053A
; CURRENT FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-444-053-19

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 75;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1290 CTAATGAAGGATTCATGAA 1309
Db 20 CCAAGAAGGACTCCATGAA 1
|||||

RESULT 35
US-09-918-686-60/c
; Sequence 60, Application US/09918686
; Patent No. 6475739
; GENERAL INFORMATION:
; APPLICANT: Brunkow, Mary
; APPLICANT: Proll, Sean
; APPLICANT: Paepfer, Bryan
; APPLICANT: Staehling-Hampton, Karen
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; FILE REFERENCE: GENOMIC DELETIONS
; FILE REFERENCE: 240083.515
; CURRENT APPLICATION NUMBER: US/09/918,686
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-918-686-60

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 75;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1116 ATGTTCAAGAGCAGTCTGC 1135
Db 20 ATGTTCAAGAGCAGTCTGC 1
|||||

RESULT 36
US-09-422-978-6588/c
; Sequence 6588, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6588
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20_bind
; OTHER INFORMATION: upstream amplification primer 99-12960 for SEQ 2654,
US-09-422-978-6588

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 75;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1042 GTTCTTTGATCTGTGGTC 1061
Db 20 GTTCTATGTTTGTAGGTC 1
|||||

```
RESULT 37
US-09-198-452A-1301
; Sequence 1301, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198.452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1301
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1301

Query Match      0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 75;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1303 CCATCAAGCTCTTGGGGAAA 1322
Db      1 CCACGAATCTCTTGGGGAAA 20

RESULT 38
US-09-198-452A-3147
; Sequence 3147, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198.452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 3147
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-3147

Query Match      0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 75;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      475 CACCATCTACAGTACTGGAA 494
Db      1 CACCACCTACAGTAATGGCA 20

RESULT 39
US-08-890-719-24/c
; Sequence 24, Application US/08890719A
; Patent No. 6075125
; GENERAL INFORMATION:
; APPLICANT: Bacon, Larry D
; APPLICANT: Hunt, Henry D
; APPLICANT: Fulton, Janet
; TITLE OF INVENTION: Production of Antisera Specific to Major
; TITLE OF INVENTION: Histocompatibility Complex Molecules in Chickens
; FILE REFERENCE: Dkt 0064.96 - Larry D. Bacon et al.
; CURRENT APPLICATION NUMBER: US/08/890.719A
; CURRENT FILING DATE: 1997-07-09
; EARLIER APPLICATION NUMBER: 60/021,685
; EARLIER FILING DATE: 1996-07-10
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1

Query Match      0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 75;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      815 GAACATCTTCATGCTATGT 834
Db      1 GAACGTCTTCATGCTTTGT 20
```

```
; SEQ ID NO 24
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Gallus gallus
US-08-890-719-24

Query Match      0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      815 GAACATCTTCATGCTATGT 834
Db      21 GAACGTCTTCATGCTTTGT 2

RESULT 40
US-08-890-719-26
; Sequence 26, Application US/08890719A
; Patent No. 6075125
; GENERAL INFORMATION:
; APPLICANT: Bacon, Larry D
; APPLICANT: Hunt, Henry D
; APPLICANT: Fulton, Janet
; TITLE OF INVENTION: Production of Antisera Specific to Major
; TITLE OF INVENTION: Histocompatibility Complex Molecules in Chickens
; FILE REFERENCE: Dkt 0064.96 - Larry D. Bacon et al.
; CURRENT APPLICATION NUMBER: US/08/890.719A
; CURRENT FILING DATE: 1997-07-09
; EARLIER APPLICATION NUMBER: 60/021,685
; EARLIER FILING DATE: 1996-07-10
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Gallus gallus
US-08-890-719-26

Query Match      0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      815 GAACATCTTCATGCTATGT 834
Db      1 GAACGTCTTCATGCTTTGT 20

RESULT 41
US-08-943-731-243/c
; Sequence 243, Application US/08943731
; Patent No. 6265157
; GENERAL INFORMATION:
; APPLICANT: PROCKOP, DARWIN J.
; APPLICANT: SPOTILA, LORETTA D.
; APPLICANT: DELTAS, CONSTANTINOS D.
; APPLICANT: SEREDA, LARISA
; APPLICANT: LARSON, ANDREA W.
; APPLICANT: PACK, MICHAEL
; APPLICANT: COLIGE, ALAIN
; APPLICANT: EARLY, JAMES
; APPLICANT: KORKKO, JARMO
; APPLICANT: ALA-KORKKO, LEENA, et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
; TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
; NUMBER OF SEQUENCES: 666
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZ JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
; STREET: FLR.
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-7086
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: PatentIn Release #1.0, Version #1.30
FILING DATE: 03-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,322
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/803,628
FILING DATE: 03-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: DOYLE LEARY Ph.D., KATHRYN
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 9598-27
TELEPHONE: 215-965-1284
TELEFAX: 215-567-2391
TELEX: 831-494
INFORMATION FOR SEQ ID NO: 243:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-943-731-243

Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2501 GATGTTTCAGACCTCCCTTTTA 2520
|||||
DB 21 GATGTTTCAGACCTCCCTTTTA 2

RESULT 42
US-09-422-978-6151
; Sequence 6151, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6151
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21
; OTHER INFORMATION: upstream amplification primer 99-9405 for SEQ 2217,
US-09-422-978-6151

Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 181 GACATTTTGGACAAGTTTA 200
|||||
DB 1 GACATTTTGGACCAGTATA 20

RESULT 43
US-09-422-978-9328/c
; Sequence 9328, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9328
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplification primer 99-25070 for SEQ 1463, in compler
US-09-422-978-9328

Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2699 TCAGTATTATTCTGTCTC 2718
|||||
DB 20 TCACAAATTATTCTGTCTC 1

RESULT 44
US-09-422-978-10352
; Sequence 10352, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10352
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplification primer 99-11340 for SEQ 2487, in compler
US-09-422-978-10352

; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-042-785A-14

Query Match 0.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3166 TCCTGTGACACACAA 3180
Db 1 TCCTGTGACACACAA 15

RESULT 49

US-08-505-509-30/c
; Sequence 30, Application US/08505509
; Patent No. 5776680
; GENERAL INFORMATION:
; APPLICANT: Liebowitz, Michael J.
; APPLICANT: Liu, Yong
; TITLE OF INVENTION: Diagnostic Probes for
; TITLE OF INVENTION: Pneumocystis Carinii
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Muccino
; STREET: P.O. Box 1267
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08551

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/505,509
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/298,087

; FILING DATE:
; APPLICATION NUMBER: US/07/922,987
; FILING DATE: 30-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Muccino, Richard R.
; REGISTRATION NUMBER: 32,538
; REFERENCE/DOCKET NUMBER: UMDI-009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 466-3407
; TELEFAX: (609) 466-2760
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-505-509-30

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 429 CAGAAGCAAGAGCTAAC 446
Db 18 CAGAAGCAAGAGCTAAC 1

RESULT 50

US-08-491-690A-30/c
; Sequence 30, Application US/08491690A
; Patent No. 5849484
; GENERAL INFORMATION:
; APPLICANT: Liebowitz, Michael J.
; APPLICANT: Liu, Yong
; TITLE OF INVENTION: In Vitro Assay For Inhibitors
; TITLE OF INVENTION: Of The Intron Self-Splicing Reaction in Pneumocystis Carinii
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Muccino
; STREET: 758 Springfield Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,690A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/068,248
; FILING DATE: 27-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Muccino, Richard R.
; REGISTRATION NUMBER: 32,538
; REFERENCE/DOCKET NUMBER: UMDI-012

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 273-4988
; TELEFAX: (908) 273-4679
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-491-690A-30

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 429 CAGAAGCAAGAGCTAAC 446
Db 18 CAGAAGCAAGAGCTAAC 1

RESULT 51

US-09-280-409-73/c
; Sequence 73, Application US/09280409
; Patent No. 6107092
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowsett
; APPLICANT: C. Frank Bennett
; APPLICANT: Bert W. O'Malley
; TITLE OF INVENTION: ANTISENSE MODULATION OF SRA EXPRESSION
; FILE REFERENCE: RTS-0048
; CURRENT APPLICATION NUMBER: US/09/280,409
; CURRENT FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 146
; SEQ ID NO 73
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

```

; OTHER INFORMATION: Antisense Oligonucleotide
US-09-280-409-73

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1334 TCTGCAGCCACACTAAG 1351
Db 18 TCTGCAGCCACAGCTGAG 1

RESULT 52
US-09-474-922A-45/c
; Sequence 45, Application US/09474922A
; Patent No. 6187586
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; APPLICANT: Richard A. Roth
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-3 EXPRESSION
; FILE REFERENCE: RTS-0036
; CURRENT APPLICATION NUMBER: US/09/474,922A
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 45
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-474-922A-45

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2423 GCAAGACTGCAGAAAT 2440
Db 18 GCAAGAGAGAGAGAGAAAT 1

RESULT 53
US-09-071-433-26
; Sequence 26, Application US/09071433A
; Patent No. 6197584
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Cowsett, Lex M
; TITLE OF INVENTION: Antisense Modulation of CD40 Expression
; FILE REFERENCE: RTS-0002
; CURRENT APPLICATION NUMBER: US/09/071,433A
; CURRENT FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-071-433-26

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1608 CTCTGTTCAGTTTCTA 1625
Db 1 CTCTGTTCAGGTGTTCTA 18

RESULT 54
US-08-679-645-545
; Sequence 545, Application US/08679645
; Patent No. 6350934
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; APPLICANT: Edington, Brent E.
; APPLICANT: McSwiggan, James A.
; APPLICANT: Merlo, Patricia Ann Owens
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Thomas A.
; APPLICANT: Young, Scott A.
; APPLICANT: Folkerts, Otto
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,645
; FILING DATE: July 12, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; APPLICATION NUMBER: 08/300,726
; FILING DATE: September 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 219/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 545:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-679-645-545

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 79;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 150 CTGCTCAGTCCACCATTTG 167
Db 1 CUGCUCGUCACCCAGUG 18

RESULT 55
US-09-287-599A-6/c
; Sequence 6, Application US/09287599A
; Patent No. 6602712
; GENERAL INFORMATION:
; APPLICANT: Handelsman, Jo
; APPLICANT: Klimowicz, Amy K
; TITLE OF INVENTION: Enterotoxin-Deficient Bacillus
```

FILE REFERENCE: 960296.95327
CURRENT APPLICATION NUMBER: US/09/287,599A
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/080943
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-287-599A-6

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1543 GAAGCGAGAGATAGTTGG 1560
Db 18 GCAGCGAAGATAGTTGG 1

RESULT 56

US-08-938-669A-22
Sequence 22, Application US/08938669A
Patent No. 6171788
GENERAL INFORMATION:
APPLICANT: Nguyen, Thai D.
APPLICANT: Polansky, Jon R.
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND
TITLE OF INVENTION: RELATED DISEASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2402

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,669A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/791,154
FILING DATE: 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mendelson, Elliot
REGISTRATION NUMBER: P-42,878
REFERENCE/DOCKET NUMBER: 07425-0034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 383-6857
TELEFAX: 202 383-6610
TELEX:

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-938-669A-22

Query Match 0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 124 CCTTCTCAGCCTTGCTGC 141
Db 1 CCTTCTCAGCCTTGCTAC 18

RESULT 57

US-09-475-947A-12/c
Sequence 12, Application US/09475947A
Patent No. 6472154
GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: UTSD0667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 19
TYPE: DNA
ORGANISM: human
US-09-475-947A-12

Query Match 0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2412 AGAAAATAAAGCAAGAA 2429
Db 19 AGAAAATAAAGCAAGAA 2

RESULT 58

US-09-306-828-22
Sequence 22, Application US/09306828
Patent No. 6475724
GENERAL INFORMATION:
APPLICANT: Nguyen, Thai D.
APPLICANT: Polansky, Jon R.
APPLICANT: Chen, Pu
APPLICANT: Chen, Hua
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
CURRENT APPLICATION NUMBER: US/09/306,828
CURRENT FILING DATE: 1999-05-07
EARLIER APPLICATION NUMBER: US 09/227,881
EARLIER FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Word 97
SEQ ID NO 22
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
US-09-306-828-22

Query Match 0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 124 CCTTCTCAGCCTTGCTGC 141
Db 1 CCTTCTCAGCCTTGCTAC 18

RESULT 59

US-08-078-683A-25
Sequence 25, Application US/08078683A
Patent No. 5486599
GENERAL INFORMATION:
APPLICANT: Saunders, Scott
APPLICANT: Bernfield, Merton

APPLICANT: Kato, Masato
TITLE OF INVENTION: Construction and Use of Synthetic
TITLE OF INVENTION: Constructs Encoding Syndecan
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/078,683A
FILING DATE: 17-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CME-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FRAGMENT TYPE: internal
US-08-078-683A-25
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 194 AAGTTTAAACGACGAGCC 211
DB 3 AAGCTTATCCAGAGCC 20
RESULT 60
US-08-079-11/c
Sequence 11, Application US/08094079
Patent No. 5512545
GENERAL INFORMATION:
APPLICANT: COOK, Anne L
APPLICANT: CRAIG, Stewart
APPLICANT: CLEMENTS, John M
APPLICANT: EDWARDS, Richard M
APPLICANT: BROWN, David
TITLE OF INVENTION: PDGF-B ANALOGUES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 S. Wacker Dr.
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/094,079
FILING DATE: 24-JAN-1992

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB92/00141
FILING DATE: 24-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9101645.1
FILING DATE: 24-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 93,640
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..20
OTHER INFORMATION: /note= "Synthetic oligonucleotide"
US-08-094-079-11
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2736 CTGTTTCTTAATAAGGAT 2753
DB 18 CTGTTACTTAGTAAGGAT 1
RESULT 61
US-08-184-422-10/c
Sequence 10, Application US/08184422
Patent No. 5565321
GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD
APPLICANT: DAVISON, BARRY
APPLICANT: FANSLAW, WILLIAM
APPLICANT: RENSHAW, BLAIR
APPLICANT: SPRIGGS, MELANIE
APPLICANT: WIDMER, MICHAEL
TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS
TITLE OF INVENTION: IN A CD40 LIGAND GENE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: MS Word for Apple 5.1, Version a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,422
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/009,258
FILING DATE: 01/22/93
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PATRICIA ANNE
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2810-A

```
/
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 2065870430
/ TELEFAX: 2065870606
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: Oligonucleotide
US-08-184-422-10

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 395 CAGGCTCTTCAGCAAAAT 412
Db 19 CAAGCTCTTCAGCAATAT 2

RESULT 62
US-09-226-568-3
/ Sequence 3, Application US/09226568
/ Patent No. 6001992
/ GENERAL INFORMATION:
/ APPLICANT: Ackermann, Elizabeth J.
/ APPLICANT: Bennett, C. Frank
/ APPLICANT: Dean, Nicholas M.
/ APPLICANT: Marcuseon, Eric G.
/ TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic
/ FILE REFERENCE: bcl-2-Related Proteins
/ FILE REFERENCE: ISPH-0337
/ CURRENT APPLICATION NUMBER: US/09/226,568
/ CURRENT FILING DATE: 1999-01-07
/ NUMBER OF SEQ ID NOS: 39
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: antisense
US-09-226-568-3

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1306 TGAAGCTGTTGGGGAAT 1323
Db 2 TGAAGCTGTTGAGCAAT 19

RESULT 63
US-09-359-757-34/c
/ Sequence 34, Application US/09359757
/ Patent No. 6080546
/ GENERAL INFORMATION:
/ APPLICANT: Brett P. Monia
/ APPLICANT: William Gaarde
/ APPLICANT: Lex M. Cowsett
/ TITLE OF INVENTION: ANTISENSE MODULATION OF MEKKS EXPRESSION
/ FILE REFERENCE: R1S-0078
/ CURRENT APPLICATION NUMBER: US/09/359,757
/ CURRENT FILING DATE: 1999-07-23
/ NUMBER OF SEQ ID NOS: 47
/ SEQ ID NO 34
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:

/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-359-757-34

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 969 CAACATAGATGTTACTG 986
Db 18 CAAAGACAGATGTTACTG 1

RESULT 64
US-08-589-771B-10/c
/ Sequence 10, Application US/08589771B
/ Patent No. 6106832
/ GENERAL INFORMATION:
/ APPLICANT: ARMITAGE, RICHARD
/ APPLICANT: DAVISON, BARRY
/ APPLICANT: FANSLON, WILLIAM
/ APPLICANT: RENSHAW, BLAIR
/ APPLICANT: SPRIGGS, MELANIE
/ APPLICANT: WIDMER, MICHAEL
/ TITLE OF INVENTION: TREATMENT OF INDIVIDUALS EXHIBITING
/ TITLE OF INVENTION: DEFECTIVE CD40L (as amended)
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: IMMUNEX CORPORATION
/ STREET: 51 UNIVERSITY STREET
/ CITY: SEATTLE
/ STATE: WASHINGTON
/ COUNTRY: USA
/ ZIP: 98101
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC Compatible
/ OPERATING SYSTEM: MS-DOS/Windows 95
/ SOFTWARE: Word for Windows 95, 7.0a
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/589,771B
/ FILING DATE: January 22, 1996
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/009,258
/ FILING DATE: 01/22/93
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: HENRY, JANIS C.
/ REGISTRATION NUMBER: 34,347
/ REFERENCE/DOCKET NUMBER: 2810-C
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 2065870430
/ TELEFAX: 2065870606
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: Oligonucleotide
US-08-589-771B-10

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 395 CAGGCTCTTCAGCAAAAT 412
Db 19 CAAGCTCTTCAGCAATAT 2

RESULT 65
US-09-249-730-193/c
```

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; Sequence 193, Application US/09249730
; Patent No. 6121000
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and
; TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase
; FILE REFERENCE: 032396-040
; CURRENT APPLICATION NUMBER: US/09/249,730
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 193
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
; US-09-249-730-193

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      277 TGTCACAAACATGAATAA 294
Db      19 TGTCGAAACTTGAATAA 2

RESULT 66
US-09-428-584-38/c
; Sequence 38, Application US/09428584
; Patent No. 6136604
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: Antisense Modulation of Methionine Aminopeptidase 2 Expression
; FILE REFERENCE: RTS-0114
; CURRENT APPLICATION NUMBER: US/09/428,584
; CURRENT FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-428-584-38

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      996 TGGACCAAGCCTGGGATG 1013
Db      19 TGGATCAAGCCTGGGATG 2

RESULT 67
US-08-765-340-82/c
; Sequence 82, Application US/08765340
; Patent No. 6150092
; GENERAL INFORMATION:
; APPLICANT: UCHIDA, K.,
; APPLICANT: UCHIDA, T.,
; APPLICANT: TANAKA, Y.,
; APPLICANT: MATSUDA, Y.,
; APPLICANT: KONDO, S.
; TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID
; NUMBER OF SEQUENCES: 185
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
```

```
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,340
; FILING DATE: 23-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 145146/94
; FILING DATE: 27-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 311130/94
; FILING DATE: 21-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SERUNIAN, LESLIE
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 1452-4005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
; US-08-765-340-82

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2411 AAGAAATAAAGCAAGA 2428
Db      20 AAGAAATAGAGCAAGA 3

RESULT 68
US-09-490-692-135/c
; Sequence 135, Application US/09490692
; Patent No. 6180353
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
; FILE REFERENCE: RTS-0120
; CURRENT APPLICATION NUMBER: US/09/490,692
; CURRENT FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 135
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-490-692-135

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      384 AGCTTCAGCTCGAGCTC 401
Db      19 AGCTTCAGCTCCTGGCTC 2
```

RESULT 69
US-09-280-805-87/c
; Sequence 87, Application US/09280805
; Patent No. 6184212
; GENERAL INFORMATION:
; APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
; APPLICANT: Graham, Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDW2
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 271
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PC
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/280,805
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/048,810
; FILING DATE: March 26, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Licata, Jane Massey
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0346
; TELEPHONE: 609-810-1515
; TELEFAX: 609-810-1454
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-09-280-805-87

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 799 GATTAAACCATTTATGA 816
Db 19 GACTAAACGATTATGA 2

RESULT 70
US-09-313-932-500/c
; Sequence 500, Application US/09313932A
; Patent No. 6228642
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: ISPH-0356
; CURRENT APPLICATION NUMBER: US/09/313,932A
; NUMBER OF SEQUENCES: 1999-05-18
; SEQ ID NO 500
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-313-932-500
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3353 GCACAAAGCAGACTCA 3370
Db 18 GCACACAGAAAGACTCA 1
RESULT 71
US-09-021-701-601/c
; Sequence 601, Application US/09021701
; Patent No. 6251588
; GENERAL INFORMATION:
; APPLICANT: Shannon, Karen W.
; APPLICANT: Wolber, Paul K.
; APPLICANT: Delenstarr, Glenda C.
; APPLICANT: Webb, Peter G.
; APPLICANT: Kincaid, Robert H.
; TITLE OF INVENTION: Methods for evaluating oligonucleotide
; TITLE OF INVENTION: Probe sequences
; NUMBER OF SEQUENCES: 1165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20
; STREET: 3000 Hanover Street
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/021,701
; FILING DATE: 10-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Choi, Wendy A.
; REGISTRATION NUMBER: 36,697
; REFERENCE/DOCKET NUMBER: 10971464-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-236-2386
; TELEFAX: 650-852-8063
; INFORMATION FOR SEQ ID NO: 601:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-021-701-601

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1073 ACTCAAGGATTTCTGGAA 1090
Db 20 ACTCAAGACTTCTGGAA 3

RESULT 72
US-09-021-701-602/c
; Sequence 602, Application US/09021701
; Patent No. 6251588

```
;
; GENERAL INFORMATION:
; APPLICANT: Shannon, Karen W.
; APPLICANT: Wolber, Paul K.
; APPLICANT: Delenstarr, Glenda C.
; APPLICANT: Webb, Peter G.
; APPLICANT: Kincaid, Robert H.
; TITLE OF INVENTION: Methods for evaluating oligonucleotide
; TITLE OF INVENTION: probe sequences
; NUMBER OF SEQUENCES: 1165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20
; STREET: 3000 Hanover Street
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/021.701
; FILING DATE: 10-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Choi, Wendy A.
; REGISTRATION NUMBER: 36,697
; REFERENCE/DOCKET NUMBER: 10971464-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-236-2386
; TELEFAX: 650-852-8063
; INFORMATION FOR SEQ ID NO: 602:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-09-021-701-602

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1073 ACTCAAGGATTCTGGAA 1090
Db 19 ACTCAAGACTTCTGGAA 2

RESULT 73
US-09-021-701-603/c
; Sequence 603, Application US/09021701
; Patent No. 6251588
; GENERAL INFORMATION:
; APPLICANT: Shannon, Karen W.
; APPLICANT: Wolber, Paul K.
; APPLICANT: Delenstarr, Glenda C.
; APPLICANT: Webb, Peter G.
; APPLICANT: Kincaid, Robert H.
; TITLE OF INVENTION: Methods for evaluating oligonucleotide
; TITLE OF INVENTION: probe sequences
; NUMBER OF SEQUENCES: 1165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20
; STREET: 3000 Hanover Street
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/021.701
; FILING DATE: 10-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Choi, Wendy A.
; REGISTRATION NUMBER: 36,697
; REFERENCE/DOCKET NUMBER: 10971464-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-236-2386
; TELEFAX: 650-852-8063
; INFORMATION FOR SEQ ID NO: 602:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-09-021-701-602

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1073 ACTCAAGGATTCTGGAA 1090
Db 19 ACTCAAGACTTCTGGAA 2

RESULT 74
US-09-207-857-4
; Sequence 4, Application US/09207857
; Patent No. 6309879
; GENERAL INFORMATION:
; APPLICANT: Burckoff, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; FILE REFERENCE: ONV-05001
; CURRENT APPLICATION NUMBER: US/09/207,857
; CURRENT FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: primer
; US-09-207-857-4

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 203 CACGAGCGCCAGACCTG 220
Db 1 CACAAAGCCCAAGACCTG 18

RESULT 75
US-09-373-845-17
; Sequence 17, Application US/09373845
; Patent No. 6316230
; GENERAL INFORMATION:
; APPLICANT: The Perkin-Elmer Corporation
; TITLE OF INVENTION: POLYMERASE EXTENSION AT 3' TERMINUS OF PNA-DNA CHIMERA
; FILE REFERENCE: 4468 US
; CURRENT APPLICATION NUMBER: US/09/373,845
; CURRENT FILING DATE: 1999-08-13
```

```
;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/021,701
; FILING DATE: 10-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Choi, Wendy A.
; REGISTRATION NUMBER: 36,697
; REFERENCE/DOCKET NUMBER: 10971464-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-236-2386
; TELEFAX: 650-852-8063
; INFORMATION FOR SEQ ID NO: 603:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-09-021-701-603

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1073 ACTCAAGGATTCTGGAA 1090
Db 18 ACTCAAGACTTCTGGAA 1

RESULT 74
US-09-207-857-4
; Sequence 4, Application US/09207857
; Patent No. 6309879
; GENERAL INFORMATION:
; APPLICANT: Burckoff, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; FILE REFERENCE: ONV-05001
; CURRENT APPLICATION NUMBER: US/09/207,857
; CURRENT FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: primer
; US-09-207-857-4

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 203 CACGAGCGCCAGACCTG 220
Db 1 CACAAAGCCCAAGACCTG 18

RESULT 75
US-09-373-845-17
; Sequence 17, Application US/09373845
; Patent No. 6316230
; GENERAL INFORMATION:
; APPLICANT: The Perkin-Elmer Corporation
; TITLE OF INVENTION: POLYMERASE EXTENSION AT 3' TERMINUS OF PNA-DNA CHIMERA
; FILE REFERENCE: 4468 US
; CURRENT APPLICATION NUMBER: US/09/373,845
; CURRENT FILING DATE: 1999-08-13
```



```
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Mouse Murine Xist gene
US-09-373-845-17

Query Match          0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1006 CTGGGATGCCAGAGAAAT 1023
Db 2 CTGGGATGCCAAAGAGCAT 19

RESULT 76
US-09-488-856A-46
; Sequence 46, Application US/09488856A
; Patent No. 6316259
; GENERAL INFORMATION:
; APPLICANT: Robert McKay
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 ALPHA EXP
; FILE REFERENCE: RTS-0115
; CURRENT APPLICATION NUMBER: US/09/488,856A
; CURRENT FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 46
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-488-856A-46

Query Match          0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2192 AGCACTGAAGTTGAAAG 2209
Db 2 AGCACTGAAGTTGAAG 19

RESULT 77
US-08-618-957A-26/c
; Sequence 26, Application US/08618957A
; Patent No. 6355237
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. Ralph
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas Joel
; APPLICANT: Shafer, Alan Wayne
; TITLE OF INVENTION: METHODS FOR USING THE OBESE
; TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
; TITLE OF INVENTION: DEVELOPMENT
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds LLP
; STREET: 1155 Avenue of The Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
```

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,957A
; FILING DATE: 20-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 008907-0033-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-618-957A-26

Query Match          0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 595 TTGGGAAAGCTGGAGATC 612
Db 20 TTGAGAAAGCTGGGATC 3

RESULT 78
US-09-702-246-15/c
; Sequence 15, Application US/09702246
; Patent No. 6383809
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF CYTOSIN-1 EXPRESSION
; FILE REFERENCE: RTS-0195
; CURRENT APPLICATION NUMBER: US/09/702,246
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-702-246-15

Query Match          0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1005 CTGGGATCCACAGAGAA 1022
Db 18 CCTGGGATCCACAGAGA 1

RESULT 79
US-09-517-467B-157/c
; Sequence 157, Application US/09517467B
; Patent No. 6451602
; GENERAL INFORMATION:
; APPLICANT: Ian Popoff
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF PAPP EXPRESSION
; FILE REFERENCE: RTS-0150
; CURRENT APPLICATION NUMBER: US/09/517,467B
; CURRENT FILING DATE: 2001-03-02
```

```
; PRIOR APPLICATION NUMBER: 09/517,467
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 345
; SEQ ID NO 157
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-517-467B-157

Query Match          0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1474 GAAGTGGAGGTGGATGGT 1491
Db 18 GAAGTGGAGAGGATGGT 1

RESULT 80
US-09-375-318-69/c
; Sequence 69, Application US/09375318
; Patent No. 6468791
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; Masco, Wilma
; Levy-Lahad, Ephrat
; Bird, Thomas D.
; Galas, David J.
; TITLE OF INVENTION: CHROMOSOME 1 GENE AND GENE PRODUCTS RELATED TO
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BEERY LLP
; STREET: 701 Fifth Ave, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/375,318
; FILING DATE: 16-Aug-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Verna, James M.
; REGISTRATION NUMBER: 33,287
; REFERENCE/DOCKET NUMBER: 920010.571C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-09-375-318-69

Query Match          0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3203 GAATCCCGAGCATGCC 3220
Db 18 GAGCTCTCAGAGCATGCC 1
```

```
RESULT 81
US-08-471-970A-25
; Sequence 25, Application US/08471970A
; Patent No. 6531295
; GENERAL INFORMATION:
; APPLICANT: Saunders, Scott
; APPLICANT: Bernfield, Merton
; APPLICANT: Kato, Masato
; TITLE OF INVENTION: Construction and Use of Synthetic
; TITLE OF INVENTION: Constructs Encoding Syndecan
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,970A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/078,683
; FILING DATE: 17-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: P-41,106
; REFERENCE/DOCKET NUMBER: CME-062DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FRAGMENT TYPE: internal
US-08-471-970A-25

Query Match          0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 194 AAGTTTACCACGAGCC 211
Db 3 AAGCTTATCCACGAGCC 20

RESULT 82
US-09-198-452A-4789/c
; Sequence 4789, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; TITLE OF INVENTION: and treatment of infection
; TITLE OF INVENTION: 9710-003-999
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4789
; LENGTH: 20
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; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-4789

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 951 TTCCCTTTGGACAGAAC 968
Db 20 TTCTCTTTGGACAGAC 3

RESULT 83
US-09-249-247-193/c
; Sequence 193, Application US/09249247
; Patent No. 6593305
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and
; TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase
; FILE REFERENCE: 032396-023
; CURRENT APPLICATION NUMBER: US/09/249,247
; CURRENT FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: US 60/023,040
; EARLIER FILING DATE: 1996-08-02
; EARLIER APPLICATION NUMBER: US 60/039,959
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: US 08/904,901
; EARLIER FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 193
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-249-247-193

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 277 TGTCGAAAACATGAATAA 294
Db 19 TGTCGAAAACATGAATAA 2

RESULT 84
US-09-081-385-33/c
; Sequence 33, Application US/09081385
; Patent No. 6593456
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, T.
; APPLICANT: Granger, G.A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
; TITLE OF INVENTION: of Use Thereof
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,385

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/964,747
; FILING DATE: 05-NOV-1997
; APPLICATION NUMBER: 60/030,761
; FILING DATE: 06-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wu, Frank
; REGISTRATION NUMBER: 41,386
; REFERENCE/DOCKET NUMBER: 22000-20577.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-081-385-33

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 589 CTGGGCTTGGAAAGCTG 606
Db 20 CTGGGCTTGGACAGCTG 3

RESULT 85
US-09-909-280A-4
; Sequence 4, Application US/09909280A
; Patent No. 6605700
; GENERAL INFORMATION:
; APPLICANT: Bumcroft, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; TITLE OF INVENTION: THERETO
; FILE REFERENCE: CIBT-P02-050
; CURRENT APPLICATION NUMBER: US/09/909,280A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/207,857
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 60/067,940
; PRIOR FILING DATE: 1997-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-909-280A-4

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 203 CACGAGCCGAGACCTG 220
Db 1 CACAAAGCCCAAGACCTG 18

RESULT 86
US-09-009-913-144
; Sequence 144, Application US/09009913
; Patent No. 6087485
; GENERAL INFORMATION:
; APPLICANT: AXYS Pharmaceuticals, Inc.
; TITLE OF INVENTION: Asthma Related Genes
```


Query Match 0.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 82;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1144 AGCTTGGGACTGGG 1159
|||||
DB 16 AGCTTGGGCCCTGGG 1

RESULT 90

US-08-373-124A-2015
; Sequence 2015, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2015:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-2015

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 89;
Matches 8; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 2544 GAGGTGATTTGTTGT 2559
|||||
DB 1 GAGGAGAUUUUGUUGU 16

RESULT 91

US-08-435-628-2015
; Sequence 2015, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628
FILING DATE: 05-MAY-1995

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,124
FILING DATE: January 13, 1995
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2015:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-435-628-2015

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 89;
Matches 8; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 2544 GAGGTGATTTGTTGT 2559
|||||
DB 1 GAGGAGAUUUUGUUGU 16

RESULT 92

US-08-985-162-40/c
; Sequence 40, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir

Db 17 AAATTCGACGACCA 2
|||||

RESULT 95
US-08-078-683A-32
; Sequence 32, Application US/08078683A
; Patent No. 5486599
; GENERAL INFORMATION:
; APPLICANT: Saunders, Scott
; APPLICANT: Bernfield, Merton
; APPLICANT: Kato, Masato
; TITLE OF INVENTION: Construction and Use of Synthetic
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/078,683A
; FILING DATE: 17-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CME-062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-078-683A-32

Query Match 0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 96;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2375 GTCATCTGATCTTCA 2390
Db 2 GCATCTGATCTTCA 17
|||||

RESULT 96
US-09-270-140A-27
; Sequence 27, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Allison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J&J1799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 27

LENGTH: 18
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:mutant RNA for
; OTHER INFORMATION: codon 41 of HIV 1 AZT resistance mutant with A to
; OTHER INFORMATION: U or C.
US-09-270-140A-27

Query Match 0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 96;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 480 TCTACAGTACTGGAAAAG 497
Db 1 UGUACAGAAUYUGAAAAG 18
:|||||:::|||||

RESULT 97
US-09-270-140A-65/C
; Sequence 65, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Allison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J&J1799
; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 65
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:antisense for
; OTHER INFORMATION: HIV 1 AZT resistance Codon 41 mutant (A to U or C)
US-09-270-140A-65

Query Match 0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 96;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 480 TCTACAGTACTGGAAAAG 497
Db 18 TGTACAGAAUYTGAAAAG 1
|||||

RESULT 98
US-08-471-970A-32
; Sequence 32, Application US/08471970A
; Patent No. 6531295
; GENERAL INFORMATION:
; APPLICANT: Saunders, Scott
; APPLICANT: Bernfield, Merton
; APPLICANT: Kato, Masato
; TITLE OF INVENTION: Construction and Use of Synthetic
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,970A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,683
FILING DATE: 17-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: P-41,106
REFERENCE/DOCKET NUMBER: CME-062DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-471-970A-32

Query Match 0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 96;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2375 GTCATCCTGATCTTCA 2390
| | | | | | | | | | | | | | | | | |
DB 2 GCCATCCTGATCTTCA 17

RESULT 99

US-09-422-978-5818/c
Sequence 5818, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CPI
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 5818
LENGTH: 18
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..18
OTHER INFORMATION: upstream amplification primer 99-7107 for SEQ 1884,
US-09-422-978-5818

Query Match 0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 96;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1607 TCTCTGTTCCATGTTT 1622
| | | | | | | | | | | | | | | | | |
DB 17 TGTCTGTTCCATGTTT 2

RESULT 100

US-09-422-978-8906/c
Sequence 8906, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CPI
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 8906
LENGTH: 19
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..19
OTHER INFORMATION: downstream amplification primer 99-1964 for SEQ 1041, in complem
US-09-422-978-8906

Query Match 0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 429 CAGAAGACACAGACAA 444
| | | | | | | | | | | | | | | | | |
DB 19 CAGAAGACACAGATCAA 4

RESULT 101

US-08-117-952-359
Sequence 359, Application US/08117952
Patent No. 5851760
GENERAL INFORMATION:
APPLICANT: Evans, Glen A.
APPLICANT: Smith, Michael W.
TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
NUMBER OF SEQUENCES: 797
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,952
FILING DATE: 07-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,471
FILING DATE: 15-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9423
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392

; INFORMATION FOR SEQ ID NO: 359:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-117-952-359

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2480 CCAGATTCCAAAACA 2495
DB 1 CCATGATCCAAAACA 16

RESULT 102

US-09-357-070-31/c
; Sequence 31, Application US/09357070
; Patent No. 6045049
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF P13 KINASE P110 DELTA EXPRESSION
; FILE REFERENCE: RTS-0076
; CURRENT APPLICATION NUMBER: US/09/357,070
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 31
; LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-070-31

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2650 GTCCAAAGACAACATG 2665
DB 20 GTCCAAAGACAACAGG 5

RESULT 103

US-09-428-219-38
; Sequence 38, Application US/09428219
; Patent No. 6177273
; GENERAL INFORMATION:

; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN-LINKED KINASE EXPRESSION
; FILE REFERENCE: RTS-0101
; CURRENT APPLICATION NUMBER: US/09/428,219
; CURRENT FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 38
; LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide
US-09-428-219-38

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2884 CTTGTATGAATATGG 2899
DB 4 CTTGTATGAATACGG 19

RESULT 104

US-09-657-481A-59/c
; Sequence 59, Application US/09657481A
; Patent No. 6258601
; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF UBIQUITIN PROTEIN LIGASE WWP1 AND W
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0087
; CURRENT APPLICATION NUMBER: US/09/657,481A
; CURRENT FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 93
; SEQ ID NO 59
; LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-657-481A-59

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1245 ATGATATGCCATATGC 1260
DB 18 ATGATATGCCATCTGC 3

RESULT 105

US-09-360-197-19/c
; Sequence 19, Application US/09360197
; Patent No. 6287859
; GENERAL INFORMATION:

; APPLICANT: Bassilana, Frederic
; APPLICANT: Lazdunski, Michel
; APPLICANT: Waldmann, Rainer
; APPLICANT: Deweille, Jan R.
; TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
; TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications
; FILE REFERENCE: 989.6706P
; CURRENT APPLICATION NUMBER: US/09/360,197
; CURRENT FILING DATE: 1997-07-23

; PRIOR APPLICATION NUMBER: 09/129,758
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: 60/095,408
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-360-197-19

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 668 GAGATGGCAAGAGCAA 683
DB 17 GAGATGGCAAGAGCAA 2

RESULT 106

```
US-09-676-610B-119
; Sequence 119, Application US/09676610B
; Patent No. 644465
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
; FILE REFERENCE: RTS-0138
; CURRENT APPLICATION NUMBER: US/09/676,610B
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-676-610B-119

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1503 AAATTCCTCCAGGACCA 1518
Db 1 AAATTCCTCCAGGACCA 16

RESULT 107
US-09-422-978-7273
; Sequence 7273, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilva
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7273
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer 99-3390 for SEQ 3339,
US-09-422-978-7273

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3123 AGAGGACATTGCTTTT 3138
Db 4 AGAGTACATTGCTTTT 19

RESULT 108
US-09-198-452A-2103/c
; Sequence 2103, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
```

```
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2103
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-2103

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3254 TGGAGTCGATCGAAAT 3269
Db 20 TGGAGGGAATCGAAAT 5

RESULT 109
US-08-664-596B-33
; Sequence 33, Application US/08664596B
; Patent No. 5807703
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Lavallie, Edward
; APPLICANT: Racie, Lisa
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Evans, Cheryl
; APPLICANT: Spaulding, Vikki
; APPLICANT: Bowman, Michael
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/664,596B
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
US-08-664-596B-33

Query Match      0.4%; Score 14.4; DB 1; Length 29;
Best Local Similarity 72.0%; Pred. No. 1.7e+02;
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Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2763 GAGTATATTAGGGAAGTGTGTAAT 2787
Db 1 GNATACATTGGCAAGTGTGACT 25

RESULT 110

US-08-233-130A-2/c
; Sequence 2, Application US/08233130A
; Patent No. 5587300
; GENERAL INFORMATION:
; APPLICANT: Malter, James S.
; TITLE OF INVENTION: Method to Increase Regulatory Molecule
; TITLE OF INVENTION: Production
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: 203 Textile Building, 119 No. 5587300th Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA

ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,130A
; FILING DATE: 26-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.

REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 119.00010101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1220
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

US-08-233-130A-2

Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 394 GCAGGCTCTCAGCAAAAT 412
Db 19 GCAGGCTCTCAGCCACAT 1

RESULT 111

US-08-913-833-35/c
; Sequence 35, Application US/08913833
; Patent No. 6087093
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; APPLICANT: LOUWAGIE, JOOST
; APPLICANT: ROSSAU, RUDI
; TITLE OF INVENTION: METHOD FOR DETECTION OF DRUG-INDUCED
; NUMBER OF SEQUENCES: 164
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS

COUNTRY: USA
ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,833
; FILING DATE: 15 Sep 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP97/00211
; FILING DATE: 17 Jan 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 96870005.4
; FILING DATE: 26 Jan 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 96870081.5
; FILING DATE: 25 Jun 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.

REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:008
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-913-833-35

Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2729 TTCGTCTCTGTTCTTAAT 2747
Db 19 TACTGTCTCTTCTTTAT 1

RESULT 112

US-09-289-380-10/c
; Sequence 10, Application US/09289380
; Patent No. 6165721
; GENERAL INFORMATION:
; APPLICANT: Rostkowski, Christine
; APPLICANT: McWilliam, Ray
; APPLICANT: Hellyer, Tobin
; TITLE OF INVENTION: Amplification and Detection of Salmonella spp.
; FILE REFERENCE: Amplif. and Detection of Salmonella sp
; CURRENT APPLICATION NUMBER: US/09/289,380
; CURRENT FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Bumper primer
; OTHER INFORMATION: for SDA of Salmonella spp.
US-09-289-380-10

Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2461 TAGCAAGGAGAAATAAT 2479
Db 19 TATCGAGAGAGAAATAAT 1

; PRIOR FILING DATE: 1997-01-17
; PRIOR APPLICATION NUMBER: EP 96870005.4
; PRIOR FILING DATE: 1996-01-26
; PRIOR APPLICATION NUMBER: EP 96870081.5
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-580-794C-35
Query Match 0.4% Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2729 TTCTGTTCTGTTCTTAAT 2747
DB 19 TACTGTTCTTTTCTTAT 1
RESULT 115
US-09-091-952A-122
; Sequence 122, Application US/09091952A
; Patent No. 6458532
; GENERAL INFORMATION:
; APPLICANT: Detera-Wadleigh, Sevilla D.
; Gershon, Elliot S.
; Badner, Judith A.
; Goldin, Lynn R.
; Berrettini, Wade H.
; Yoshikawa, Takeo
; Sanders, Alan R.
; Esterling, Lisa E.
; TITLE OF INVENTION: Chromosomal Markers and Diagnostic
; Tests for Manic-Depressive Illness
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/091,952A
; FILING DATE: 19-Apr-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/029,278
; FILING DATE: 28-OCT-1996
; APPLICATION NUMBER: PCT/US97/19381
; FILING DATE: 28-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Timothy L.
; REGISTRATION NUMBER: 35,367
; REFERENCE/DOCKET NUMBER: 015280-297100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid

; PRIOR FILING DATE: 1997-01-17
; PRIOR APPLICATION NUMBER: EP 96870005.4
; PRIOR FILING DATE: 1996-01-26
; PRIOR APPLICATION NUMBER: EP 96870081.5
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 164
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-580-794C-35
Query Match 0.4% Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3354 CACAAAGCAGCACACTCAAT 3372
DB 19 CACAAAGCAGCACACTCAAT 1
RESULT 114
US-09-580-794C-35/c
; Sequence 35, Application US/09580794C
; Patent No. 6331389
; GENERAL INFORMATION:
; APPLICANT: Stuyver, Lieven
; APPLICANT: Louwaghe, Joost
; APPLICANT: Rossau, Rudi
; TITLE OF INVENTION: METHOD FOR DETECTION OF DRUG-INDUCED MUTATIONS IN THE REVERSE
; TITLE OF INVENTION: TRANSCRIPTASE GENE
; FILE REFERENCE: INNS008--2
; CURRENT APPLICATION NUMBER: US/09/580,794C
; CURRENT FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 08/913,833 now US/6,087,093
; PRIOR FILING DATE: 1997-09-15
; PRIOR APPLICATION NUMBER: PCT/EP 97/00211

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1...19
; OTHER INFORMATION: Clone 7 forward primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 122:
US-09-091-952A-122

Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 325 GGAACAGTCCACACTTGGC 343
Db 1 GGAACAGTGTACACTTCC 19

RESULT 116
US-09-422-978-6079
; Sequence 6079, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET 020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6079
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-8799 for SEQ 2145,
US-09-422-978-6079

Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 726 AAGTAATGGGTAGATGG 744
Db 1 ACGAAATGGGGAGATGG 19

RESULT 117
US-09-422-978-9062/c
; Sequence 9062, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET 020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23

; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9062
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: downstream amplification primer 99-21167 for SEQ 1197, in comple
US-09-422-978-9062

Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3127 GACATTGCTTTTCACATTC 3145
Db 19 GGCATTGCTTTTCAGTTC 1

RESULT 118
US-07-807-529A-34
; Sequence 34, Application US/07807529A
; Patent No. 5547669
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenstern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-Chang
; APPLICANT: Morville, Malcolm
; TITLE OF INVENTION: RECOMBITOPE PEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: One Kendall Square, Building 600
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/807,529A
; FILING DATE: 199111213
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/662,276
; FILING DATE: 28-FEB-1991
; APPLICATION NUMBER: US 07/431,565
; FILING DATE: 03-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Channing, Stacey L.
; REGISTRATION NUMBER: 31,095
; REFERENCE/DOCKET NUMBER: IPC-027/imi-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 494-0060
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 9..20

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US-07-807-529A-34
Query Match          0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2400 GAGATCGGAGGAGGATGTC 2418
Db 2 GGGATCCGAGAGACAAA 20

RESULT 119
US-08-999-996-33
; Sequence 33, Application US/08089996
; Patent No. 5703054
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett
; TITLE OF INVENTION: Oligonucleotide Modulation of Protein
; TITLE OF INVENTION: Kinase C
; NUMBER OF SEQUENCES: 62
; ADDRESS: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & No. 5703054ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/089,996
; FILING DATE: 19930709
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 852,852
; FILING DATE: March 16, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Rebecca Ralph Gaumond
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: ISIS-1154
; TELEPHONE: (215) 568-3439
; TELEFAX: (215) 568-3100
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
; US-08-089-996-33

Query Match          0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2096 TTTGGGGAGGAGGATGTC 2114
Db 1 TTTGGGGATGAGGGTGAC 19

RESULT 120
US-08-478-178A-33
; Sequence 33, Application US/08478178A
; Patent No. 5882927
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett
; TITLE OF INVENTION: Oligonucleotide Modulation of
; TITLE OF INVENTION: Protein Kinase C
; NUMBER OF SEQUENCES: 121
; ADDRESS: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & No. 5885970ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,177
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; US-08-478-178A-33

Query Match          0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2096 TTTGGGGAGGAGGATGTC 2114
Db 1 TTTGGGGATGAGGGTGAC 19

RESULT 121
US-08-488-177-33
; Sequence 33, Application US/08488177
; Patent No. 5885970
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett
; TITLE OF INVENTION: Oligonucleotide Modulation of
; TITLE OF INVENTION: Protein Kinase C
; NUMBER OF SEQUENCES: 121
; ADDRESS: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & No. 5885970ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,177
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; US-08-488-177-33
```

APPLICATION NUMBER: 852,852
FILING DATE: March 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS-1995
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-08-488-177-33

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2096 TTTGGGGAGGAGGATGTC 2114
Db 1 TTTGGGGATGAGGGTGAGC 19

RESULT 122
US-08-481-072A-33
Sequence 33, Application US/08481072A
Patent No. 5916807
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett
TITLE OF INVENTION: Oligonucleotide Modulation of
Kinase C
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & No. 5916807ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,072A
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: March 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumond
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-1154
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-08-481-072A-33

Query Match 0.4%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2096 TTTGGGGAGGAGGATGTC 2114
Db 1 TTTGGGGATGAGGGTGAGC 19

RESULT 123
US-08-540-804-20/c
Sequence 20, Application US/08540804
Patent No. 5919666
GENERAL INFORMATION:
APPLICANT: Young, Richard A.
APPLICANT: Koleske, Anthony J.
APPLICANT: Thompson, Craig M.
APPLICANT: Chao, David M.
TITLE OF INVENTION: No. 5919666el Factors Which Modify Gene
Transcription and Methods of Use Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/540,804
FILING DATE: 11-OCT-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/521,872
FILING DATE: 21-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,265
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI94-03A2
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-540-804-20

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2119 GGCTAATTGAAACCAAGA 2137
Db 19 GCGGAGTTTGAGCAAGA 1

RESULT 124
US-08-218-265-20/c
Sequence 20, Application US/08218265
Patent No. 5922585
GENERAL INFORMATION:
APPLICANT: Young, Richard A.

APPLICANT: Koleske, Anthony J.
APPLICANT: Thompson, Craig M.
TITLE OF INVENTION: No. 5922585el Factors Which Modify Gene
TITLE OF INVENTION: Transcription and Methods of Use Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/218,265
FILING DATE: 25-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI94-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-9540
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-218-265-20

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2119 GGCTAATTGAAACCAAGA 2137
||| ||||| |||||
Db 19 GCGAGTTGAGACCAAGA 1

RESULT 125
US-08-664-336-33
Sequence 33, Application US/08664336
Patent No. 5922686
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett
TITLE OF INVENTION: Oligonucleotide Modulation of Protein
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & No. 5922686ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 720 kb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/664,336
FILING DATE: herewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852

FILING DATE: March 16, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 089,996
FILING DATE: July 9, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS-2345
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: YES
US-08-664-336-33
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2096 TTGGGGGAGGAGGATGTC 2114
||| ||||| |||||
Db 1 TTGGGGATGAGGGTGAGC 19
RESULT 126
US-08-975-211-8
Sequence 8, Application US/08975211
Patent No. 5948902
GENERAL INFORMATION:
APPLICANT: Honkanen, Richard E
APPLICANT: Dean, Nicholas M
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jaseckle Fleischmann & Muegel, LLP
STREET: 39 State Street
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14614-1310
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,211
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87647.97R407
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-262-3640
TELEFAX: 716-262-4133
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
ANTI-SENSE: YES
US-08-975-211-8
Query Match 0.4%; Score 14.2; DB 1; Length 20;


```
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1471 AGAGAGTGGAGGTGGATG 1489
Db 1 AGAGCCCTGGAGGTGGATG 19

RESULT 127
US-08-481-066A-33
; Sequence 33, Application US/08481066A
; Patent No. 5959096
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett
; TITLE OF INVENTION: Oligonucleotide Modulation of
; TITLE OF INVENTION: Protein Kinase C
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & No. 5959096ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,066A
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 852,852
; FILING DATE: March 16, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Rebecca Ralph Gaumond
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: ISIS-1154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
US-08-481-066A-33

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2096 TTGTGGGAGGAGTGTGC 2114
Db 1 TTGTGGGAGTGGGTGAGC 19

RESULT 128
US-08-888-982A-21
; Sequence 21, Application US/08888982A
; Patent No. 5981731
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation
; TITLE OF INVENTION: of raf Gene Expression
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2327 TGGCTGATGTTTGGGAG 2345
Db 1 TGGATGGGTGTTTGGAG 19

RESULT 129
US-09-205-860-3
; Sequence 3, Application US/09205860
; Patent No. 5981732
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-13 EXPRESSION
; FILE REFERENCE: RTS-0031
; CURRENT APPLICATION NUMBER: US/09/205,860
; CURRENT FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-205-860-3

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 389 CAGCTGCAGGCTCTTCAGC 407
Db 1 CAGCTGCAGGCTCTTCAGC 407
```



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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 852,852
; FILING DATE: 16-MAR-1992
; APPLICATION NUMBER: 08/089,996
; FILING DATE: 09-JUL-1993
; APPLICATION NUMBER: 08/199,779
; FILING DATE: 22-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-1568
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
; US-08-578-615A-33

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2096 TTGGGGAGGAGGATGTC 2114
Db 1 TTGGGGATGAGGGTGAC 19

RESULT 133
US-08-300-928C-83
; Sequence 83, Application US/08300928C
; Patent No. 6019972
; GENERAL INFORMATION:
; APPLICANT: GETTER, Malcolm L. et al.
; TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
; TITLE OF INVENTION: PROTEIN (TRFP)
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMLOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02145
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/300,928C
; FILING DATE: September 2, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,529
; FILING DATE: December 13, 1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: AMY E. MANDRAGOURAS
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: 002.6US (IMI-044)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

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; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 9..20
; US-08-300-928C-83

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2400 GAGATCGGAAGAGAAAAA 2418
Db 2 GGGATCCGAGAGACAAA 20

RESULT 134
US-08-430-944D-83
; Sequence 83, Application US/08430944D
; Patent No. 6025162
; GENERAL INFORMATION:
; APPLICANT: Bruce L. Rogers et al.
; TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,944D
; FILING DATE: 28-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430,014
; FILING DATE: 27-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,928
; FILING DATE: 02-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-044DV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 9..20
; US-08-430-944D-83

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2400 GAGATCGGAAGAGAAAAA 2418
Db 2 GGGATCCGAGAGACAAA 20
```

RESULT 135
US-08-430-014-83
; Sequence 83, Application US/08430014
; Patent No. 6048962
; GENERAL INFORMATION:
; APPLICANT: GETTER, Malcolm L. et al.
; TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
; TITLE OF INVENTION: PROTEIN (TRFP)
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02145
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,014
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/300,928
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: AMY E. MANDRAGOURAS
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: 002.6US (IMI-044)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 9..20
US-08-430-014-83

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2400 GAGATCGGAAGAGAAAA 2418
DB 2 GCGATCCGAGAGACAAA 20

RESULT 136
US-09-120-853-11/c
; Sequence 11, Application US/09120853
; Patent No. 6057437
; GENERAL INFORMATION:
; APPLICANT: Kamiya, Kinya
; APPLICANT: Matsuda, Yoko
; APPLICANT: Uchida, Kiyoshi
; TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID COMPOUND
; FILE REFERENCE: 07898/030001
; CURRENT APPLICATION NUMBER: US/09/120,853
; CURRENT FILING DATE: 1998-07-21
; EARLIER APPLICATION NUMBER: JP 213838/1997
; EARLIER FILING DATE: 1997-07-25
; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: nucleic acid sequence
US-09-120-853-11

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1597 TGACCCCGCATCTCTTC 1615
DB 19 TGACCCCGCTCTCTCTTC 1

RESULT 137
US-08-431-184-83
; Sequence 83, Application US/08431184
; Patent No. 6120769
; GENERAL INFORMATION:
; APPLICANT: Bruce L. Rogers et al.
; TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,184
; FILING DATE: 28-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430,014
; FILING DATE: 27-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,928
; FILING DATE: 02-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-044DV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 9..20
US-08-431-184-83

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2400 GAGATCGGAAGAGAAAA 2418


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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/021,701
; FILING DATE: 10-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Choi, Wendy A.
; REGISTRATION NUMBER: 36,697
; REFERENCE/DOCKET NUMBER: 10971464-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-236-2386
; TELEFAX: 650-852-8063
; INFORMATION FOR SEQ ID NO: 553:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-09-021-701-553

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2068 TTTAAAGTAAATAATCAG 2086
Db 20 TTTAAAGTAAATAATCAG 2

RESULT 144
US-09-021-701-554/c
; Sequence 554, Application US/09021701
; Patent No. 6251588
; GENERAL INFORMATION:
; APPLICANT: Shannon, Karen W.
; APPLICANT: Wolber, Paul K.
; APPLICANT: Delenstarr, Glenda C.
; APPLICANT: Webb, Peter G.
; APPLICANT: Kincaid, Robert H.
; TITLE OF INVENTION: Methods for evaluating oligonucleotide
; NUMBER OF SEQUENCES: 1165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20
; STREET: 3000 Hanover Street
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/021,701
; FILING DATE: 10-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Choi, Wendy A.
; REGISTRATION NUMBER: 36,697
; REFERENCE/DOCKET NUMBER: 10971464-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-236-2386
; TELEFAX: 650-852-8063
; INFORMATION FOR SEQ ID NO: 554:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-09-021-701-554

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2068 TTTAAAGTAAATAATCAG 2086
Db 19 TTTAAAGTAAATAATCAG 1

RESULT 145
US-09-489-868A-19
; Sequence 19, Application US/09489868A
; Patent No. 6265216
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF COT ONCOGENE EXPRESSION
; FILE REFERENCE: RTS-0113
; CURRENT APPLICATION NUMBER: US/09/489,868A
; CURRENT FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-489-868A-19

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 33 GAAATCTCATGAGGAGGT 51
Db 2 GAGAGTCTCATGAGGTGGT 20

RESULT 146
US-09-593-711A-86/c
; Sequence 86, Application US/09593711A
; Patent No. 6271030
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION
; FILE REFERENCE: RTS-0118
; CURRENT APPLICATION NUMBER: US/09/593,711A
; CURRENT FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 244
; SEQ ID NO 86
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-593-711A-86

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 126 TTCTCAGCCTTGTGCTGT 144
Db 20 TTCTAGGCGTTGTGCTGT 2
```

```
RESULT 147
US-09-467-642-23/c
; Sequence 23, Application US/09457642
; Patent No. 6300132
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF TELOMERIC REPEAT BINDING FACTOR 2 EXPRES
; FILE REFERENCE: RTS-0106
; CURRENT APPLICATION NUMBER: US/09/467,642
; CURRENT FILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-467-642-23

Query Match          0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 769 GATTGAGATCTGGAACAT 787
Db 20 GATTGAGAGGGGAAAAAT 2

RESULT 148
US-09-657-042A-39
; Sequence 39, Application US/09657042A
; Patent No. 6329203
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-1 EXPRES
; FILE REFERENCE: RTS-0148
; CURRENT APPLICATION NUMBER: US/09/657,042A
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-657-042A-39

Query Match          0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 136 TGTGCTGTAACGTGCTGCT 154
Db 2 TGTGCTGGAGCTGCTGCT 20

RESULT 149
US-08-829-637A-33
; Sequence 33, Application US/08829637A
; Patent No. 6339066
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Phillip Dan Cook
; APPLICANT: Nicholas Dean
; APPLICANT: Glenn Hoke
; TITLE OF INVENTION: OLIGONUCLEOTIDES WHICH HAVE
; TITLE OF INVENTION: PHOSPHOROTHIATE LINKAGES OF HIGH CHIRAL PURITY AND
; TITLE OF INVENTION: WHICH MODULATE at, all, , k, n, AND ISOFORMS OF
; TITLE OF INVENTION: PROTEIN KINASE C
; NUMBER OF SEQUENCES: 136
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John W. Caldwell (28,937) Woodcock
; ADDRESSEE: Washburn Kurtz Mackiewicz & No. 6339066ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,637A
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,066
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,129
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,851
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/468,569
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/089,996
; FILING DATE: 09-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/058,023
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/777,007
; FILING DATE: 16-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/777,760
; FILING DATE: 15-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/852,852
; FILING DATE: 16-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/00243
; FILING DATE: 11-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/566,977
; FILING DATE: 13-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,358
; FILING DATE: 11-JAN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: ISIS-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
; US-08-829-637A-33

Query Match          0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 2096 TTTCGGGAGGAGGATGTC 2114
|||||
Db 1 TTTCGGGATGAGGTGAGC 19

RESULT 150
US-09-232-346-56
; Sequence 56, Application US/09232346
; Patent No. 6352830
; GENERAL INFORMATION:
; APPLICANT: Crabtree, Gerald R.
; APPLICANT: No. 6352830throp, Jeffrey P.
; APPLICANT: Ho, Steffan M.
; APPLICANT: Flanagan, William M.
; TITLE OF INVENTION: NF-AT POLYPEPTIDES AND POLYNUCLEOTIDES AND SCREENING
; TITLE OF INVENTION: METHODS FOR IMMOSUPPRESSIVE AGENTS
; FILE REFERENCE: APV-008.04
; CURRENT APPLICATION NUMBER: US/09/232.346
; CURRENT FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: 08/507,032
; PRIOR FILING DATE: 1995-07-31
; PRIOR APPLICATION NUMBER: 08/228,944
; PRIOR FILING DATE: 1994-04-18
; PRIOR APPLICATION NUMBER: 07/749,385
; PRIOR FILING DATE: 1991-08-22
; PRIOR APPLICATION NUMBER: 08/260,174
; PRIOR FILING DATE: 1994-06-13
; PRIOR APPLICATION NUMBER: 08/124,981
; PRIOR FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: putative NF-AT
US-09-232-346-56

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2405 CGGAGAGAGAAATAAAG 2423
|||||
Db 1 CAGAGAGGAAATGAG 19

RESULT 151
US-09-629-645A-62
; Sequence 62, Application US/09629645A
; Patent No. 6365354
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF LYSOPHOSPHOLIPASE I EXPRESSION
; FILE REFERENCE: RTS-0137
; CURRENT APPLICATION NUMBER: US/09/629.645A
; CURRENT FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 164
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-629-645A-62

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 39 CTCATGAGGAGGTTTAGT 57
|||||
Db 1 CTCATGAGGAGATATTATT 19

RESULT 152
US-09-658-687A-60/c
; Sequence 60, Application US/09658687A
; Patent No. 6387699
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF A20 EXPRESSION
; FILE REFERENCE: RTS-0141
; CURRENT APPLICATION NUMBER: US/09/658.687A
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-658-687A-60

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1029 AGGAGCCGAGAACTTCTT 1047
|||||
Db 19 AGGAGCCGAGAACTTCTT 1

RESULT 153
US-09-462-261-21
; Sequence 21, Application US/09462261
; Patent No. 6391636
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: Antisense Oligonucleotide
; TITLE OF INVENTION: Modulation of raf Gene Expression
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: Pentium
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/462.261
; FILING DATE: 01-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/756,806
; FILING DATE: No. 6391636member 26, 1996
; APPLICATION NUMBER: PCT/US95/07111
; FILING DATE: May 31, 1995
; APPLICATION NUMBER: 08/250,856
; FILING DATE: May 31, 1994
; APPLICATION NUMBER: 08/888,982
; FILING DATE: July 7, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0312
; TELECOMMUNICATION INFORMATION:


```
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1487 ATGGCTCTTAAGGGGAAA 1505
Db 1 ATGGCTCTTAAGAGGAAA 19
|||||
|

RESULT 158
US-09-517-467B-130
; Sequence 130, Application US/09517467B
; Patent No. 6451602
; GENERAL INFORMATION:
; APPLICANT: Ian Popoff
; APPLICANT: Lex M. Cowseart
; TITLE OF INVENTION: ANTISENSE MODULATION OF PAPP EXPRESSION
; FILE REFERENCE: RTS-0150
; CURRENT APPLICATION NUMBER: US/09/517,467B
; CURRENT FILING DATE: 2001-03-02
; PRIOR FILING DATE: 09/517,467
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 345
; SEQ ID NO 130
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-517-467B-130

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2037 CATCTGTGCATATCATAT 2055
Db 1 CATCTGTGCATATCATAT 19
|||||
|

RESULT 159
US-09-920-672-77/c
; Sequence 77, Application US/09920672
; Patent No. 6455308
; GENERAL INFORMATION:
; APPLICANT: Mark J. Graham
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF SERUM AMYLOID A4 EXPRESSION
; FILE REFERENCE: RTS-0251
; CURRENT APPLICATION NUMBER: US/09/920,672
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 77
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-920-672-77

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 105 TGTCAAGCTCTCTGGCT 123
Db 19 TCTATAGCTCTCTGGCT 1
|||||
|

RESULT 160
US-09-254-322-33
; Sequence 33, Application US/09254322
; Patent No. 6465439
; GENERAL INFORMATION:
; APPLICANT: Nicklin, Paul
; APPLICANT: Phillips, Judith
; APPLICANT: Love, William
; APPLICANT: Hamilton, Karen
; TITLE OF INVENTION: Pharmaceutical Compositions
; FILE REFERENCE: 4-21026/MA 2138/PCT
; CURRENT APPLICATION NUMBER: US/09/254,322
; CURRENT FILING DATE: 1999-03-04
; EARLIER APPLICATION NUMBER: PCT/EP97/04796
; EARLIER FILING DATE: 1997-09-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
US-09-254-322-33

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2096 TTTGGGGAGGAGTGTC 2114
Db 1 TTTGGGGAGGAGGTGAGC 19
|||||
|

RESULT 161
US-09-535-008-16
; Sequence 16, Application US/09535008
; Patent No. 6465629
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; TITLE OF INVENTION: BCL1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
; FILE REFERENCE: 2318-259
; CURRENT APPLICATION NUMBER: US/09/535,008
; CURRENT FILING DATE: 2000-03-23
; EARLIER APPLICATION NUMBER: U.S. 60/125,806
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 77
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-09-535-008-16

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 974 ATAGATGTTACTGATGCAA 992
Db 1 ACAGATGCTACTGATGCCA 19
|||||
|

RESULT 162
US-09-600-770A-70/c
; Sequence 70, Application US/09600770A
; Patent No. 6489110
; GENERAL INFORMATION:
; APPLICANT: Oudshoorn, Pieter
; APPLICANT: Klatser, Paul
; TITLE OF INVENTION: EF-Tu mRNA AS A MARKER FOR VIABILITY OF BACTERIA
; FILE REFERENCE: 9250.21
; CURRENT APPLICATION NUMBER: US/09/600,770A
; CURRENT FILING DATE: 2000-07-21
```

; PRIOR APPLICATION NUMBER: PCT/EP99/00323
; PRIOR FILING DATE: 1999-01-19
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 70
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(20)
; OTHER INFORMATION: Synthetic oligonucleotide to Klebsiella pneumoniae EF-Tu.
US-09-600-770A-70

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 201 ACCACGAAGCCGAGACCT 219
Db 19 ACCACGACGAGACACCT 1

RESULT 163
US-09-659-845A-150
; Sequence 150, Application US/09659845A
; Patent No. 6492170
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 9 EXPRESSION
; FILE REFERENCE: RTS-0183
; CURRENT APPLICATION NUMBER: US/09/659,845A
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 150
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-845A-150

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2916 GACAGTCCCTGGGAACCTGG 2934
Db 1 GACAGCACCCGGGAACCTGG 19

RESULT 164
US-09-658-688A-13/c
; Sequence 13, Application US/09658688A
; Patent No. 6498035
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: William Gaarde
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF MEK3 EXPRESSION
; FILE REFERENCE: RTS-0143
; CURRENT APPLICATION NUMBER: US/09/658,688A
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-658-688A-13

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 710 TGGAGAGGAGACTATGAAG 728
Db 19 TGGATATGAGACCATGAAG 1

RESULT 165
US-09-815-585-13
; Sequence 13, Application US/09815585
; Patent No. 6500622
; GENERAL INFORMATION:
; APPLICANT: Bruchez Jr., Marcel P.
; APPLICANT: Lai, Jennifer H.
; APPLICANT: Phillips, Vince E.
; APPLICANT: Watson, Andrew R.
; APPLICANT: Wong, Edith Y.
; TITLE OF INVENTION: METHODS OF USING SEMICONDUCTOR NANOCRYSTALS IN
; TITLE OF INVENTION: BEAD-BASED NUCLEIC ACID ASSAYS
; FILE REFERENCE: 5100-0701
; CURRENT APPLICATION NUMBER: US/09/815,585
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/191,227
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/237,000
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide LDLrb
US-09-815-585-13

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 92 TCACAGGGGACGATGTCAA 110
Db 1 TCACAGGTTCCGATGTCAA 19

RESULT 166
US-09-898-361-40
; Sequence 40, Application US/09898361
; Patent No. 6503152
; GENERAL INFORMATION:
; APPLICANT: Susan Murray
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA RECEPTOR
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0158
; CURRENT APPLICATION NUMBER: US/09/898,361
; CURRENT FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 163
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-361-40

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 319 TTTAAAGGACAGTCCACA 337
Db 2 TTACAGACAGTCCAAA 20

RESULT 167

US-09-668-313A-78
; Sequence 78, Application US/09668313A
; Patent No. 6503756
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF SYNTAXIN 4 INTERACTING PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0127
; CURRENT APPLICATION NUMBER: US/09/668,313A
; CURRENT FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 247
; SEQ ID NO 78
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-668-313A-78

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1503 AAATTCCTCCAAAGACCAAGTG 1521
Db 1 AAATACCCCAAGTCCAGAG 19

RESULT 168

US-09-216-393B-296/c
; Sequence 296, Application US/09216393B
; Patent No. 6514694
; GENERAL INFORMATION:
; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: TX-1-C2
; CURRENT APPLICATION NUMBER: US/09/216,393B
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,825
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 296
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-216-393B-296

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2348 GTGATGGGAGTCATAGTCG 2366
Db 20 GTGATGGGAGTCACAGTAG 2

RESULT 169

US-09-422-978-6606
; Sequence 6606, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel

; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6606
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer 99-13579 for SEQ 2672,
US-09-422-978-6606

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 542 GGTTCGAATGAATAATG 560
Db 2 GGTCTGAATGAATAATG 20

RESULT 170

US-09-422-978-11734
; Sequence 11734, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11734
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-4102 for SEQ 3869, in complete
US-09-422-978-11734

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1014 CACAGAGAATATTCAGGA 1032
Db 1 CACAGATAAATTCAGGA 19

RESULT 171

US-10-025-139-33
; Sequence 33, Application US/10025139

```
; Patent No. 6537973
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Holmlund, Jon T.
; APPLICANT: Dorr, F. Andrew
; TITLE OF INVENTION: Oligonucleotide Modulation Of Protein Kinase C
; FILE REFERENCE: US194954
; CURRENT APPLICATION NUMBER: US/10/025,139
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 08/829,637
; PRIOR FILING DATE: 1997-03-31
; PRIOR APPLICATION NUMBER: US 08/478,178
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/089,996
; PRIOR FILING DATE: 1993-07-09
; PRIOR APPLICATION NUMBER: US 07/852,852
; PRIOR FILING DATE: 1992-03-16
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-10-025-139-33

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2096  TTGGGGAGGAGTGTC 2114
Db      1      TTTGGGGATGAGGGTGAC 19

RESULT 172
US-09-096-724B-36/c
; Sequence 36, Application US/09096724B
; Patent No. 6548290
; GENERAL INFORMATION:
; APPLICANT: McGarity, Thomas J.
; APPLICANT: Kroll, Kristen
; APPLICANT: Kirschner, Marc W.
; TITLE OF INVENTION: Geminin Gene and Protein
; FILE REFERENCE: 0725.1055-001
; CURRENT APPLICATION NUMBER: US/09/096,724B
; CURRENT FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/085,371
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primers
; US-09-096-724B-36

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1606  ATCTCTGTTCATGTTCT 1624
Db      19  ATCTCTGCTCATGTGCT 1

RESULT 173
US-09-198-452A-1694
; Sequence 1694, Application US/09198452A
```

```
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1694
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; US-09-198-452A-1694

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2115  GAGTGGCTAATTGAAACC 2133
Db      1      GAGGGCAAAATTGGAACC 19

RESULT 174
US-09-198-452A-1954/c
; Sequence 1954, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1954
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; US-09-198-452A-1954

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      96     AGGGGAGGATGTCAGGCTC 114
Db      19     AGGGGAGGATCTCAAGTTC 1

RESULT 175
US-09-198-452A-2441/c
; Sequence 2441, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2441
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; US-09-198-452A-2441

Query Match      0.4%; Score 14.2; DB 1; Length 20;
```

```
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4647
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-4647

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 768 TGATTGAAGATGTGGAACA 786
Db 20 TGATTGAACAGTGGACCA 2

RESULT 176
US-09-198-452A-4041/c
; Sequence 4041, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4041
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-4041

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 761 GCCCAGTTGATGAAGATG 779
Db 19 GCCCAGTTGATGAAGAG 1

RESULT 177
US-09-198-452A-4044/c
; Sequence 4044, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4044
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-4044

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 761 GCCCAGTTGATGAAGATG 779
Db 19 GCCCAGTTGATGAAGAG 1

RESULT 178
US-09-198-452A-4647/c
; Sequence 4647, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4647
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-4647
```

```
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4647
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-4647

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 383 AAGCTTCAGCTGCAGGCTC 401
Db 19 AATCTTCTGATGCAGGCTC 1

RESULT 179
US-09-198-452A-4770
; Sequence 4770, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4770
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-4770

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3074 CTTTCTTCAAGTGACAGG 3092
Db 1 CTTGGTTAAAGTGACAGG 19

RESULT 180
US-09-649-728-10
; Sequence 10, Application US/09649728
; Patent No. 6562564
; GENERAL INFORMATION:
; APPLICANT: Honkanen, Richard E
; TITLE OF INVENTION: DECREASING CELL PROLIFERATION BY DECREASING LEVELS OF PFS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: Braman & Rogalsky, LLP
; STREET: P.O. Box 352
; CITY: Canandaigua
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/649,728
; FILING DATE: 28-Aug-2000
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 08/975,127
FILING DATE: 20-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Broman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 004.00126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-393-3002
TELEFAX: 716-393-3001
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
ANTI-SENSE: YES
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-649-728-10

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1471 AGAGAGCTGGAGGTGGATG 1489
DB 1 AGAGCCCTGGAGGTGGATG 19

RESULT 181
US-09-909-595-24/c
Sequence 24, Application US/09909595
Patent No. 6586245
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Brenda F. Baker
APPLICANT: Jacqueline Wyatt
APPLICANT: Scott E. Davis
TITLE OF INVENTION: ANTISENSE MODULATION OF CD40 LIGAND EXPRESSION
FILE REFERENCE: RTS-0223
CURRENT APPLICATION NUMBER: US/09/909,595
CURRENT FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 24
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-909-595-24

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2743 TTATTAAGAGTTTCTATT 2761
DB 20 TTCATGAAGATTTCGTATT 2

RESULT 182
US-09-389-956-87/c
Sequence 87, Application US/09389956
Patent No. 6586579
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: PR-Domain Containing Nucleic Acids, Polypeptides,
TITLE OF INVENTION: Antibodies and Methods
FILE REFERENCE: P-LJ 3611
CURRENT APPLICATION NUMBER: US/09/389,956
CURRENT FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 87
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-09-389-956-87

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1496 AAAGGGGAATTCCTCAAG 1514
DB 19 AAAGGGAATTCCTCGAG 1

RESULT 183
US-09-823-634A-14
Sequence 14, Application US/09823634A
Patent No. 6596489
GENERAL INFORMATION:
APPLICANT: Applied Gene Technologies, Inc.
APPLICANT: Dattagupta, Nanibhushan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
TITLE OF INVENTION: MISMATCHES USING RNASE H
FILE REFERENCE: 47541-20006.00
CURRENT APPLICATION NUMBER: US/09/823,634A
CURRENT FILING DATE: 2002-02-28
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligo AGT02021
US-09-823-634A-14

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2640 AAAAAAATTCCTCAAGA 2658
DB 2 AAAAAAATTCCTCAAGAAA 20

RESULT 184
US-09-823-647B-14
Sequence 14, Application US/09823647B
Patent No. 6596490
GENERAL INFORMATION:
APPLICANT: Applied Gene Technologies, Inc.
APPLICANT: Dattagupta, Nanibhushan
TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 47541-20004.20
CURRENT APPLICATION NUMBER: US/09/823,647B
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: US 09/616,761
PRIOR FILING DATE: 2000-07-14
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligo AGT02021
US-09-823-647B-14

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2640 AAAAAAAAAATTGTCACAAAGA 2658
Db 2 AAAAAAAAAATTGTAACAAA 20

RESULT 185

US-09-825-497A-8
; Sequence 8, Application US/09825497A
; Patent No. 6599742

GENERAL INFORMATION:

; APPLICANT: Honkanen, Richard E.
; APPLICANT: Dean, Nicholas M.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF HUMAN SERINE/THREONINE PRO
; FILE REFERENCE: ISPH-0572
; CURRENT APPLICATION NUMBER: US/09/825,497A
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

US-09-825-497A-8

Query Match

Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1471 AGAGAGTGGAGTGGATG 1489
Db 1 AGAGCCTGGAGTGGATG 19

RESULT 186

US-09-112-580-207/c
; Sequence 207, Application US/09112580
; Patent No. 6610539

GENERAL INFORMATION:

; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE SEQUENCES AS INHIBITORS OF
; FILE REFERENCE: 032396-016
; CURRENT APPLICATION NUMBER: US/09/112,580
; CURRENT FILING DATE: 1998-07-09
; EARLIER APPLICATION NUMBER: US 60/052,160
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 265
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 207
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-112-580-207

Query Match

Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1520 TGGATGAAAGTGGTGGG 1538
Db 19 TGTATGAAAGTGGCGG 1

RESULT 187

US-09-628-129-2
; Sequence 2, Application US/09628129
; Patent No. 6613327

; GENERAL INFORMATION:
; APPLICANT: Ling, Vincent
; APPLICANT: Gray, Gary
; APPLICANT: Keith, Jr., James C.
; APPLICANT: Maganti, Srinivas
; TITLE OF INVENTION: METHODS OF PREVENTING IMMUNE-MEDIATED ABORTION BY
; FILE REFERENCE: GNN-010CP
; CURRENT APPLICATION NUMBER: US/09/628,129
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/362,812
; PRIOR FILING DATE: 1999-07-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-09-628-129-2

Query Match

Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2489 CAAACACTGATGATGTC 2507
Db 1 CACACACTGATGATGTC 19

RESULT 188

US-09-495-714C-130
; Sequence 130, Application US/09495714C
; Patent No. 6670465

GENERAL INFORMATION:

; APPLICANT: University Technologies International Inc.
; TITLE OF INVENTION: RETINAL CALCIUM CHANNEL (ALPHA) 1P-SUBUNIT GENE
; FILE REFERENCE: 45499.4 (formerly 45074.6)
; CURRENT APPLICATION NUMBER: US/09/495,714C
; CURRENT FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-495-714C-130

Query Match

Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1226 GAGATGGGGCATATCCAGT 1244
Db 1 GAGATGGGGCACAAACAGT 19

RESULT 189

US-09-495-714C-131/c
; Sequence 131, Application US/09495714C
; Patent No. 6670465

GENERAL INFORMATION:

; APPLICANT: University Technologies International Inc.
; TITLE OF INVENTION: RETINAL CALCIUM CHANNEL (ALPHA) 1P-SUBUNIT GENE
; FILE REFERENCE: 45499.4 (formerly 45074.6)
; CURRENT APPLICATION NUMBER: US/09/495,714C
; CURRENT FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 20

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-495-714C-131

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1226 GAGATGGGCATATCCAGT 1244
    |||||
Db 20 GAGATGGGCACAAACAGT 2

RESULT 190
PCT-US93-02213-33
; Sequence 33, Application PC/TUS9302213
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett
; TITLE OF INVENTION: Oligonucleotide Modulation of Protein
; TITLE OF INVENTION: Kinase C
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSER: Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02213
; FILING DATE: 19930225
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 852,852
; FILING DATE: March 16, 1992
; APPLICATION NUMBER: 08/089,996
; FILING DATE: July 9, 1993
; APPLICATION NUMBER: 08/199,779
; FILING DATE: February 22, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rebecca Ralph Gaumond
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: ISIS-1546
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
; PCT-US94-07770-33

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2096 TTTGGGGAGGAGGTGTC 2114
    |||||
Db 1 TTTGGGGATGAGGGTGAGC 19

RESULT 192
5171843-3
; Patent No. 5171843
; APPLICANT: NUSSENZWEIG, VICTOR
; TITLE OF INVENTION: IMMUNOGENIC POLYPEPTIDE AND METHOD FOR
; PURIFYING IT
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/175,112
; FILING DATE: 30-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 754,645
; FILING DATE: 9-JUL-1985
; APPLICATION NUMBER: 115,634
; FILING DATE: 26-OCT-1987
; APPLICATION NUMBER: 649,903
; FILING DATE: 12-SEP-1984
; SEQ ID NO: 3:
; LENGTH: 20
5171843-3

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2096 TTTGGGGAGGAGGTGTC 2114
    |||||
Db 1 TTTGGGGATGAGGGTGAGC 19

RESULT 191
PCT-US94-07770-33
; Sequence 33, Application PC/TUS9407770
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett and
; APPLICANT: Russell T. Boggs
; TITLE OF INVENTION: Oligonucleotide Modulation of
```

```
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 119
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSER: Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07770
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 852,852
; FILING DATE: March 16, 1992
; APPLICATION NUMBER: 08/089,996
; FILING DATE: July 9, 1993
; APPLICATION NUMBER: 08/199,779
; FILING DATE: February 22, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rebecca Ralph Gaumond
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: ISIS-1546
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
; PCT-US94-07770-33

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2096 TTTGGGGAGGAGGTGTC 2114
    |||||
Db 1 TTTGGGGATGAGGGTGAGC 19

RESULT 192
5171843-3
; Patent No. 5171843
; APPLICANT: NUSSENZWEIG, VICTOR
; TITLE OF INVENTION: IMMUNOGENIC POLYPEPTIDE AND METHOD FOR
; PURIFYING IT
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/175,112
; FILING DATE: 30-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 754,645
; FILING DATE: 9-JUL-1985
; APPLICATION NUMBER: 115,634
; FILING DATE: 26-OCT-1987
; APPLICATION NUMBER: 649,903
; FILING DATE: 12-SEP-1984
; SEQ ID NO: 3:
; LENGTH: 20
5171843-3
```

Kinase C

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1923 GTACCGACTGGAGCCCAT 1941
DB 1 GCACCGAATGACTCCCAT 19

RESULT 193

US-08-832-021-13/c
Sequence 13, Application US/08832021
Patent No. 6045998
GENERAL INFORMATION:
APPLICANT: Combates, N.
APPLICANT: Pardini, J.
APPLICANT: Parimoo, S.
APPLICANT: Prouty, S.
APPLICANT: Stenn, K.
TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
FILE REFERENCE: JBP-382
CURRENT APPLICATION NUMBER: US/08/832,021
CURRENT FILING DATE: 1997-04-02
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 13
LENGTH: 14
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-13

Query Match 0.4%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3392 TCAAAAAAAAAAAAA 3405
DB 14 TCAAAAAAAAAAAAA 1

RESULT 194

US-08-724-466B-13/c
Sequence 13, Application US/08724466B
Patent No. 6063606
GENERAL INFORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
CITY: Toronto
ZIP: M5L 1A9
COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,466B
FILING DATE: October 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00004
TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-724-466B-13

Query Match 0.4%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3392 TCAAAAAAAAAAAAA 3405
DB 14 TCAAAAAAAAAAAAA 1

RESULT 195

US-08-882-164D-13/c
Sequence 13, Application US/08882164D
Patent No. 6306624
GENERAL INFORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5L 1A9
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,164D
FILING DATE: June 25, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-882-164D-13

Query Match 0.4%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3392 TCAAAAAAAAAAAAA 3405
DB 14 TCAAAAAAAAAAAAA 1

RESULT 196

US-08-292-620A-234/c
; Sequence 234, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwigen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 234:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-832-021-25/c
; Sequence 25, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-25

Query Match 0.4%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3392 TCAAAAAAAAAA 3405
Db 14 TCAAAAAAAAAA 1

RESULT 198
US-08-832-021-26/c
; Sequence 26, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-26

Query Match 0.4%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3392 TCAAAAAAAAAA 3405
Db 14 TCAAAAAAAAAA 1

RESULT 199
US-08-832-021-28/c
; Sequence 28, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64

Query Match 0.4%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3363 GACACTCAATAAT 3376
Db 15 GACACTCAATAAT 2

RESULT 197
US-08-832-021-25/c
; Sequence 25, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.

two

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-28

Query Match      0.4%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3392 TCAAAAAAAAAA 3405
DB      14 TCAAAAAAAAAA 1

RESULT 200
US-09-071-845-234/c
; Sequence 234, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 234:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-09-071-845-234
Query Match      0.4%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3363 GACACTCAATAAAT 3376
DB      15 GACACTCAATAAAT 2

RESULT 201
US-09-422-978-6934/c
; Sequence 6934, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6934
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-21533 for SEQ 3000,
US-09-422-978-6934

Query Match      0.4%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3052 GTGATGTTTGAAT 3065
DB      15 GTGATGTTTGAAT 2

RESULT 202
US-09-422-978-7203
; Sequence 7203, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7203
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
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; NAME/KEY: primer_bind
; LOCATION: 1.19
; OTHER INFORMATION: upstream amplification primer 99-2903 for SEQ 3269,
US-09-422-978-7203

Query Match          0.4%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

QY 2426 AGAAGTGGAGAAA 2439
    |||||
Db 1 AGAAGTGGAGAAA 14

RESULT 203
US-08-712-610-7/c
; Sequence 7, Application US/08712610
; Patent No. 6048897
; GENERAL INFORMATION:
; APPLICANT: Charles N. Serhan
; TITLE OF INVENTION: Lipoxin Compounds
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/712,610
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/260,030
; FILING DATE: 15-JUNE-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,300
; FILING DATE: 15-JUNE-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: BWI-112CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; ANTI-SENSE: NO
US-08-712-610-7

Query Match          0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

QY 160 CACCATTGAGGAAC 173
    |||||
Db 15 CACCATTGAGGAAC 2

RESULT 204
US-08-714-071-6/c
; Sequence 6, Application US/08714071
; Patent No. 6136584

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; GENERAL INFORMATION:
; APPLICANT: Tsutomu, FUJIWARA
; APPLICANT: Shiro, OKUNO
; APPLICANT: Hisanobu, HIRANO
; APPLICANT: Sadahito, SHIN
; TITLE OF INVENTION: FK506 BINDING PROTEIN GENE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,071
; FILING DATE:
; CLASSIFICATION: 435
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-714-071-6

Query Match          0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

QY 2710 TTCTGTCTCTGGAT 2723
    |||||
Db 20 TTCTGTCTCTGGAT 7

RESULT 205
US-09-309-423-7/c
; Sequence 7, Application US/09309423
; Patent No. 6316648
; GENERAL INFORMATION:
; APPLICANT: Charles N. Serhan
; TITLE OF INVENTION: Lipoxin Compounds
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/309,423
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/260,030
; FILING DATE: 15-JUNE-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,300

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; Software: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/968,445
; FILING DATE: 01-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/260,030
; FILING DATE: 15-JUNE-1994
; APPLICATION NUMBER: 08/077,300
; FILING DATE: 15-JUNE-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: BWI-112CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-968-445-7

Query Match 0.4% Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels

Qy 160 CACCATGAGGAAC 173
Db 15 CACCATGAGGAAC 2

RESULT 208
US-10-175-268-7/c
; Sequence 7, Application US/10175268
; Patent No. 6620919
; GENERAL INFORMATION:
; APPLICANT: Charles N. Serhan
; TITLE OF INVENTION: Lipoxin Compounds
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; Software: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/175,268
; FILING DATE: 19-Jun-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/712,610
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/077,300
; FILING DATE: 15-JUNE-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: BWI-112CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400

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; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 816:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-435-628-816

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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 35.3%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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QY 2699 TCAGTATTATTCTGT 2715
DB 1 UCAGUAUUUUUCCUGU 17

```

```

RESULT 217
US-08-584-040-1556/c
; Sequence 1556 Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwigen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITILE OF INVENTION: TREATMENT OF DISEASES OR
; TITILE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITILE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITILE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage

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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1556:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-1556

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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

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QY 315 CCTTTTAAAGGAACAG 331
DB 17 CTTTTTAAAGTAACAG 1

```

```

RESULT 218
US-08-584-040-1557/c
; Sequence 1557 Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwigen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITILE OF INVENTION: TREATMENT OF DISEASES OR
; TITILE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITILE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITILE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.

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Tue Sep 28 08:41:41 2004

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US-08-584-040-2518
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 35.3%; Pred. No. 1.2e+02;
Matches 6; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

QY 2526 ATCTATGTTTTCCTCT 2542
Db 1 AUCUUGUUGUCCUCU 17

RESULT 220
US-08-679-645-36
; Sequence 36, Application US/08679645
; Patent No. 6350934
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; APPLICANT: Edington, Brent E.
; APPLICANT: McSwiggen, James A.
; APPLICANT: Merlo, Patricia Ann Owens
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Thomas A.
; APPLICANT: Young, Scott A.
; APPLICANT: Folkerts, Otto
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,645
; FILING DATE: July 12, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; APPLICATION NUMBER: 08/300,726
; FILING DATE: September 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 219/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-679-645-36

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 1.2e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 151 TGCTCAGTCACCATTG 167

```

Db 1 UGCUCCGUCACCAGUG 17
:||:| |:|||||:|

RESULT 221
US-08-679-645-699
; Sequence 699, Application US/08679645
; Patent No. 6350934
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; APPLICANT: Edington, Brent E.
; APPLICANT: McSwiggen, James A.
; APPLICANT: Merlo, Patricia Ann Owens
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Thomas A.
; APPLICANT: Young, Scott A.
; APPLICANT: Folkerts, Otto
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,645
; FILING DATE: July 12, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; APPLICATION NUMBER: 08/300,726
; FILING DATE: September 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 219/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 699:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-679-645-699

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 1.2e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1294 TGAGGATTCCATGAAG 1310
:|||||:|:|:|

Db 1 UGAGGAUUUCAUGAUG 17

RESULT 222
US-09-371-772B-101/c
; Sequence 101, Application US/09371772B

; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 101
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-101

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 315 CCTTTTAAAGGAACAG 331
:|||||:|:|:|

Db 17 CTTTTTAAAGTAACAG 1

RESULT 223
US-09-371-772B-102/c
; Sequence 102, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 102
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-102

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2064 ACTTTTAAAGTAAAG 2080
:|||||:|:|:|

Db 17 ACTTTTAAAGTAACA 1

RESULT 224
US-09-371-772B-1042
; Sequence 1042, Application US/09371772B
; Patent No. 6566127


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; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 319
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-319
```

```
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2406 GGAAGAGAAATATAA 2422
||||| ||||| ||||| |||||
Db 1 GGAAGAGAGAAAGAAA 17
```

```
RESULT 229
US-09-827-998-483
; Sequence 483, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMPF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 483
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-483
```

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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 2413 GAAATAAAGCAAGAA 2429
||||| ||||| ||||| |||||
Db 1 GAAATAAAGCAAGAA 17
```

```
RESULT 230
US-09-866-108A-1698
; Sequence 1698, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
```

```
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1698
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1698
```

```
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 2046 CATATGCTATGAGGAG 2062
||||| ||||| ||||| |||||
Db 1 CAGATGCTATGAGGAG 17
```

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RESULT 231
US-09-866-108A-7340/c
; Sequence 7340, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
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Tue Sep 28 08:41:41 2004

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; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7340
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7340

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3270 TCCAACTGTATGTTTCAC 3286
Db 17 TCCAACTGTATGTTTCAC 1

RESULT 232
US-09-866-108A-7341/c
; Sequence 7341, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866.108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7341
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7341

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3269 TTCCAACGTGTATGTTCA 3285
Db 17 TTCCAACGTGTATGTTCA 1

RESULT 233
US-09-866-108A-7613/c
; Sequence 7613, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866.108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7613
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7613

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3077 TCTTCAAGTGCACAGGT 3093
Db 17 TCTTCAAGTGCACAGGT 1

RESULT 234
US-09-866-108A-8648/c
; Sequence 8648, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866.108A
```


; CURRENT FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 15755
 ; SOFTWARE: Acomica Sequence Listing Engine
 ; Patent No. 6686188
 ; SEQ ID NO 8648
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-866-108A-8848

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 381 TCACGCTTCAGTGCAG 397
 DB 17 TCCAGCTGCAGCTGCAG 1

RESULT 235
 US-09-866-108A-8847/c
 ; Sequence 8847, Application US/09866108A
 ; Patent No. 6686188
 ; GENERAL INFORMATION:
 ; APPLICANT: GU, Yizhong
 ; APPLICANT: JI, Yonggang
 ; APPLICANT: PENN, Sharron G.
 ; APPLICANT: HANZEL, David K.
 ; APPLICANT: RANK, David R.
 ; APPLICANT: CHEN, Wensheng
 ; APPLICANT: SHANNON, Mark
 ; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
 ; FILE REFERENCE: AEOMICA-7
 ; CURRENT APPLICATION NUMBER: US/09/866,108A
 ; CURRENT FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 15755
 ; SOFTWARE: Acomica Sequence Listing Engine
 ; Patent No. 6686188
 ; SEQ ID NO 8648
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-866-108A-8848

; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 15755
 ; SOFTWARE: Acomica Sequence Listing Engine
 ; Patent No. 6686188
 ; SEQ ID NO 8847
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-866-108A-8847

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2221 GTCCCGAGCCGTATCA 2237
 DB 17 GTCCCGAGCCGTATCA 1

RESULT 236
 US-09-866-108A-8848/c
 ; Sequence 8848, Application US/09866108A
 ; Patent No. 6686188
 ; GENERAL INFORMATION:
 ; APPLICANT: GU, Yizhong
 ; APPLICANT: JI, Yonggang
 ; APPLICANT: PENN, Sharron G.
 ; APPLICANT: HANZEL, David K.
 ; APPLICANT: RANK, David R.
 ; APPLICANT: CHEN, Wensheng
 ; APPLICANT: SHANNON, Mark
 ; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
 ; FILE REFERENCE: AEOMICA-7
 ; CURRENT APPLICATION NUMBER: US/09/866,108A
 ; CURRENT FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 15755
 ; SOFTWARE: Acomica Sequence Listing Engine
 ; Patent No. 6686188
 ; SEQ ID NO 8848
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-866-108A-8848

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.2e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2220 TGTCCCGAGCCGTATC 2236

Db 17 TGTCCGAGCCGGATC 1
|||||

```
RESULT 237
US-09-866-108A-8852/c
; Sequence 8852, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aecomica Sequence Listing Engine
; NUMBER OF SEQ ID NOS: 15755
; Patent No. 6686188
; SEQ ID NO 8852
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-8852

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2216 AGGATGTCGGAGCCG 2232
Db 17 AGGCTGTCCGAGCCG 1
|||||

RESULT 238
US-09-866-108A-8853/c
; Sequence 8853, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 89.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2216 AGGATGTCGGAGCCG 2232
Db 17 AGGCTGTCCGAGCCG 1
|||||

RESULT 239
US-09-866-108A-8854/c
; Sequence 8854, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aecomica Sequence Listing Engine
; NUMBER OF SEQ ID NOS: 15755
; Patent No. 6686188
; SEQ ID NO 8852
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-8852

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2215 CAGGATGTCCGAGCC 2231
Db 17 CAGGCTGTCCGAGCC 1
|||||
```

```
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 8854
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-8854

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2214 TCAGGATGTCGCGAGC 2230
Db      17 TCAGGCTGTCCCGAAG 1

RESULT 240
US-09-866-108A-8855/c
; Sequence 8855, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 8855
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-8855

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2213 ATCAGGATGTCGCGAG 2229
Db      17 ATCAGGCTGTCCCGAAG 1

RESULT 241
US-09-866-108A-10338/c
; Sequence 10338, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10338
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10338

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      398 GCTCTTCAGCAAAATGG 414
Db      17 GCTCTTCTTCAAAATGG 1

RESULT 242
US-09-866-108A-10339/c
; Sequence 10339, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
```

ashen923-4.rni

Tue Sep 28 08:41:41 2004

```

; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10339
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-10339

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 397 GGCTCTTCAGCAAAATG 413
Db 17 GGCTCTTCAGCAAAATG 1

RESULT 243
US-07-977-284A-151/c
; Sequence 151, Application US/07977284A
; Patent No. 5558988
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Ala-Kokko, Leena
; APPLICANT: Williams, Charlene J.
; APPLICANT: Ritvaniemi, Pertti
; APPLICANT: Baldwin, Clinton
; APPLICANT: Hopkinson, Ian
; APPLICANT: Ahmad, Nilofar Nina
; TITLE OF INVENTION: METHODS OF DETECTING A GENETIC
; TITLE OF INVENTION: PREDISPOSITION FOR OSTEOARTHRITIS
; NUMBER OF SEQUENCES: 261
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5558988ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,284A
; FILING DATE: 13-NOV-1992
; CLASSIFICATION: 435

; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10339
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-10339

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1842 ATGTAGGCCCACTGCTC 1858
Db 17 ATCTGAGGCCCACTGCTC 1

RESULT 244
US-08-411-796-317
; Sequence 317, Application US/08411796
; Patent No. 5677149
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Mair H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Oline, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Polazzi, Joseph O.
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Interleukin-3 (IL-3) Mutant Polypeptides
; NUMBER OF SEQUENCES: 549
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/411,796
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/981044
; FILING DATE: 24-NOV-1992
; PRIOR APPLICATION DATA: PCT/US93/11198
; APPLICATION NUMBER: 22-NOV-1993
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C2713/1

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
TELEFAX: (708)470-6881
INFORMATION FOR SEQ ID NO: 317:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
US-08-411-796-317

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1053 CTGTTGGTCTTCTTAAT 1069
|||||
Db 1 CTGTTGGTCTTCTTCCCAT 17
|||||

RESULT 245

US-08-428-257A-45/c
Sequence 45, Application US/08428257A
Patent No. 5885808

GENERAL INFORMATION:
APPLICANT: Spooner, Robert A.
APPLICANT: Epenetos, A.A.
TITLE OF INVENTION: Compounds to target cells
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:

ADDRESSEE: Jules E. Goldberg
STREET: 261 Madison Avenue
CITY: New York
STATE: NY
COUNTRY: USA

ZIP: 10016-2391

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/428,257A
FILING DATE: 07/05/95

CLASSIFICATION: 514

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Adenovirus

STRAIN: Ad5

US-08-428-257A-45

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 521 GAATGCTTATTACTTGA 537
|||||
Db 18 GAATCTTATTACTCGA 2
|||||

RESULT 246

US-08-256-426B-151/c

Sequence 151, Application US/08256426B
Patent No. 5948611

GENERAL INFORMATION:
APPLICANT: Prockop, Darwin J.
APPLICANT: Ala-Kokko, Leena
APPLICANT: Williams, Charlene J.
APPLICANT: Ritvaniemi, Pertti
APPLICANT: Baldwin, Clinton
APPLICANT: Hopkinson, Ian
APPLICANT: Ahmad, Nilofer Nina
TITLE OF INVENTION: Methods of Detecting A Genetic
NUMBER OF SEQUENCES: 293
CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5948611 Iris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 3.1

SOFTWARE: WORDPERFECT 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/256,426B

FILING DATE: 03-FEB-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/10964

FILING DATE: 12-NOV-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/977,284

FILING DATE: 13-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: Mark DeLuca

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TJU-1082

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 151:

SEQUENCE CHARACTERISTICS:

LENGTH: 18

TYPE: NUCLEIC ACID

STRANDEDNESS: SINGLE

TOPOLOGY: LINEAR

ANTI-SENSE: NO

US-08-256-426B-151

Query Match

Best Local Similarity 0.4%; Score 13.8; DB 1; Length 18;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1842 ATGTAAGGCCACTGCTC 1858

|||||

Db 17 ATCTGAGGCCACTGCTC 1

RESULT 247

US-08-363-276B-18

Sequence 18, Application US/08363276B

Patent No. 5969109

GENERAL INFORMATION:

APPLICANT: BONA ET AL.

TITLE OF INVENTION: CHIMERIC ANTIBODIES

TITLE OF INVENTION: COMPRISING ANTIGEN BINDING SITES AND B AND T CELL EPITOPES

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brumbaugh, Graves, Donohue &

ADDRESS: Raymond

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: NY

COUNTRY: USA

Tue Sep 28 08:41:41 2004

```

;
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,276B
; FILING DATE: 22-DECEMBER-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 07/486,546
; FILING DATE: 28-FEBRUARY-1990 (ABANDONED)
; APPLICATION NUMBER: USSN 07/687,376
; FILING DATE: 18-APRIL-1991 (ABANDONED)
; APPLICATION NUMBER: USSN 08/327,636
; FILING DATE: 24-OCTOBER-1994 (ABANDONED)
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Richard S
; REGISTRATION NUMBER: 26,154
; REFERENCE/DOCKET NUMBER: 29889-165/29528
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2558
; TELEFAX: 212-765-2519
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM:
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: primer
US-08-363-276B-18

```

```

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 3348 GCTGAGCACAAGCAGA 3364
Db 2 GCTGAGCACAAGCAGA 18

```

```

RESULT 248
US-09-256-496-15
; Sequence 15, Application US/09256496
; Patent No. 5998206
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-12 EXPRESSION
; FILE REFERENCE: RTS-0056
; CURRENT APPLICATION NUMBER: US/09/256,496
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 86
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-256-496-15

```

```

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 389 CAGCTGAGGCTCTTCA 405

```

```

Db 1 CAGCAGCAGGATCTTCA 17

```

```

RESULT 249
US-08-875-540-5
; Sequence 5, Application US/08875540A
; Patent No. 6015888
; GENERAL INFORMATION:
; APPLICANT: Heath, Paul Roy
; APPLICANT: Orange, Paul Richard
; APPLICANT: Pearson, Ronald Carl Alan
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO THE DETECTION OF VARIATIONS IN
; TITLE OF INVENTION: HUMAN HISTAMINE H2 RECEPTORS
; FILE REFERENCE: 09347/002001
; CURRENT APPLICATION NUMBER: US/08/875,540A
; CURRENT FILING DATE: 1998-01-05
; EARLIER APPLICATION NUMBER: PCT/EP96/00397
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: GB9503866.7
; EARLIER FILING DATE: 1995-01-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: Synthetic Oligonucleotide
US-08-875-540-5

```

```

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 3110 CCAGGGAACAGGTAGAG 3126
Db 1 CCAGGGAACAGGTAGAG 17

```

```

RESULT 250
US-08-875-540-6/c
; Sequence 6, Application US/08875540A
; Patent No. 6015888
; GENERAL INFORMATION:
; APPLICANT: Heath, Paul Roy
; APPLICANT: Orange, Paul Richard
; APPLICANT: Pearson, Ronald Carl Alan
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO THE DETECTION OF VARIATIONS IN
; TITLE OF INVENTION: HUMAN HISTAMINE H2 RECEPTORS
; FILE REFERENCE: 09347/002001
; CURRENT APPLICATION NUMBER: US/08/875,540A
; CURRENT FILING DATE: 1998-01-05
; EARLIER APPLICATION NUMBER: PCT/EP96/00397
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: GB9503866.7
; EARLIER FILING DATE: 1995-01-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: Synthetic Oligonucleotide
US-08-875-540-6

```

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Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 3110 CCAGGACAGCTAGAG 3126
Db 18 CCAGCAACAGGAGAG 2

RESULT 251

US-08-471-039-317
; Sequence 317, Application US/08471039
; Patent No. 6017523
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Maire H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olin, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Polazzi, Joseph O.
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Interleukin-3 (IL-3) Mutant Polypeptides
; NUMBER OF SEQUENCES: 549
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSEE: Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,039
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/981,044
; FILING DATE: 24-NOV-1992
; APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11198
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C2713/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708)470-6501
; TELEFAX: (708)470-6881
; INFORMATION FOR SEQ ID NO: 317:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
US-08-471-039-317

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1053 CTGTGCTCTTCCCTAAT 1069
Db 1 CTGTGGTCTTCCCAT 17

RESULT 252

US-08-826-532-17

; Sequence 17, Application US/08826532B
; Patent No. 6027923
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robert B.
; TITLE OF INVENTION: Linked Linear Amplification of Nucleic Acids
; FILE REFERENCE: 3239-102P
; CURRENT APPLICATION NUMBER: US/08/826,532B
; CURRENT FILING DATE: 1997-04-02
; EARLIER APPLICATION NUMBER: US 08/475,605
; EARLIER FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA
; OTHER INFORMATION: Molecule:synthesized primer
US-08-826-532-17

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 1.3e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2726 GACTTCTGTTCTGTTTC 2742
Db 2 GATTCTGTGTTGTTTC 18

RESULT 253

US-08-826-532-19
; Sequence 19, Application US/08826532B
; Patent No. 6027923
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robert B.
; TITLE OF INVENTION: Linked Linear Amplification of Nucleic Acids
; FILE REFERENCE: 3239-102P
; CURRENT APPLICATION NUMBER: US/08/826,532B
; CURRENT FILING DATE: 1997-04-02
; EARLIER APPLICATION NUMBER: US 08/475,605
; EARLIER FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-826-532-19

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2726 GACTTCTGTTCTGTTTC 2742
Db 2 GATTCTGTGTTGTTTC 18

RESULT 254

US-09-034-205-58
; Sequence 58, Application US/09034205
; Patent No. 6194149
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Nerl, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
; TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP

ashen923-4.rn1

Tue Sep 28 08:41:41 2004

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; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/034,205
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-03268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; US-09-034-205-58

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3051 AGTCATGTTTGGATCG 3067
Db 1 AGTCAGTTTGGAAACCG 17

RESULT 255
US-09-071-433-56
; Sequence 56, Application US/09071433A
; Patent No. 6197584
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Antisense Modulation of CD40 Expression
; FILE REFERENCE: RTS-0002
; CURRENT APPLICATION NUMBER: US/09/071,433A
; CURRENT FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-071-433-56

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2787 TTGCTCTCACAGGCTGT 2803
Db 1 TTGCTCTCACAGTGT 17

RESULT 256
US-09-071-433-73/c
; Sequence 73, Application US/09071433A
; Patent No. 6197584
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Antisense Modulation of CD40 Expression
; FILE REFERENCE: RTS-0002
; CURRENT APPLICATION NUMBER: US/09/071,433A
; CURRENT FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-071-433-73

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 109 AAGCTCTTCTCGCTCC 125
Db 18 ACGATCTTCTCGCTCC 2

RESULT 257
US-09-071-433-74/c
; Sequence 74, Application US/09071433A
; Patent No. 6197584
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Antisense Modulation of CD40 Expression
; FILE REFERENCE: RTS-0002
; CURRENT APPLICATION NUMBER: US/09/071,433A
; CURRENT FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-071-433-74

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 109 AAGCTCTTCTCGCTCC 125
Db 18 ACGATCTTCTCGCTCC 2

RESULT 258
US-09-228-324A-17
; Sequence 17, Application US/09228324A
; Patent No. 6335184
; GENERAL INFORMATION:
; APPLICANT: Reyes, Antonio A.
; APPLICANT: Wallace, Robert B.
; APPLICANT: Ugozzoli, Luis A.
; TITLE OF INVENTION: Linked Linear Amplification of Nucleic Acids
; FILE REFERENCE: 3239-103P
; CURRENT APPLICATION NUMBER: US/09/228,324A
; CURRENT FILING DATE: 1999-01-11
; PRIOR APPLICATION NUMBER: US 08/826,532
; PRIOR FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0

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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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US-09-677-192-58

QY 3110 CCAGGACAGGTAGAG 3126
 Db 18 CCAGGACAGGAGAG 2

RESULT 263
 US-09-677-218B-58
 ; Sequence 58, Application US/09677218B
 ; Patent No. 6355437
 ; GENERAL INFORMATION:
 ; APPLICANT: Lyamichiev, Victor I.
 ; Brow, Mary Ann D.
 ; Fors, Lance
 ; Neri, Bruce P.

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
 STRUCTURE-BRIDGING OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 68
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MEDLEN & CARROLL, LLP
 STREET: 220 Montgomery Street, Suite 2200
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94104

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/677,218B
 FILING DATE: 02-Oct-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/034,205
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: MacKnight, Kamrin T.
 REGISTRATION NUMBER: 38,230
 REFERENCE/DOCKET NUMBER: FORS-03268
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 58:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "DNA"
 SEQUENCE DESCRIPTION: SEQ ID NO: 58:

US-09-677-218B-58
 Query Match 0.4%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3051 AGTGATGTTTGAATCG 3067
 Db 1 AGTGACGTTTGAACCG 17

RESULT 264
 US-09-677-192-58
 ; Sequence 58, Application US/09677192
 ; Patent No. 6358691
 ; GENERAL INFORMATION:
 ; APPLICANT: Lyamichiev, Victor I.
 ; APPLICANT: Brow, Mary Ann D.
 ; APPLICANT: Fors, Lance
 ; APPLICANT: Neri, Bruce P.

US-09-677-192-58

QY 3051 AGTGATGTTTGAATCG 3067
 Db 1 AGTGACGTTTGAACCG 17

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
 STRUCTURE-BRIDGING OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 68
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MEDLEN & CARROLL, LLP
 STREET: 220 Montgomery Street, Suite 2200
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94104

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/677,218B
 FILING DATE: 02-Oct-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/034,205
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: MacKnight, Kamrin T.
 REGISTRATION NUMBER: 38,230
 REFERENCE/DOCKET NUMBER: FORS-03268
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 58:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "DNA"
 SEQUENCE DESCRIPTION: SEQ ID NO: 58:

US-09-677-192-58
 Query Match 0.4%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3110 CCAGGACAGGTAGAG 3126
 Db 1 CCAGGACAGGAGAG 17

RESULT 265
 US-09-677-634-6/c
 ; Sequence 6, Application US/09473634
 ; Patent No. 6440670
 ; GENERAL INFORMATION:
 ; APPLICANT: Heath, Paul Roy
 ; APPLICANT: Orange, Paul Richard
 ; APPLICANT: Pearson, Ronald Carl Alan

US-09-677-192-58

QY 3051 AGTGATGTTTGAATCG 3067
 Db 1 AGTGACGTTTGAACCG 17

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
 STRUCTURE-BRIDGING OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 68
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MEDLEN & CARROLL, LLP
 STREET: 220 Montgomery Street, Suite 2200
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94104

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/677,218B
 FILING DATE: 02-Oct-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/034,205
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: MacKnight, Kamrin T.
 REGISTRATION NUMBER: 38,230
 REFERENCE/DOCKET NUMBER: FORS-03268
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 58:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "DNA"
 SEQUENCE DESCRIPTION: SEQ ID NO: 58:

US-09-677-192-58
 Query Match 0.4%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3110 CCAGGACAGGTAGAG 3126
 Db 1 CCAGGACAGGAGAG 17

RESULT 266
 US-09-677-634-6/c
 ; Sequence 6, Application US/09473634
 ; Patent No. 6440670
 ; GENERAL INFORMATION:
 ; APPLICANT: Heath, Paul Roy
 ; APPLICANT: Orange, Paul Richard
 ; APPLICANT: Pearson, Ronald Carl Alan

; APPLICANT: Wright, Simon Ralph
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO THE DETECTION OF VARIATIONS IN
; FILE REFERENCE: 09347/002001
; CURRENT APPLICATION NUMBER: US/09/473,634
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 1998-01-05
; PRIOR APPLICATION NUMBER: PCT/EP96/00397
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: GB9503866.7
; PRIOR FILING DATE: 1995-01-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-473-634-6

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3110 CCAGGGAACAGGTAGAG 3126
|||||
Db 18 CCAGGGAACAGGAAGAG 2

RESULT 267
US-08-559-390-317
; Sequence 317, Application US/08559390
; Patent No. 6479261
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Mairé H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olin, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Polazzi, Joseph O.
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Interleukin-3 (IL-3) Mutant Polypeptides
; NUMBER OF SEQUENCES: 549
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSEE: Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,390
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/411,796
; FILING DATE:
; APPLICATION NUMBER: US 07/981044
; FILING DATE: 24-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11198

; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C2713/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708)470-6501
; TELEFAX: (708)470-6881
; INFORMATION FOR SEQ ID NO: 317:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
US-08-559-390-317

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1053 CTGTTGGTCTCTCCTAAT 1069
|||||
Db 1 CTGTTGGTCTCTCCCAT 17

RESULT 268
US-09-216-393B-314
; Sequence 314, Application US/09216393B
; Patent No. 6514694
; GENERAL INFORMATION:
; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: TX-1-C2
; CURRENT APPLICATION NUMBER: US/09/216,393B
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,825
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 314
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-216-393B-314

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3244 TCTCTAACTGTGGAGTG 3260
|||||
Db 1 TCTCCGACTGTGGAGTG 17

RESULT 269
US-09-422-978-5256/c
; Sequence 5256, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23

Tue Sep 28 08:41:41 2004

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; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5256
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-22857 for SEQ 1322,
US-09-422-978-5256

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 170 GAACAGGCCAAGACATT 186
Db 18 GAAGAGACCAAGACATT 2

RESULT 270
US-09-422-978-7513/c
; Sequence 7513, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7513
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-6549 for SEQ 3579,
US-09-422-978-7513

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2728 CTTCTGTCCTGTTCTT 2744
Db 18 CTTCTGTCCTGTTGTT 2

RESULT 271
US-09-422-978-8735
; Sequence 8735, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850

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; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 8735
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-17889 for SEQ 870, in complete
US-09-422-978-8735

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2150 TTCTTTGTCACCTGCACC 2166
Db 2 TTTTTCCTCCTGCACC 18

RESULT 272
US-09-422-978-9788/c
; Sequence 9788, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9788
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-7373 for SEQ 1923, in complete
US-09-422-978-9788

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1586 GAACATACCTGTCACC 1602
Db 18 GAACATCCTATGACC 2

RESULT 273
US-09-422-978-11574
; Sequence 11574, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI

```

```
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11574
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-9847 for SEQ 3709, in complete
US-09-422-978-11574

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Gaps 0;

QY 3355 ACAAGAGAGACTCTCA 3371
Db 1 ACAGAGGAGACTCTCA 17

RESULT 274
US-09-344-510B-25/c
; Sequence 25, Application US/09344510B
; Patent No. 6579850
; GENERAL INFORMATION:
; APPLICANT: Nabeshima, Youichi
; Kuroo, Makoto
; Sekine, Susumu
; Iida, Akhiro
; TITLE OF INVENTION: No. 6579850el Polypeptide, No. 6579850el DNA and No. 657985
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10112-3801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 1.44 mb, DS, DD
; COMPUTER: Compaq DeskPro EN
; OPERATING SYSTEM: Windows 98
; SOFTWARE: WordPad
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/344,510B
; FILING DATE: 25-Jun-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP97/04585
; FILING DATE: 12-DEC-1997
; APPLICATION NUMBER: JP 347871
; FILING DATE: 26-DEC-1996
; APPLICATION NUMBER: JP 205815
; FILING DATE: 31-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Perry, Lawrence S.
; REGISTRATION NUMBER: 31865
; REFERENCE/DOCKET NUMBER: 766.32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 218-2100
; TELEFAX: (212) 218-2200
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: nucleic acid
; STRANDEDNESS: single
```

```
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-344-510B-25

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 988 TGCAATGGTGGACGAGG 1004
Db 17 TGAATGGTGGACGAGG 1

RESULT 275
PCT-US93-11198-317
; Sequence 317, Application PC/TUS9311198
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Maire H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKeen, John P.
; APPLICANT: Olin, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Polazzi, Joseph O.
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Interleukin-3 (IL-3) Mutant Polypeptides
; NUMBER OF SEQUENCES: 549
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESS: Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11198
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/981044
; FILING DATE: 24-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C2713/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 470-6501
; TELEFAX: (708) 470-6881
; INFORMATION FOR SEQ ID NO: 317:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
PCT-US93-11198-317

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1053 CTGTTGGTCTTCTTAAT 1069
|||||
```

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DB          1  CTGTTGGTCTTCCCAT 17

RESULT 276
PCT-US95-16718-18
; Sequence 18, Application PC/TUS9516718
; GENERAL INFORMATION:
; APPLICANT: MOUNT SINAI SCHOOL OF MEDICINE OF THE
; APPLICANT: CITY UNIVERSITY OF NEW YORK
; TITLE OF INVENTION: CHIMERIC ANTIBODIES
; TITLE OF INVENTION: COMBINING ANTIGEN BINDING SITES AND B AND T CELL EPITOPES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue &
; ADDRESSEE: Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16718
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Richard S
; REGISTRATION NUMBER: 26,154
; REFERENCE/DOCKET NUMBER: 29889-165/29528
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2558
; TELEFAX: 212-765-2519
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM:
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: primer
;
PCT-US95-16718-18

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3348 GCTGAGCACAAGCAGA 3364
DB 2 GCTGAGCACAAGAGA 18
||||| ||||| |||

RESULT 277
US-07-820-154A-42/c
; Sequence 42, Application US/07820154A
; Patent No. 5382425
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D., Mark D
; APPLICANT: Junker M.S., David E
; TITLE OF INVENTION: Recombinant Swinepox Virus

```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 163:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-117-952-163

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 885 GCCTCCCTGCTCATTTG 901
Db 2 GCCTCCCTGCTCATTTG 18

RESULT 279
US-08-097-554A-42/c
; Sequence 42, Application US/08097554A
; Patent No. 5869312
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D., Mark D
; APPLICANT: Junker M.S., David E
; TITLE OF INVENTION: Recombinant Swinepox Virus
; NUMBER OF SEQUENCES: 112
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,554A
; FILING DATE: July 22, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; ORIGINAL SOURCE:
; ORGANISM: Pseudorabies virus \ Synthetic oligonucleotide primer
; US-08-097-554A-42

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1333 TTCTGCAGCCACCTTA 1349
Db 18 TTACAGCAGCCACTCCTA 2

RESULT 280
US-08-480-640A-42/c
; Sequence 42, Application US/08480640A
; Patent No. 6033904
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; APPLICANT: Junker, David E.
; TITLE OF INVENTION: Recombinant Swinepox Virus
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,640A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; ORIGINAL SOURCE:
; ORGANISM: Pseudorabies virus
; ORGANISM: Synthetic oligonucleotide primer
; US-08-480-640A-42

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1333 TTCTGCAGCCACCTTA 1349
Db 18 TTACAGCAGCCACTCCTA 2

RESULT 281
US-08-851-350-30/c
; Sequence 30, Application US/08851350
; Patent No. 6057122
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME AND METHODS
; TITLE OF INVENTION: FOR INHIBITING ANGIOGENESIS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; US-08-851-350-30/c
```

STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851.350
FILING DATE: 05-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-851-350-30

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1109 CCAGGAATGTTCTGAA 1125
Db 17 CCAGGAAGGTTCTGAA 1

RESULT 282
US-08-295-802-42/c
Sequence 42, Application US/08295802
Patent No. 6127163
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 188
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295.802
FILING DATE: Herewith
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523

INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
ORIGINAL SOURCE:
ORGANISM: Pseudorabies virus \ Synthetic oligonucleotide primer
US-08-295-802-42

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1333 TTCTGCAGCCACCTA 1349
Db 18 TTCAGCAGCCACTCCTA 2

RESULT 283
US-08-974-549A-442
Sequence 442, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974.549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997


```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA: WO PCT/US97/17618
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA: WO PCT/US97/17885
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 442:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..19
; OTHER INFORMATION: /note= "TCP1.69 primer"
; US-08-974-549A-442

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 ACCAAGCCGACACCTG 220
Db 1 ACCAAGCCGACACCTG 17

RESULT 284
US-08-686-968C-72/c
; Sequence 72, Application US/08686968C
; Patent No. 6221361
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: Recombinant Swinepox Virus
; FILE REFERENCE: 39119-H/JML
; CURRENT APPLICATION NUMBER: US/08/686,968C
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 72
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; US-08-686-968C-72

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1333 TTCTGCAGCCACCTA 1349
Db 18 TTCAGCAGCCACTCCTA 2

RESULT 285
US-08-488-237A-42/c
; Sequence 42, Application US/08488237A
; Patent No. 6251403
; GENERAL INFORMATION:
```

```
; APPLICANT: Cochran, Mark D.
; APPLICANT: Junker, David E.
; TITLE OF INVENTION: Recombinant Swinepox Virus
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,237A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; ORIGINAL SOURCE:
; ORGANISM: Pseudorabies virus
; ORGANISM: Synthetic oligonucleotide primer
; US-08-488-237A-42

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1333 TTCTGCAGCCACCTA 1349
Db 18 TTCAGCAGCCACTCCTA 2

RESULT 286
US-09-277-078-19
; Sequence 19, Application US/09277078
; Patent No. 6312949
; GENERAL INFORMATION:
; APPLICANT: Sakurada, Kazuhiro
; APPLICANT: Palmer, Theo
; APPLICANT: Gage, Fred H.
; TITLE OF INVENTION: REGULATION OF TYROSINE HYDROXYLASE
; FILE REFERENCE: 07251/031001
; CURRENT APPLICATION NUMBER: US/09/277,078
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for PCR
; US-09-277-078-19

Query Match 0.4%; Score 13.8; DB 1; Length 19;
```

Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 885 GCCTCCCTGCTCATTG 901
||| ||||| ||||| |||
Db 1 GCCACCCCTGCTCATCTG 17

RESULT 287
US-08-375-992A-42/c
; Sequence 42, Application US/08375992A
; Patent No. 6328975
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; APPLICANT: Junker, David E.
; TITLE OF INVENTION: Recombinant Swinepox Virus
; NUMBER OF SEQUENCES: 220
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/375,992A
; FILING DATE: Herewith
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; ORIGINAL SOURCE:
; ORGANISM: Pseudorabies virus
; ORGANISM: Synthetic oligonucleotide primer
US-08-375-992A-42

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1333 TTTCGACCCACACCTA 1349
||| ||||| ||||| |||
Db 18 TTCAGCAGCCACTCCTA 2

RESULT 288
US-09-345-882-123/c
; Sequence 123, Application US/09345882
; Patent No. 6399373
; GENERAL INFORMATION:
; APPLICANT: Bouqueleret, Lydie
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
; FILE REFERENCE: GENSET-031A
; CURRENT APPLICATION NUMBER: US/09/345,882
; CURRENT FILING DATE: 1999-06-30

; PRIOR APPLICATION NUMBER: US 60/091,315
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/111,909
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: Patent.pm
; SEQ ID NO 123
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: potential microsequencing oligo for 5-124-273.mis2
US-09-345-882-123

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.4e+02;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2706 TTATTTCTGTCCTGGATT 2724
||||| ||||| ||||| |||
Db 19 TTATTACTGTACTGGWTT 1

RESULT 289
US-08-912-951-209
; Sequence 209, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; TITLE OF INVENTION: THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

US-08-472-679H-42

```
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-3519 for SEQ 3363,
US-09-422-978-7297

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2337 TTTTGGAGTTGTGATG 2353
      ||||| ||||| |||||
Db 17 TTTTGTAGTTCGATG 1

RESULT 293
US-09-402-181B-442
; Sequence 442, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenius, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 442:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..19
; OTHER INFORMATION: /note= "TCP1.69 primer"
; SEQUENCE DESCRIPTION: SEQ ID NO: 442:
US-09-402-181B-442

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 ACGAAGCCGAGACCTG 220
      ||||| ||||| |||||
Db 1 ACGAAGCCGTACACCTG 17

RESULT 294
US-09-721-456-442
; Sequence 442, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,456
; FILING DATE: 22-No. 6617110-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
```

NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 442:

SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:

NAME/KEY: -
LOCATION: 1..19
OTHER INFORMATION: /note= "TcP1.69 primer"

SEQUENCE DESCRIPTION: SEQ ID NO: 442:

US-09-721-456-442

Query Match

Best Local Similarity 0.4%; Score 13.8; DB 1; Length 19;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 204 ACGAAGCCGAGACCTG 220

Db 1 ACGAAGCCGTACACCTG 17

RESULT 295

PCT-US93-00324-42/c

Sequence 42, Application PC/TUS9300324

GENERAL INFORMATION:

APPLICANT: Cochran Ph.D., Mark D

APPLICANT: Junker M.S., David E

TITLE OF INVENTION: Recombinant Swinepox Virus

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/00324

FILING DATE: 19930113

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: White, John P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEFAX: (212) 664-0525

TELEX: 422523

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: N

ANTI-SENSE: N

ORIGINAL SOURCE:

ORGANISM: Pseudorabies virus \ Synthetic oligonucleotide primer

PCT-US93-00324-42

Query Match

0.4%; Score 13.8; DB 1; Length 19;

Best Local Similarity 88.2%; Pred No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1333 TTCTGAGCCACACCTA 1349

Db 18 TTCAGCAGCCACTCCTA 2

RESULT 296

US-08-311-486C-51/c

Sequence 51, Application US/08311486C

Patent No. 5811300

GENERAL INFORMATION:

APPLICANT: Sean Sullivan

APPLICANT: Kenneth Draper

APPLICANT: Kevin Kisich

APPLICANT: Dan T. Stinchcomb

APPLICANT: James McSwiggen

TITLE OF INVENTION: RIBOZYME TREATMENT OF

TITLE OF INVENTION: DISEASES OR CONDITIONS

TITLE OF INVENTION: RELATED TO LEVELS OF

TITLE OF INVENTION: TNF-

NUMBER OF SEQUENCES: 1157

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/311,486C

FILING DATE: September 23, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below:

APPLICATION NUMBER: 08/008,895

FILING DATE: January 19, 1993

APPLICATION NUMBER: 07/989,849

FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/166

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-311-486C-51

Query Match

0.4%; Score 13.4; DB 1; Length 15;

Best Local Similarity 93.3%; Pred No. 1.2e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 20 GGCTGATTAGAGA 34

Db 15 GGCTGATTAGAGA 1

RESULT 297

US-08-292-620A-365/c
; Sequence 365, Application US/08292620A

; Patent No. 5837542

; GENERAL INFORMATION:

; APPLICANT: Susan Grimm

; APPLICANT: Dan T. Stinchcomb

; APPLICANT: James McSwiggen

; APPLICANT: Sean Sullivan

; APPLICANT: Kenneth G. Draper

; TITLE OF INVENTION: RIBOZYME TREATMENT OF

; TITLE OF INVENTION: DISEASES OR CONDITIONS

; TITLE OF INVENTION: RELATED TO LEVELS OF

; TITLE OF INVENTION: INTRACELLULAR ADHESION

; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)

; NUMBER OF SEQUENCES: 2390

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/292,620A

; FILING DATE: August 17, 1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below:

; APPLICATION NUMBER: 08/008,895

; FILING DATE: January 19, 1993

; APPLICATION NUMBER: 07/989,849

; FILING DATE: December 7, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 208/149

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 365:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-292-620A-365

Query Match 0.4%; Score 13.4; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 1.2e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3391 CTCAAAAAAAAAAAAA 3405

Db 15 CTGAAAAAAAAAAAAA 1

RESULT 298

US-08-585-684B-735/c

; Sequence 735, Application US/08585684B

; Patent No. 5877021

; GENERAL INFORMATION:

; APPLICANT: Stinchcomb, Daniel T.

; APPLICANT: Jarvis, Thale

; APPLICANT: McSwiggen, James

; TITLE OF INVENTION: METHOD AND REAGENT FOR THE

; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE

; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES

; NUMBER OF SEQUENCES: 2751

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/585,684B

; FILING DATE: January 16, 1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/000,951

; FILING DATE: July 7, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 218/078

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 735:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-585-684B-735

Query Match 0.4%; Score 13.4; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 1.2e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 19 AGGCTGATAAGAGAG 33

Db 15 AGGATGATAAGAGAG 1

RESULT 299

US-08-585-684B-736/c

; Sequence 736, Application US/08585684B

; Patent No. 5877021

; GENERAL INFORMATION:

; APPLICANT: Stinchcomb, Daniel T.

; APPLICANT: Jarvis, Thale

; TITLE OF INVENTION: METHOD AND REAGENT FOR THE

; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE

; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES

; NUMBER OF SEQUENCES: 2751

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 736:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-585-684B-736

Query Match 0.4%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 AGCGTGTAAAGAG 33
||| |||||
Db 15 AGGATGATAAGAG 1

RESULT 300

US-08-585-684B-737/c
Sequence 737, Application US/08585684B
Patent No. 5877021
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: McSwigen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 737:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-585-684B-737

Query Match 0.4%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 AGCGTGTAAAGAG 33
||| |||||
Db 15 AGGATGATAAGAG 1

RESULT 301

US-08-832-021-19/c
Sequence 19, Application US/08832021
Patent No. 6045998
GENERAL INFORMATION:
APPLICANT: Combates, N.
APPLICANT: Pardinas, J.
APPLICANT: Parimoo, S.
APPLICANT: Prouty, S.
APPLICANT: Stenn, K.
TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
FILE REFERENCE: JBP-382
CURRENT APPLICATION NUMBER: US/08/832,021
CURRENT FILING DATE: 1997-04-02
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-19

Query Match 0.4%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3391 CTCAAAAA 3405
||| |||||
Db 15 CTTAAAAA 1

RESULT 302

US-08-832-021-23/c
Sequence 23, Application US/08832021
Patent No. 6045998
GENERAL INFORMATION:
APPLICANT: Combates, N.
APPLICANT: Pardinas, J.
APPLICANT: Parimoo, S.
APPLICANT: Prouty, S.
APPLICANT: Stenn, K.
TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
FILE REFERENCE: JBP-382
CURRENT APPLICATION NUMBER: US/08/832,021
CURRENT FILING DATE: 1997-04-02
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer

US-08-832-021-23

Query Match 0.4%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3391 CTCACAAAAA 3405
DB 15 CTCACAAAAA 1

RESULT 303

US-08-832-021-39/c
; Sequence 39, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-39

Query Match 0.4%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3391 CTCACAAAAA 3405
DB 15 CTCACAAAAA 1

RESULT 304

US-08-832-021-44/c
; Sequence 44, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-44

Query Match 0.4%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3390 ACTCAAAAAA 3404

DB 15 ACTCAAAAAA 1

RESULT 305

US-08-832-021-51/c
; Sequence 51, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-51

Query Match 0.4%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3391 CTCACAAAAA 3405
DB 15 CTCACAAAAA 1

RESULT 306

US-08-832-021-63/c
; Sequence 63, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardinas, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-63

Query Match 0.4%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3391 CTCACAAAAA 3405
DB 15 CTCACAAAAA 1

RESULT 307

US-09-071-845-365/c
; Sequence 365, Application US/09071845

Patent No. 6132967
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
CITY: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 365:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-365

Query Match 0.4%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3391 CTCGAAAAA 3405
DB 15 CTGAAAAA 1

RESULT 308
US-09-038-073-735/c
Sequence 735, Application US/09038073
Patent No. 6194150
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: McSwiggen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
INDUCTION OF GRAFT TOLERANCE

TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
CITY: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,073
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,684
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 735:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-038-073-735

Query Match 0.4%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 AGCGTATGAAGAG 33
DB 15 AGGATGATAAGAG 1

RESULT 309
US-09-038-073-736/c
Sequence 736, Application US/09038073
Patent No. 6194150
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: McSwiggen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
CITY: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,666
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 736:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-038-073-736

Query Match 0.4%; Score
Best Local Similarity 93.3%; Prior
Matches 14; Conservative 0;

QY 19 AGGCTGATAGAGAG 33
Db 15 AGGATGATAGAGAG 1

RESULT 310
US-09-038-073-737/c
; Sequence 737, Application US/090308
; Patent No. 6194150
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND
; TITLE OF INVENTION: INDUCTION
; TITLE OF INVENTION: AND REVERS
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette,
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. D
; SOFTWARE: FastSeq Version 1.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,666
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 737:
; SEQUENCE CHARACTERISTICS:

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/ APPLICATION NUMBER: US/08/390,850
/ FILING DATE: February 17, 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/354,920
/ FILING DATE: December 13, 1994
/ APPLICATION NUMBER: 08/152,487
/ FILING DATE: No. 5612215ember 12, 1993
/ APPLICATION NUMBER: 07/989,848
/ FILING DATE: December 7, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 211/084
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 582:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-390-850-582

Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 315 CTTTAAAGGAAC 329
Db 2 CAUUUUUAAAGGAAC 16

RESULT 313
US-08-373-124A-1156/c
/ Sequence 1156, Application US/08373124A
/ Patent No. 5646042
/ GENERAL INFORMATION:
/ APPLICANT: Stinchcomb, Dan T.
/ APPLICANT: Draper, Kenneth
/ APPLICANT: McSwiggen, James
/ APPLICANT: Jarvis, Thale
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
/ TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
/ TITLE OF INVENTION: CANCER USING RIBOZYMES
/ NUMBER OF SEQUENCES: 2627
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: Storage
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/373,124A
/ FILING DATE: January 13, 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/245,466
/ FILING DATE: May 18, 1994
/ APPLICATION NUMBER: 08/192,943
/ FILING DATE: February 7, 1994
/ APPLICATION NUMBER: 07/987,132
/ FILING DATE: December 7, 1992
/ APPLICATION NUMBER: 07/936,422
/ FILING DATE: August 26, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 209/035
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 1158:

/ APPLICATION NUMBER: US/08/390,850
/ FILING DATE: February 17, 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/354,920
/ FILING DATE: December 13, 1994
/ APPLICATION NUMBER: 08/152,487
/ FILING DATE: No. 5612215ember 12, 1993
/ APPLICATION NUMBER: 07/989,848
/ FILING DATE: December 7, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 209/035
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 1158:

Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3388 ACACCTCAAAAAAAA 3402
Db 16 ACACCTCAAAAAAAA 2

RESULT 314
US-08-373-124A-1158/c
/ Sequence 1158, Application US/08373124A
/ Patent No. 5646042
/ GENERAL INFORMATION:
/ APPLICANT: Stinchcomb, Dan T.
/ APPLICANT: Draper, Kenneth
/ APPLICANT: McSwiggen, James
/ APPLICANT: Jarvis, Thale
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
/ TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
/ TITLE OF INVENTION: CANCER USING RIBOZYMES
/ NUMBER OF SEQUENCES: 2627
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: Storage
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/373,124A
/ FILING DATE: January 13, 1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/245,466
/ FILING DATE: May 18, 1994
/ APPLICATION NUMBER: 08/192,943
/ FILING DATE: February 7, 1994
/ APPLICATION NUMBER: 07/987,132
/ FILING DATE: December 7, 1992
/ APPLICATION NUMBER: 07/936,422
/ FILING DATE: August 26, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 209/035
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 1158:
```

SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-1158

Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3388 ACACTCAAAAAAAA 3402
Db 15 ACACTCAAAACAAA 1

RESULT 315

US-08-373-124A-2017
Sequence 2017, Application US/08373124A
Patent No. 5646042

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.

APPLICANT: Draper, Kenneth
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND

TITLE OF INVENTION: CANCER USING RIBOZYMES

NUMBER OF SEQUENCES: 2627

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/373.124A

FILING DATE: January 13, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/245,466

FILING DATE: May 18, 1994

APPLICATION NUMBER: 08/192,943

FILING DATE: February 7, 1994

APPLICATION NUMBER: 07/987,132

FILING DATE: December 7, 1992

APPLICATION NUMBER: 07/936,422

FILING DATE: August 26, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/035

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 2017:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-373-124A-2017

Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 46.7%; Pred. No. 1.4e+02;

Matches 7; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
QY 2545 AGGTGATTTTGTGT 2559
Db 1 AGGAGUUUUUUUU 15

RESULT 316

US-08-435-634-582
Sequence 582, Application US/08435634
Patent No. 5731295

GENERAL INFORMATION:

APPLICANT: Draper, Kenneth G.

APPLICANT: Pavco, Pamela

APPLICANT: McSwiggen, James

APPLICANT: Gustofson, John

APPLICANT: Stinchcomb, Dan T.

TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT

TITLE OF INVENTION: OF ARTHRITIC CONDITIONS

NUMBER OF SEQUENCES: 1151

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/435,634

FILING DATE: 05-MAY-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/390,850

FILING DATE: February 17, 1995

APPLICATION NUMBER: 08/354,920

FILING DATE: December 13, 1994

APPLICATION NUMBER: 08/152,487

FILING DATE: No. 5731295ember 12, 1993

APPLICATION NUMBER: 07/989,848

FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 211/084

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 582:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-435-634-582

Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;

Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 315 CCTTTTAAAGAAC 329

Db 2 CAUUUUAAAGAAC 16

RESULT 317

```

US-08-435-628-1156/c
; Sequence 1156, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1156:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-628-1156
Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3388 ACACCTCAAAAAAAA 3402
Db 16 ACACCTCAAAAAAAA 2

RESULT 318
US-08-435-628-1158/c
; Sequence 1158, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth

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; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1158:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-628-1158
Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3388 ACACCTCAAAAAAAA 3402
Db 15 ACACCTCAAAAAAAA 1

RESULT 319
US-08-435-628-2017
; Sequence 2017, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627

```

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;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2017:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; US-08-435-628-2017
;
; Query Match 0.4%; Score 13.4; DB 1; Length 17;
; Best Local Similarity 46.7%; Pred. No. 1.4e+02;
; Matches 7; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
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; QY 2545 AGGTGATTTTGTCT 2559
; Db 1 AGGAGUUUUUUUU 15
;
; RESULT 320
; US-08-584-040-1555/c
; Sequence 1555, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1555:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-584-040-1555

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;
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1555:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-584-040-1555
;
; Query Match 0.4%; Score 13.4; DB 1; Length 17;
; Best Local Similarity 93.3%; Pred. No. 1.4e+02;
; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 318 TTTTAAAGGAACAGT 332
; Db 17 TTTTAAAGTAACAGT 3
;
; RESULT 321
; US-08-584-040-1555/c
; Sequence 1558, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040

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/ FILING DATE: January 11, 1996
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/005,974
/ FILING DATE: October 26, 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 218/064
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 1558:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-08-584-040-1558

Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2064 ACTTTTAAAGTAA 2078
Db 16 ACTTTTAAAGTAA 2

RESULT 322
US-08-584-040-2187/c
/ Sequence 2187, Application US/08584040
/ Patent No. 6346398
/ GENERAL INFORMATION:
/ APPLICANT: Pavco, Pamela
/ APPLICANT: McSwiggen, James
/ APPLICANT: Stinchcomb, Dan T.
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: METHOD AND REAGENT FOR THE
/ TITLE OF INVENTION: TREATMENT OF DISEASES OR
/ TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
/ TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
/ TITLE OF INVENTION: GROWTH FACTOR
/ NUMBER OF SEQUENCES: 8502
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/584,040
/ FILING DATE: January 11, 1996
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/005,974
/ FILING DATE: October 26, 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 218/064
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 2188:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-08-584-040-2188

Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 2187:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-08-584-040-2187

Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3390 ACTCAAAAAAAAAA 3404
Db 17 AGTCAAAAAAAAAA 3

RESULT 323
US-08-584-040-2188/c
/ Sequence 2188, Application US/08584040
/ Patent No. 6346398
/ GENERAL INFORMATION:
/ APPLICANT: Pavco, Pamela
/ APPLICANT: McSwiggen, James
/ APPLICANT: Stinchcomb, Dan T.
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: METHOD AND REAGENT FOR THE
/ TITLE OF INVENTION: TREATMENT OF DISEASES OR
/ TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
/ TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
/ TITLE OF INVENTION: GROWTH FACTOR
/ NUMBER OF SEQUENCES: 8502
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/584,040
/ FILING DATE: January 11, 1996
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/005,974
/ FILING DATE: October 26, 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 218/064
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 2188:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-08-584-040-2188

Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 3390 ACTCAAAAAAAAAA 3404
 Db 16 AGTCAAAAAAAAAA 2

RESULT 324

US-08-584-040-2189/c
 ; Sequence 2189, Application US/08584040
 ; Patent No. 6346398
 ; GENERAL INFORMATION:
 ; APPLICANT: Pavco, Pamela
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Stinchcomb, Dan T.
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 ; TITLE OF INVENTION: TREATMENT OF DISEASES OR
 ; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
 ; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
 ; TITLE OF INVENTION: GROWTH FACTOR
 ; NUMBER OF SEQUENCES: 8502
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/584,040
 ; FILING DATE: January 11, 1996
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/005,974
 ; FILING DATE: October 26, 1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 218/064
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 2189:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 17 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-584-040-2189

Query Match 0.4%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 1.4e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3390 ACTCAAAAAAAAAA 3404
 Db 15 AGTCAAAAAAAAAA 1

RESULT 325

US-08-584-040-2460
 ; Sequence 2460, Application US/08584040
 ; Patent No. 6346398
 ; GENERAL INFORMATION:
 ; APPLICANT: Pavco, Pamela

; APPLICANT: McSwiggen, James
 ; APPLICANT: Stinchcomb, Dan T.
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 ; TITLE OF INVENTION: TREATMENT OF DISEASES OR
 ; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
 ; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
 ; TITLE OF INVENTION: GROWTH FACTOR
 ; NUMBER OF SEQUENCES: 8502
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/584,040
 ; FILING DATE: January 11, 1996
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/005,974
 ; FILING DATE: October 26, 1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 218/064
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 2460:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 17 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-584-040-2460

Query Match 0.4%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 73.3%; Pred. No. 1.4e+02;
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1329 CACTTCTGCAGCCA 1343
 Db 3 CACCUUCGAGCCA 17

RESULT 326

US-08-584-040-2726/c
 ; Sequence 2726, Application US/08584040
 ; Patent No. 6346398
 ; GENERAL INFORMATION:
 ; APPLICANT: Pavco, Pamela
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Stinchcomb, Dan T.
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 ; TITLE OF INVENTION: TREATMENT OF DISEASES OR
 ; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
 ; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
 ; TITLE OF INVENTION: GROWTH FACTOR
 ; NUMBER OF SEQUENCES: 8502
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street


```
/ STREET: Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/584,040
/ FILING DATE: January 11, 1996
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/005,974
/ FILING DATE: October 26, 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 218/064
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 2726:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-584-040-2726

Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2577 ATGGTATAGAAATA 2591
Db 15 ATGGTATACAAATA 1
|||||

RESULT 327
US-08-584-040-7969
/ Sequence 7969, Application US/08584040
/ Patent No. 6346398
/ GENERAL INFORMATION:
/ APPLICANT: Pavco, Pamela
/ APPLICANT: McSwiggen, James
/ APPLICANT: Stinchcomb, Dan T.
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: METHOD AND REAGENT FOR THE
/ TITLE OF INVENTION: TREATMENT OF DISEASES OR
/ TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
/ TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
/ TITLE OF INVENTION: GROWTH FACTOR
/ NUMBER OF SEQUENCES: 8502
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: 60/001,135
/ FILING DATE: July 13, 1995
/ APPLICATION NUMBER: 08/300,726
/ FILING DATE: September 2, 1994
/ ATTORNEY/AGENT INFORMATION:

/ STREET: Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: 60/005,974
/ FILING DATE: October 26, 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 218/064
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 7969:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-584-040-7969

Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2575 TCATGGTATAGAAA 2589
Db 2 UCAUGGUCUAGAAA 16
|||||

RESULT 328
US-08-679-645-247/c
/ Sequence 247, Application US/08679645
/ Patent No. 6350934
/ GENERAL INFORMATION:
/ APPLICANT: Zwick, Michael G.
/ APPLICANT: Edington, Brent E.
/ APPLICANT: McSwiggen, James A.
/ APPLICANT: Merlo, Patricia Ann Owens
/ APPLICANT: Guo, Lining
/ APPLICANT: Skokut, Thomas A.
/ APPLICANT: Young, Scott A.
/ APPLICANT: Folkerts, Otto
/ APPLICANT: Merlo, Donald J.
/ TITLE OF INVENTION: COMPOSITION AND METHODS FOR
/ TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
/ TITLE OF INVENTION: IN PLANTS
/ NUMBER OF SEQUENCES: 1263
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/679,645
/ FILING DATE: July 12, 1996
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/001,135
/ FILING DATE: July 13, 1995
/ APPLICATION NUMBER: 08/300,726
/ FILING DATE: September 2, 1994
/ ATTORNEY/AGENT INFORMATION:
```

NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 247:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-679-645-247

Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1694 CAAGCAGCTAAACAT 1708
Db 17 CAAGCAGCTACAT 3
|||||

RESULT 329
US-09-527-223-17/c
Sequence 17, Application US/09527223
Patent No. 6432646
GENERAL INFORMATION:
APPLICANT: GASSER, Robin B.
APPLICANT: WOODS, Wayne G.
APPLICANT: RICHARDS, David G.
APPLICANT: WHITHEAR, Kevin G.
TITLE OF INVENTION: PCR-BASED IDENTIFICATION OF EIMERIA SPECIES AND STRAINS
FILE REFERENCE: Q58329
CURRENT APPLICATION NUMBER: US/09/527,223
CURRENT FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 17
TYPE: DNA
ORGANISM: synthetic construct
US-09-527-223-17

Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1393 AGACACTGAAACAGA 1407
Db 17 AGACACTGAAACAGA 3
|||||

RESULT 330
US-09-474-432B-691/c
Sequence 691, Application US/09474432B
Patent No. 6528640
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Burgin, Alex
APPLICANT: Beaudry, Amber
APPLICANT: Karpelesky, Alex
APPLICANT: Adamic, Jasenka
APPLICANT: Sweedler, David
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleotides
FILE REFERENCE: MBHB00-831-B (247/276)
CURRENT APPLICATION NUMBER: US/09/474,432B
CURRENT FILING DATE: 1999-12-19
PRIOR APPLICATION NUMBER: US 60/064,866
PRIOR FILING DATE: 1997-11-05

PRIOR APPLICATION NUMBER: US 60/084,727
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: US 09/186,675
PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: US 09/301,511
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 1526
SOFTWARE: PatentIn version 3.0
SEQ ID NO 691
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-474-432B-691

Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1796 CCTGGACCCCTAGCA 1810
Db 16 CCTGGACCCCGCA 2
|||||

RESULT 331
US-09-371-772B-100/c
Sequence 100, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 100
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-371-772B-100

Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 318 TTTTAAAGGAACAGT 332
Db 17 TTTTAAAGTAACAGT 3
|||||

RESULT 332
US-09-371-772B-103/c
Sequence 103, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B

; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-103

Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2064 ACTTTTAAAGTAA 2078
||||| |||||
Db 16 ACTTTTAAAGTAA 2

RESULT 333
US-09-371-772B-732/c
; Sequence 732, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 732
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-732

Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3390 ACTCAAAAAA 3404
||||| |||||
Db 17 AGTCAAAAAA 3

RESULT 334
US-09-371-772B-733/c
; Sequence 733, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10

; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 733
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-733

Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3390 ACTCAAAAAA 3404
||||| |||||
Db 16 AGTCAAAAAA 2

RESULT 335
US-09-371-772B-734/c
; Sequence 734, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 734
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-734

Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3390 ACTCAAAAAA 3404
||||| |||||
Db 15 AGTCAAAAAA 1

RESULT 336
US-09-371-772B-984
; Sequence 984, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974

; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 984
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-984

Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 73.3%; Pred. No. 1.4e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1329 CACTTCTGCAGCCA 1343
||| :||:|||||
Db 3 CACCUUCGACGCA 17

RESULT 337

US-09-371-772B-1250/c
; Sequence 1250, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1250
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1250

Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2577 ATGGTATAGAAATA 2591
|||||:|||||
Db 15 ATGGTATACAAAATA 1

RESULT 338

US-09-371-772B-3752
; Sequence 3752, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26

; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3752
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3752

Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2575 TCATGGTATAGAAA 2589
|||:|||||
Db 2 UCAUGGUCUAGAAA 16

RESULT 339

US-09-371-772B-5338
; Sequence 5338, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5338
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5338

Query Match 0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 73.3%; Pred. No. 1.4e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1329 CACTTCTGCAGCCA 1343
|||:|||||
Db 2 CACCUUCGACGCA 16

RESULT 340

US-09-476-387-690/c
; Sequence 690, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleo
; FILE REFERENCE: MHB00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29


```
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7928
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-7928

Query Match      0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      578 AATGAGAGGCTCTGG 592
Db      1 AAGGAGAGGCTCTGG 15

RESULT 344
PCT-US92-01015-24/c
; Sequence 24, Application PC/TUS9201015
; GENERAL INFORMATION:
; APPLICANT: Davis, Geneva R
; APPLICANT: Provow, Sally P
; TITLE OF INVENTION: Production of Human Serum Albumin in
; TITLE OF INVENTION: Methyloleophilic Yeast Cells
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitch, Even, Tabin & Flannery
; STREET: 135 South LaSalle Street, Suite 900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19920204
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/650,040
; FILING DATE: 04-FEB-1991
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 50857PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)552-1311
; TELEFAX: (619)552-0095
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US92-01015-24

Query Match      0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1170 TCAGGATCCTTAGT 1184
Db      16 TCAGGATCCTTAGT 2

RESULT 345
5240847-21
; Patent No. 5240847
; APPLICANT: HECKL, KONRAD; SPEVAK, WALTER; OSTERMANN, ELINBORG;
; ZOPHEL, ANDREAS; KRISTEK, EDELTRAUD; MAURER-FOGY, INGRID;
; WICHE-CASTANON, MARIA J.; STRATOWA, CHRISTIAN; HAUPTMANN, RUDOLF
; TITLE OF INVENTION: HUMAN MANGANESE SUPEROXIDE DISMUTASE
; (HMN-SOD)
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/167,261
; FILING DATE: 11-MAR-1986
; SEQ ID NO: 21
; LENGTH: 17
5240847-21

Query Match      0.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      267 CTGAAGAGAATGTCC 281
Db      3 CTGAAGAGAATGTCC 17

RESULT 346
US-08-432-871C-28/c
; Sequence 28, Application US/08432871C
; Patent No. 5877010
; GENERAL INFORMATION:
; APPLICANT: Loeb, Lawrence A.
; APPLICANT: Black, Margaret E.
; TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432,871C
; FILING DATE: 02-MAY-1995
```


; TITLE OF INVENTION: ANTISENSE MODULATION OF SRA EXPRESSION
; FILE REFERENCE: RTS-0048
; CURRENT APPLICATION NUMBER: US/09/280,409
; CURRENT FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 146
; SEQ ID NO 44
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

US-09-280-409-44

Query Match 0.4%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 67 GTCATTCAGTGGATG 81
||| ||||| |||||
Db 17 GTCAGTCAGTGGATG 3

RESULT 351

US-09-071-433-57
; Sequence 57, Application US/09071433A
; Patent No. 6197584
; GENERAL INFORMATION:

; APPLICANT: Bennett, C. Frank

; APPLICANT: Cowert, Lex M

; TITLE OF INVENTION: Antisense Modulation of CD40 Expression

; FILE REFERENCE: RTS-0002

; CURRENT APPLICATION NUMBER: US/09/071,433A

; CURRENT FILING DATE: 1998-05-01

; NUMBER OF SEQ ID NOS: 91

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 57

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-071-433-57

Query Match 0.4%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2783 GTATTGGTCTCACA 2797
||| ||||| |||||
Db 4 GTCTTGGTCTCACA 18

RESULT 352

US-09-527-223-27/c
; Sequence 27, Application US/09527223
; Patent No. 6432646
; GENERAL INFORMATION:

; APPLICANT: GASSER, Robin B.

; APPLICANT: WOODS, Wayne G.

; APPLICANT: RICHARDS, David G.

; APPLICANT: WHITHEAR, Kevin G.

; TITLE OF INVENTION: PCR-BASED IDENTIFICATION OF EIMERIA SPECIES AND STRAINS

; FILE REFERENCE: Q58329

; CURRENT APPLICATION NUMBER: US/09/527,223

; CURRENT FILING DATE: 2000-03-16

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 27

; LENGTH: 18

; TYPE: DNA

; ORGANISM: synthetic construct

US-09-527-223-27

Query Match 0.4%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1393 AGACATGAAACAGA 1407
||| ||||| |||||
Db 18 AGACACTGAAACAGA 4

RESULT 353

US-09-527-223-33/c

; Sequence 33, Application US/09527223

; Patent No. 6432646

; GENERAL INFORMATION:

; APPLICANT: GASSER, Robin B.

; APPLICANT: WOODS, Wayne G.

; APPLICANT: RICHARDS, David G.

; APPLICANT: WHITHEAR, Kevin G.

; TITLE OF INVENTION: PCR-BASED IDENTIFICATION OF EIMERIA SPECIES AND STRAINS

; FILE REFERENCE: Q58329

; CURRENT APPLICATION NUMBER: US/09/527,223

; CURRENT FILING DATE: 2000-03-16

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 33

; LENGTH: 18

; TYPE: DNA

; ORGANISM: synthetic construct

US-09-527-223-33

Query Match 0.4%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1393 AGACATGAAACAGA 1407
||| ||||| |||||
Db 18 AGACACTGAAACAGA 4

RESULT 354

US-09-270-956-28/c

; Sequence 28, Application US/09270956

; Patent No. 6451571

; GENERAL INFORMATION:

; APPLICANT: Loeb, Lawrence A.

; APPLICANT: Black, Margaret E.

; TITLE OF INVENTION: THYMIDINE KINASE MUTANTS

; NUMBER OF SEQUENCES: 104

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: US

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/270,956

; FILING DATE: 17-MAR-1999

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: McMasters, David D.

; REGISTRATION NUMBER: 33,963

; REFERENCE/DOCKET NUMBER: 240052.409C3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; TELEX: 3723836

; INFORMATION FOR SEQ ID NO: 28:


```
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-09-270-956-28

Query Match          0.4%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 394 GCAGGCTCTTCAGCA 408
Db 16 GCAGGCTCTTCAGCA 2

RESULT 355
US-09-422-978-7303/c
; Sequence 7303, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7303
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-3563 for SEQ 3369,
US-09-422-978-7303

Query Match          0.4%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1521 GGATGAAGAAGTGGT 1535
Db 15 GGATGAAGAAGTGGT 1

RESULT 356
US-09-422-978-9960
; Sequence 9960, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
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/ SEQ ID NO 9960
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: primer_bind
/ LOCATION: 1..18
/ OTHER INFORMATION: downstream amplification primer 99-8487 for SEQ 2095, in complete
US-09-422-978-9960

Query Match          0.4%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 477 CCATCTACAGTACTG 491
Db 4 CCATCTACTGTACTG 18

RESULT 357
US-09-422-978-10104
; Sequence 10104, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10104
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-952 for SEQ 2239, in complete
US-09-422-978-10104

Query Match          0.4%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 327 AACAGTCCACACTTG 341
Db 1 AACAGTACACACTTG 15

RESULT 358
US-09-747-391-35/c
; Sequence 35, Application US/09747391
; Patent No. 6670124
; GENERAL INFORMATION:
; APPLICANT: Chow, Robert
; APPLICANT: Tonal, Richard
; APPLICANT: StemCyte, Inc.
; TITLE OF INVENTION: High Throughput Methods of HLA Typing
; FILE REFERENCE: 020035-000210US
; CURRENT APPLICATION NUMBER: US/09/747,391
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/172,768
; PRIOR FILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: FastSEQ for Windows Version 3.0
```

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; SEQ ID NO 35
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-747-391-35

Query Match      0.4%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1145 GCTTGGGACCTGGG 1159
Db      15 GCTTGCACCTGGG 1

RESULT 359
PCT-US92-01015-11
; Sequence 11, Application PC/TUS9201015
; GENERAL INFORMATION:
; APPLICANT: Davis, Geneva R
; TITLE OF INVENTION: Production of Human Serum Albumin in
; TITLE OF INVENTION: Methylothrophic Yeast Cells
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitch, Even, Tabin & Flannery
; STREET: 135 South LaSalle Street, Suite 900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/01015
; FILING DATE: 19920204
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/650,040
; FILING DATE: 04-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 50857PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)552-1311
; TELEFAX: (619)552-0095
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US92-01015-11

Query Match      0.4%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2143 CTTTAAATTTCTTTGT 2157
Db      2 CTTTCATTTCTTTGT 16

RESULT 360
PCT-US95-04094-21
; Sequence 21, Application PC/TUS9504094
; GENERAL INFORMATION:
; APPLICANT: ALMS, William
```

```
; APPLICANT: WHITE, Barbara
; TITLE OF INVENTION: HUMAN INTERLEUKIN VARIANTS GENERATED BY
; TITLE OF INVENTION: ALTERNATIVE SPLICING
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04094
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/224,010
; FILING DATE: 06-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 028754-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US95-04094-21

Query Match      0.4%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      468 CAATGAGCACCACCT 482
Db      3 CAATGAGCACCACCT 17

RESULT 361
US-08-161-673A-8
; Sequence 8, Application US/08161673A
; Patent No. 5578716
; GENERAL INFORMATION:
; APPLICANT: Szyf, Moshe
; APPLICANT: von Hofe, Eric
; TITLE OF INVENTION: Antisense Oligonucleotides Having
; TITLE OF INVENTION: Tumorigenicity-Inhibiting Activity
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 S. Wacker
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/161,673A
; FILING DATE: December 1, 1993
```

```
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Greenfield, Michael S.
/ REGISTRATION NUMBER: 37,142
/ REFERENCE/DOCKET NUMBER: 93,1027
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-715-1000
/ TELEFAX: 312-715-1234
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1..19
/ OTHER INFORMATION: /note= "SENSE PRIMER"
US-08-161-673A-8
Query Match 0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3034 TATGGTGATTGCT 3048
Db 2 TATGGTGATTGCT 16

RESULT 362
US-08-468-037A-33
/ Sequence 33, Application US/08468037A
/ Patent No. 5859221
/ GENERAL INFORMATION:
/ APPLICANT: Phillip Dan Cook
/ APPLICANT: A. Kawasaki
/ TITLE OF INVENTION: 2'-Modified Oligonucleotides
/ NUMBER OF SEQUENCES: 37
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 5859221ris
/ STREET: One Liberty Place - 46th Floor
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: U.S.A.
/ ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch disk, 720 Kb
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WordPerfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/468,037A
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 835,932
/ FILING DATE: 05-MAR-1992
/ REGISTRATION NUMBER: 33,307
/ REFERENCE/DOCKET NUMBER: ISIS-2004
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 215-568-3100
/ TELEFAX: 215-568-3439
/ INFORMATION FOR SEQ ID NO: 33:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 bases
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-468-037A-33

Query Match 0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3034 TATGGTGATTGCT 3048
Db 2 TATGGTGATTGCT 16

RESULT 364
US-08-481-876-8
/ Sequence 8, Application US/08481876
/ Patent No. 5919772
/ GENERAL INFORMATION:
/ APPLICANT: Szyf, Moshe
/ APPLICANT: von Hofe, Eric
/ TITLE OF INVENTION: Antisense Oligonucleotides Having
/ NUMBER OF SEQUENCES: 12
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Banner & Allegretti, Ltd.
/
```

STREET: 10 S. Wacker
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481.876
FILING DATE: June 7, 1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield, Michael S.
REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 93,1027-B
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..19
OTHER INFORMATION: /note= "SENSE PRIMER"
US-08-481-876-8

Query Match 0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3034 TATGGTGATTGCCT 3048
|||||
DB 2 TATGGTGATTGCCT 16

RESULT 365
US-08-465-880-28
Sequence 28, Application US/08465880
Patent No. 595589
GENERAL INFORMATION:
APPLICANT: Philip Dan Cook
TITLE OF INVENTION: Gapped 2' Modified Oligonucleotides
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5955589ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465.880
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 244,993
FILING DATE: 21-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307

REFERENCE/DOCKET NUMBER: ISIS-2002
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-465-880-28

Query Match 0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3391 CTCAAAAA 3405
|
DB 1 CGCAAAAAA 15

RESULT 366
US-09-035-357-33
Sequence 33, Application US/09035357
Patent No. 6005087
GENERAL INFORMATION:
APPLICANT: Philip Dan Cook
APPLICANT: A. Kawasaki
TITLE OF INVENTION: 2'-Modified Oligonucleotides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6005087ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035.357
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/468,037
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-2004
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-035-357-33

Query Match 0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3391 CTCAAAAA 3405
|
DB 1 CGCAAAAAA 15

```
RESULT 367
US-08-181-664-26
; Sequence 26, Application US/08181664
; Patent No. 6025127
; GENERAL INFORMATION:
; APPLICANT: Sidransky, David
; TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION IN
; TITLE OF INVENTION: HISTOLOGIC TISSUE
; NUMBER OF SEQUENCES: 82
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Spensley Horn Jubas & Lubitz
; STREET: 1890 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/181,664
; FILING DATE: JANUARY 14, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-3055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..19
US-08-181-664-26

Query Match 0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3256 GAGTGAATGGAATT 3270
Db 5 GAGTGAAGGAATT 19
|||||

RESULT 368
US-09-185-437-8
; Sequence 8, Application US/09185437
; Patent No. 6054439
; GENERAL INFORMATION:
; APPLICANT: SZYF, Moshe
; APPLICANT: von Hofe, Eric
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES HAVING
; TITLE OF INVENTION: TUMORIGENICITY-INHIBITING ACTIVITY
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: United States of America
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

Query Match 0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3391 CTCAAAAAAGAAAAA 3405
Db 1 CGCAAAAAAAGAAAAA 15
|||||

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/185,437
; FILING DATE: 17-FEB-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: KEOWN, Wayne A.
; REGISTRATION NUMBER: 33,923
; REFERENCE/DOCKET NUMBER: 106.101.138
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 526 6000
; TELEFAX: 617 526 5000
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..19
; OTHER INFORMATION: /note= "SENSE PRIMER"
US-09-185-437-8

Query Match 0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3034 TATGGTGAATTGCCT 3048
Db 2 TATGGTGGTTGCCT 16
|||||

RESULT 369
US-09-016-520-4
; Sequence 4, Application US/09016520A
; Patent No. 6127533
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/016,520A
; CURRENT FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; EARLIER FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-016-520-4

Query Match 0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3391 CTCAAAAAAGAAAAA 3405
Db 1 CGCAAAAAAAGAAAAA 15
|||||

RESULT 370
US-09-144-611-12
; Sequence 12, Application US/09144611A
; Patent No. 6146829
```

```
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Monia, Brett P
; TITLE OF INVENTION: Gapped 2' Modified Oligonucleotides
; FILE REFERENCE: ISIS153
; CURRENT APPLICATION NUMBER: US/09/144,611A
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 08/861,306
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6146829e1
; OTHER INFORMATION: Sequence
US-09-144-611-12

Query Match          0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3391 CTCAAAAAATAAAAA 3405
Db      1 CGCAAAAAAATAAAAA 15

RESULT 371
US-09-130-973-4
; Sequence 4, Application US/09130973
; Patent No. 6172209
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides And Methods For
; TITLE OF INVENTION: Making Same
; FILE REFERENCE: ISIS2955
; CURRENT APPLICATION NUMBER: US/09/130,973
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6172209e1
; OTHER INFORMATION: Sequence
US-09-130-973-4

Query Match          0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3391 CTCAAAAAATAAAAA 3405
Db      1 CGCAAAAAAATAAAAA 15

RESULT 372
US-08-899-330-20
; Sequence 20, Application US/08899330
; Patent No. 6177275
; GENERAL INFORMATION:
; APPLICANT: CORUZZI, GLORIA
; APPLICANT: LAM, HON-MING
; APPLICANT: HSIEH, MING-HSIUN
; TITLE OF INVENTION: PLANT NITROGEN REGULATORY
; TITLE OF INVENTION: P-FII GENES
```

```
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,330
; FILING DATE: 23-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/022,328
; FILING DATE: 24-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 5914-042-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)7909090
; TELEFAX: (212)8699741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
US-08-899-330-20

Query Match          0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      964 GAAACCAACATAGA 978
Db      1 GAAACCAACACAGA 15

RESULT 373
US-09-477-902-4
; Sequence 4, Application US/09477902
; Patent No. 6194598
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: Aminoxy-Modified Oligonucleotides
; FILE REFERENCE: ISIS2824
; CURRENT APPLICATION NUMBER: US/09/477,902
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 09/016,520
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/037,143
; PRIOR FILING DATE: 1997-02-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-477-902-4
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Query Match          0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3391 CTCAAAAA 3405
DB 1 CGCAAAAAA 15

RESULT 374
US-08-557-006C-15/c
; Sequence 15, Application US/08557006C
; Patent No. 6258547
; GENERAL INFORMATION:
; APPLICANT: Berli, Rajindar K.
; APPLICANT: Carling, David
; APPLICANT: Forder, Robert A.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
; FILE REFERENCE: NGAP/PHM37588/UST
; CURRENT APPLICATION NUMBER: US/08/557,006C
; CURRENT FILING DATE: 1996-03-06
; PRIOR APPLICATION NUMBER: PCT/GB94/01093
; PRIOR FILING DATE: 1994-05-20
; PRIOR APPLICATION NUMBER: GB 9310489.1
; PRIOR FILING DATE: 1993-05-21
; PRIOR APPLICATION NUMBER: GB 9318010.7
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA artificial
US-08-557-006C-15

Query Match          0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 125 CTCTCAGCCTGTT 139
DB 19 CTCTCAGCATGTT 5

RESULT 375
US-09-453-514A-12
; Sequence 12, Application US/09453514A
; Patent No. 6326199
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Monia, Brett P.
; TITLE OF INVENTION: Gapped 2-Modified Oligonucleotides
; FILE REFERENCE: ISIS-4231
; CURRENT APPLICATION NUMBER: US/09/453,514A
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/144,611
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. 6326199el Sequence
US-09-453-514A-12

Query Match          0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3391 CTCAAAAA 3405
DB 1 CGCAAAAAA 15

RESULT 376
US-09-135-202-33
; Sequence 33, Application US/09135202
; Patent No. 6399754
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; APPLICANT: Andrew Kawasaki
; TITLE OF INVENTION: Sugar Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6399754aris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,202
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/471,973
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-135-202-33

Query Match          0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3391 CTCAAAAA 3405
DB 1 CGCAAAAAA 15

RESULT 377
US-08-802-331-29
; Sequence 29, Application US/08802331
; Patent No. 6451991
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D.
; APPLICANT: Monia, Brett
; APPLICANT: Martin, Pierre
; APPLICANT: Altman, Karl-Heinz
; TITLE OF INVENTION: Sugar-Modified Gapped Oligonucleotides
; FILE REFERENCE: ISNO0083
; CURRENT APPLICATION NUMBER: US/08/802,331
; CURRENT FILING DATE: 1997-02-11
; NUMBER OF SEQ ID NOS: 32
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6451991el Sequence
US-08-802-331-29

Query Match          0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3391 CTCAAAAAATAAAA 3405
Db 1 CGCAAAAAAATAAAA 15

RESULT 378
US-09-291-541-14/c
; Sequence 14, Application US/09291541
; Patent No. 6461864
; GENERAL INFORMATION:
; APPLICANT: Soriano, Philippe
; APPLICANT: Robertson, Elizabeth J.
; TITLE OF INVENTION: METHODS AND VECTOR CONSTRUCTS FOR MAKING TRANSGENIC
; TITLE OF INVENTION: NON-HUMAN ANIMALS WHICH UBIQUITOUSLY EXPRESS A
; TITLE OF INVENTION: HETEROLOGOUS GENE
; FILE REFERENCE: 14538A-44-1
; CURRENT APPLICATION NUMBER: US/09/291,541
; CURRENT FILING DATE: 1999-04-14
; EARLIER APPLICATION NUMBER: US 60/081,894
; EARLIER FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence. Primer for
; OTHER INFORMATION: detecting ROSA26 antisense region (R26alt2)
US-09-291-541-14

Query Match          0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2189 CCTAGACTGAAGTT 2203
Db 16 CCTAGACTGGAGT 2

RESULT 379
US-08-899-367-21
; Sequence 21, Application US/08899367
; Patent No. 6472170
; GENERAL INFORMATION:
; APPLICANT: Yang et al.
; TITLE OF INVENTION: BCL-X{SYMBOL 103 \f "Symbol"}, A NOVEL BCL-X
; TITLE OF INVENTION: ISOFORM, AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,367
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-899-367-21

Query Match          0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2828 TCTGTTCAATTTCTG 2842
Db 5 TCTGTTGATTTCTG 19

RESULT 380
US-09-389-283-33
; Sequence 33, Application US/09389283
; Patent No. 6531584
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; APPLICANT: A. Kawasaki
; TITLE OF INVENTION: 2'-Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6531584rls
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/389,283
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/035,357
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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US-09-389-283-33

Query Match 0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3391 CTCACAAAAA 3405
Db 1 CGCAAAAAA 15

RESULT 381

US-09-422-978-4334/c

; Sequence 4334, Application US/09422978

; Patent No. 6537751

; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel

; APPLICANT: Blumenfeld, Marta

; APPLICANT: Chumakov, Ilya

; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

; FILE REFERENCE: GENSET.020CP1

; CURRENT APPLICATION NUMBER: US/09/422,978

; CURRENT FILING DATE: 1999-10-20

; EARLIER APPLICATION NUMBER: US 09/298,850

; EARLIER FILING DATE: 1999-04-21

; EARLIER APPLICATION NUMBER: US 60/109,732

; EARLIER FILING DATE: 1998-11-23

; EARLIER APPLICATION NUMBER: US 60/082,614

; EARLIER FILING DATE: 1998-04-21

; NUMBER OF SEQ ID NOS: 11796

; SEQ ID NO 4334

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: primer_bind

; LOCATION: 1..19

; OTHER INFORMATION: upstream amplification primer 99-14662 for SEQ 400,

US-09-422-978-4334

Query Match 0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2524 AAATCTATGTTTTC 2538
Db 15 AAATCTATGTTTCTC 1

RESULT 382

US-09-422-978-7392/c

; Sequence 7392, Application US/09422978

; Patent No. 6537751

; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel

; APPLICANT: Blumenfeld, Marta

; APPLICANT: Chumakov, Ilya

; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

; FILE REFERENCE: GENSET.020CP1

; CURRENT APPLICATION NUMBER: US/09/422,978

; CURRENT FILING DATE: 1999-10-20

; EARLIER APPLICATION NUMBER: US 09/298,850

; EARLIER FILING DATE: 1999-04-21

; EARLIER APPLICATION NUMBER: US 60/109,732

; EARLIER FILING DATE: 1998-11-23

; EARLIER APPLICATION NUMBER: US 60/082,614

; EARLIER FILING DATE: 1998-04-21

; NUMBER OF SEQ ID NOS: 11796

; SEQ ID NO 7392

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-4225 for SEQ 3458,
US-09-422-978-7392

Query Match 0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 294 ATGCTGGGACAAAT 308
Db 17 ATGCTGGGACACAT 3

RESULT 383

US-09-614-614-10

; Sequence 10, Application US/09614614

; Patent No. 6544741

; GENERAL INFORMATION:

; APPLICANT: MUGASIMANGALAM, RAJA

; TITLE OF INVENTION: SEQUENCE SPECIFIC AND SEQUENCE NON-SPECIFIC METHODS AND

; FILE REFERENCE: cDNA NORMALIZATION AND SUBTRACTION

; CURRENT APPLICATION NUMBER: US/09/614,614

; CURRENT FILING DATE: 2000-07-12

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 10

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: misc.feature

; LOCATION: (1)..(19)

; OTHER INFORMATION: killer primer

US-09-614-614-10

Query Match 0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 546 TGAATGAATAATGG 560
Db 1 TGAATGAATAAAGG 15

RESULT 384

US-09-083-852A-7

; Sequence 7, Application US/09083852A

; Patent No. 6596930

; GENERAL INFORMATION:

; APPLICANT: MORRIS, CRAIG F.

; APPLICANT: GIROUX, MICHAEL J.

; TITLE OF INVENTION: MODIFICATION OF CEREAL GRAIN HARDNESS VIA EXPRESSION OF

; FILE REFERENCE: PUROINDOLINE PROTEINS

; CURRENT APPLICATION NUMBER: US/09/083,852A

; CURRENT FILING DATE: 1998-05-22

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Triticum aestivum

US-09-083-852A-7

Query Match 0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1707 ATGAAGGCCCTCTGC 1721
Db 1 ATGAAGGCCCTCTTC 15

RESULT 385
US-09-370-541-4
; Sequence 4, Application US/09370541
; Patent No. 6639062
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Nucleosidic Compounds And Oligomeric
; TITLE OF INVENTION: Compounds Prepared Therefrom
; FILE REFERENCE: ISIS3993
; CURRENT APPLICATION NUMBER: US/09/370,541
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: 09/130,973
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 09/016,520
; EARLIER FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; EARLIER FILING DATE: 1997-02-14
; EARLIER APPLICATION NUMBER: 09/344,260
; EARLIER FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: sequence
US-09-370-541-4

Query Match 0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3391 CTCAAAAA 3405
Db 1 CGCAAAAA 15

RESULT 386
US-09-989-706-14
; Sequence 14, Application US/09989706
; Patent No. 6653108
; GENERAL INFORMATION:
; APPLICANT: PARK, HAN-CH
; APPLICANT: JEON, JIN-TAE
; APPLICANT: JANG, MI-SOOK
; TITLE OF INVENTION: PROCESS FOR PREPARATION OF FULL-LENGTH CDNA AND ANCHOR
; TITLE OF INVENTION: USED FOR THE SAME
; FILE REFERENCE: 024018-0119
; CURRENT APPLICATION NUMBER: US/09/989,706
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: KR 10-2001-0022956
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-989-706-14

Query Match 0.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1140 CCACAGCTTGGAGC 1154
Db 1 CCACAGCTTGGAGC 15

Search completed: September 28, 2004, 08:37:24
Job time : 15 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 28, 2004, 08:39:18 ; Search time 9 Seconds
(without alignments)

3.431 Million cell updates/sec

Title: US-10-798-923A-4

Perfect score: 3405

Sequence: 1 cgcaccaaccagttcaag.....acacactcaaaaaaaaaa 3405

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 219 seqs, 4534 residues

Total number of hits satisfying chosen parameters: 438

Minimum DB seq length: 8

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 219 summaries

Database : rnpb4.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	1.8	60	1	US-09-308-975-8608
2	41	1.2	41	1	US-10-005-956-665
3	39.4	1.2	41	1	US-10-005-956-697
4	27	0.8	27	1	US-10-005-956-1231
5	26	0.8	26	1	US-10-005-956-1228
6	26	0.8	27	1	US-10-005-956-1219
7	24	0.7	24	1	US-10-005-956-1227
8	20.2	0.6	25	1	US-09-866-108-13747
9	20.2	0.6	25	1	US-10-723-361-13747
10	19.2	0.6	25	1	US-09-866-108-13746
11	19.2	0.6	25	1	US-09-866-108-13748
12	19.2	0.6	25	1	US-10-723-361-13746
13	19.2	0.6	25	1	US-10-723-361-13748
14	19	0.6	19	1	US-10-005-956-601
15	18.6	0.5	26	1	US-10-187-975-224
16	18.2	0.5	25	1	US-10-085-906-3
17	18.2	0.5	25	1	US-09-866-108-13745
18	18.2	0.5	25	1	US-09-866-108-13749
19	18.2	0.5	25	1	US-10-723-361-13749
20	18.2	0.5	25	1	US-10-005-956-1232
21	18	0.5	18	1	US-10-098-263B-2714
22	17.8	0.5	25	1	US-09-866-108-15237
23	17.6	0.5	25	1	US-09-866-108-15238
24	17.6	0.5	25	1	US-10-098-263B-2714
25	17.6	0.5	25	1	US-10-098-263B-2714
26	17.6	0.5	25	1	US-10-098-263B-2714
27	17.6	0.5	25	1	US-10-098-263B-2714
28	17.4	0.5	25	1	US-10-098-263B-2714
29	17.2	0.5	23	1	US-09-971-894-1
30	17.2	0.5	24	1	US-09-940-188-2386
31	16.8	0.5	22	1	US-10-162-497-14
32	16.8	0.5	22	1	US-10-629-313-14
33	16.4	0.5	20	1	US-10-092-208-34

1	US-10-126-355-28	20	0.5	16.4	Sequence 28, Appl
1	US-10-173-208-43	20	0.5	16.4	Sequence 43, Appl
1	US-10-173-208-74	20	0.5	16.4	Sequence 74, Appl
1	US-10-335-977-9818	22	0.5	16.4	Sequence 9818, Ap
1	US-10-455-470-10	21	0.5	16.2	Sequence 10, Appl
1	US-09-912-976-82	22	0.5	16.2	Sequence 82, Appl
1	US-10-116-993-24	22	0.5	16.2	Sequence 24, Appl
1	US-10-743-163-24	22	0.5	16.2	Sequence 24, Appl
1	US-10-449-741B-30	22	0.5	16.2	Sequence 30, Appl
1	US-10-349-143-4843	19	0.5	16	Sequence 4843, Ap
1	US-10-262-473-17	20	0.5	15.8	Sequence 17, Appl
1	US-09-978-385-11	20	0.5	15.8	Sequence 11, Appl
1	US-10-319-893-79	20	0.5	15.8	Sequence 79, Appl
1	US-09-216-393-193	22	0.5	15.8	Sequence 193, App
1	US-10-321-856-193	22	0.5	15.8	Sequence 193, App
1	US-10-321-039-468	22	0.5	15.8	Sequence 468, App
1	US-08-983-605-250	22	0.5	15.6	Sequence 250, App
1	US-09-938-689-47	22	0.5	15.6	Sequence 47, Appl
1	US-10-115-482-125	22	0.5	15.6	Sequence 125, App
1	US-10-182-230-12	22	0.5	15.6	Sequence 12, Appl
1	US-10-379-008-24	22	0.5	15.6	Sequence 24, Appl
1	US-09-780-533A-2672	17	0.5	15.4	Sequence 2672, Ap
1	US-09-780-533A-2673	17	0.5	15.4	Sequence 2673, Ap
1	US-09-930-423-294	17	0.5	15.4	Sequence 294, App
1	US-09-745-237A-294	17	0.5	15.4	Sequence 294, App
1	US-10-349-143-6432	18	0.5	15.4	Sequence 6432, Ap
1	US-09-752-983-245	20	0.5	15.4	Sequence 245, App
1	US-09-730-617-98	20	0.5	15.4	Sequence 98, Appl
1	US-10-005-344-245	20	0.5	15.4	Sequence 245, App
1	US-10-292-849-45	20	0.5	15.4	Sequence 45, Appl
1	US-10-304-111-43	20	0.5	15.4	Sequence 43, Appl
1	US-10-304-111-68	20	0.5	15.4	Sequence 68, Appl
1	US-09-969-373-2297	21	0.5	15.4	Sequence 2297, Ap
1	US-10-032-552-5294	22	0.5	15.4	Sequence 5294, Ap
1	US-09-918-686-60	22	0.4	15.2	Sequence 60, Appl
1	US-09-969-373-3418	20	0.4	15.2	Sequence 3418, Ap
1	US-09-828-344-150	20	0.4	15.2	Sequence 150, App
1	US-10-353-150-60	20	0.4	15.2	Sequence 60, Appl
1	US-10-177-573-20	20	0.4	15.2	Sequence 20, Appl
1	US-10-104-047-3957	20	0.4	15.2	Sequence 3957, Ap
1	US-10-349-143-6588	20	0.4	15.2	Sequence 6588, Ap
1	US-10-289-762-1301	20	0.4	15.2	Sequence 1301, Ap
1	US-10-289-762-3147	20	0.4	15.2	Sequence 3147, Ap
1	US-10-211-859-41	20	0.4	15.2	Sequence 41, Appl
1	US-10-211-859-72	20	0.4	15.2	Sequence 72, Appl
1	US-10-274-085-106	20	0.4	15.2	Sequence 106, App
1	US-10-628-109-134	20	0.4	15.2	Sequence 134, App
1	US-10-755-889-695	20	0.4	15.2	Sequence 695, App
1	US-10-731-739-371	20	0.4	15.2	Sequence 371, App
1	US-09-080-140-20	21	0.4	15.2	Sequence 20, Appl
1	US-10-399-091-11	21	0.4	15.2	Sequence 11, Appl
1	US-10-335-977-9991	21	0.4	15.2	Sequence 9991, Ap
1	US-10-349-143-6151	21	0.4	15.2	Sequence 6151, Ap
1	US-10-349-143-9328	21	0.4	15.2	Sequence 9328, Ap
1	US-10-349-143-10352	21	0.4	15.2	Sequence 10352, A
1	US-10-349-143-10665	21	0.4	15.2	Sequence 10665, A
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1	US-09-969-373-1896	18	0.4	15	Sequence 1896, Ap
1	US-10-600-816-32	19	0.4	15	Sequence 32, Appl
1	US-09-800-629A-116	20	0.4	15	Sequence 116, App
1	US-10-012-456A-24	20	0.4	15	Sequence 24, Appl
1	US-10-092-208-16	20	0.4	15	Sequence 16, Appl
1	US-10-679-532-116	20	0.4	15	Sequence 116, App
1	US-09-067-638B-26	18	0.4	14.8	Sequence 26, Appl
1	US-09-287-599-6	18	0.4	14.8	Sequence 6, Appli
1	US-09-933-638A-10	18	0.4	14.8	Sequence 10, Appl
1	US-09-961-077-545	18	0.4	14.8	Sequence 545, App
1	US-10-194-584-2	18	0.4	14.8	Sequence 2, Appli
1	US-10-211-296-1	18	0.4	14.8	Sequence 1, Appli
1	US-10-116-325-26	18	0.4	14.8	Sequence 26, Appl
1	US-10-169-771-45	18	0.4	14.8	Sequence 45, Appl
1	US-10-388-263-26	18	0.4	14.8	Sequence 26, Appl
1	US-10-108-260A-5168	18	0.4	14.8	Sequence 5168, Ap

107	14.8	0.4	18	1	US-10-108-260A-5396	Sequence 5396, App
108	14.8	0.4	19	1	US-09-985-637A-18	Sequence 18, Appl
109	14.8	0.4	19	1	US-10-467-721-43	Sequence 43, Appl
110	14.8	0.4	19	1	US-10-464-633-22	Sequence 22, Appl
111	14.8	0.4	19	1	US-10-251-117-97	Sequence 97, Appl
112	14.8	0.4	19	1	US-10-251-117-346	Sequence 346, App
113	14.8	0.4	19	1	US-10-741-339-18	Sequence 18, Appl
114	14.8	0.4	20	1	US-09-752-983-87	Sequence 87, Appl
115	14.8	0.4	20	1	US-09-752-639-33	Sequence 33, Appl
116	14.8	0.4	20	1	US-09-984-198-33	Sequence 33, Appl
117	14.8	0.4	20	1	US-09-791-243-15	Sequence 15, Appl
118	14.8	0.4	20	1	US-09-909-280A-4	Sequence 4, Appli
119	14.8	0.4	20	1	US-09-824-322B-500	Sequence 500, App
120	14.8	0.4	20	1	US-09-771-933-114	Sequence 114, App
121	14.8	0.4	20	1	US-09-784-674-602	Sequence 602, App
122	14.8	0.4	20	1	US-09-784-674-602	Sequence 602, App
123	14.8	0.4	20	1	US-09-784-674-603	Sequence 603, App
124	14.8	0.4	20	1	US-09-865-993-35	Sequence 35, Appl
125	14.8	0.4	20	1	US-09-953-047-59	Sequence 59, Appl
126	14.8	0.4	20	1	US-10-630-401-59	Sequence 59, Appl
127	14.8	0.4	20	1	US-10-618-540-1	Sequence 1, Appli
128	14.8	0.4	20	1	US-10-095-929-26	Sequence 26, Appl
129	14.8	0.4	20	1	US-10-045-621-17	Sequence 17, Appl
130	14.8	0.4	20	1	US-10-181-846-135	Sequence 135, App
131	14.8	0.4	20	1	US-10-035-485A-84	Sequence 84, Appl
132	14.8	0.4	20	1	US-10-003-319-47	Sequence 47, Appl
133	14.8	0.4	20	1	US-10-017-621-60	Sequence 60, Appl
134	14.8	0.4	20	1	US-10-180-781-69	Sequence 69, Appl
135	14.8	0.4	20	1	US-10-058-597-13	Sequence 13, Appl
136	14.8	0.4	20	1	US-10-005-344-87	Sequence 87, Appl
137	14.8	0.4	20	1	US-10-181-875-46	Sequence 46, Appl
138	14.8	0.4	20	1	US-10-189-256-70	Sequence 70, Appl
139	14.8	0.4	20	1	US-10-189-256-133	Sequence 133, App
140	14.8	0.4	20	1	US-10-289-762-4789	Sequence 4789, App
141	14.8	0.4	20	1	US-10-447-136-193	Sequence 193, App
142	14.8	0.4	20	1	US-10-150-811-132	Sequence 132, App
143	14.8	0.4	20	1	US-10-161-493-167	Sequence 167, App
144	14.8	0.4	20	1	US-10-210-230-18	Sequence 18, Appl
145	14.8	0.4	20	1	US-10-210-290-94	Sequence 94, Appl
146	14.8	0.4	20	1	US-10-210-802-18	Sequence 18, Appl
147	14.8	0.4	20	1	US-10-210-802-94	Sequence 94, Appl
148	14.8	0.4	20	1	US-10-304-107-60	Sequence 60, Appl
149	14.8	0.4	20	1	US-10-304-107-126	Sequence 126, App
150	14.8	0.4	20	1	US-10-317-270-86	Sequence 86, Appl
151	14.8	0.4	20	1	US-10-317-270-157	Sequence 157, App
152	14.8	0.4	20	1	US-10-745-377-21	Sequence 21, Appl
153	14.8	0.4	20	1	US-10-652-795-500	Sequence 500, App
154	14.8	0.4	20	1	US-10-647-918-500	Sequence 500, App
155	14.8	0.4	20	1	US-08-983-605-185	Sequence 185, App
156	14.8	0.4	21	1	US-08-983-605-297	Sequence 297, App
157	14.8	0.4	21	1	US-09-987-456-95	Sequence 95, Appl
158	14.8	0.4	21	1	US-09-818-991-49	Sequence 49, Appl
159	14.8	0.4	21	1	US-09-845-042-5	Sequence 5, Appli
160	14.8	0.4	21	1	US-09-997-213-10	Sequence 10, Appl
161	14.8	0.4	21	1	US-10-061-395-84	Sequence 84, Appl
162	14.8	0.4	21	1	US-10-052-942-127	Sequence 127, App
163	14.8	0.4	21	1	US-10-184-085A-124	Sequence 124, App
164	14.8	0.4	21	1	US-10-277-161-49	Sequence 49, Appl
165	14.8	0.4	21	1	US-10-405-877-112	Sequence 112, App
166	14.8	0.4	21	1	US-10-349-143-10297	Sequence 10297, A
167	14.8	0.4	21	1	US-10-294-228-56	Sequence 56, Appl
168	14.8	0.4	21	1	US-10-294-228-57	Sequence 57, Appl
169	14.8	0.4	21	1	US-10-287-226-556	Sequence 536, App
170	14.8	0.4	21	1	US-10-600-816-45	Sequence 45, Appl
171	14.4	0.4	16	1	US-09-829-855-76	Sequence 76, Appl
172	14.4	0.4	16	1	US-10-607-077A-76	Sequence 76, Appl
173	14.4	0.4	17	1	US-09-780-533A-2674	Sequence 2674, Ap
174	14.4	0.4	17	1	US-09-848-754A-40	Sequence 40, Appl
175	14.4	0.4	17	1	US-09-848-754A-3125	Sequence 3125, Ap
176	14.4	0.4	17	1	US-09-930-423-295	Sequence 295, App
177	14.4	0.4	17	1	US-09-745-237A-295	Sequence 295, App
178	14.4	0.4	17	1	US-10-339-782-462	Sequence 462, App
179	14.4	0.4	17	1	US-10-339-793-135	Sequence 135, App

c 180	14.4	0.4	17	1	US-10-339-793-332	Sequence 332, App
c 181	14.4	0.4	17	1	US-10-138-674-4306	Sequence 4306, Ap
c 182	14.4	0.4	17	1	US-10-287-949A-4306	Sequence 4306, Ap
c 183	14.4	0.4	18	1	US-09-925-548-17	Sequence 17, Appl
c 184	14.4	0.4	18	1	US-09-969-373-2519	Sequence 2519, Ap
c 185	14.4	0.4	18	1	US-10-321-589-2	Sequence 2, Appli
c 186	14.4	0.4	18	1	US-10-321-589-4	Sequence 4, Appli
c 187	14.4	0.4	18	1	US-10-349-143-5818	Sequence 5818, Ap
c 188	14.4	0.4	19	1	US-10-128-560-86	Sequence 86, Appl
c 189	14.4	0.4	19	1	US-10-128-560-186	Sequence 186, App
c 190	14.4	0.4	19	1	US-10-251-117-573	Sequence 573, App
c 191	14.4	0.4	19	1	US-10-251-117-880	Sequence 880, App
c 192	14.4	0.4	19	1	US-10-240-689-30	Sequence 30, Appl
c 193	14.4	0.4	19	1	US-10-349-143-8906	Sequence 8906, Ap
c 194	14.4	0.4	20	1	US-09-754-167-65	Sequence 65, Appl
c 195	14.4	0.4	20	1	US-09-912-724-49	Sequence 49, Appl
c 196	14.4	0.4	20	1	US-09-920-033-106	Sequence 106, App
c 197	14.4	0.4	20	1	US-10-282-174-132	Sequence 132, App
c 198	14.4	0.4	20	1	US-10-238-443-41	Sequence 41, Appl
c 199	14.4	0.4	20	1	US-10-309-362-41	Sequence 41, Appl
c 200	14.4	0.4	20	1	US-10-012-984-66	Sequence 66, Appl
c 201	14.4	0.4	20	1	US-10-388-281-26	Sequence 26, Appl
c 202	14.4	0.4	20	1	US-10-126-355-109	Sequence 109, App
c 203	14.4	0.4	20	1	US-10-147-196-106	Sequence 106, App
c 204	14.4	0.4	20	1	US-10-380-931-119	Sequence 119, App
c 205	14.4	0.4	20	1	US-10-388-263-642	Sequence 642, App
c 206	14.4	0.4	20	1	US-10-174-559-73	Sequence 73, Appl
c 207	14.4	0.4	20	1	US-10-174-014-24	Sequence 24, Appl
c 208	14.4	0.4	20	1	US-10-174-014-56	Sequence 56, Appl
c 209	14.4	0.4	20	1	US-10-349-143-7273	Sequence 7273, Ap
c 210	14.4	0.4	20	1	US-10-188-883-38	Sequence 38, Appl
c 211	14.4	0.4	20	1	US-10-289-762-2103	Sequence 2103, Ap
c 212	14.4	0.4	20	1	US-10-131-827-9057	Sequence 9057, Ap
c 213	14.4	0.4	20	1	US-10-120-429-23	Sequence 23, Appl
c 214	14.4	0.4	20	1	US-10-363-828-59	Sequence 59, Appl
c 215	14.4	0.4	20	1	US-10-302-027-80	Sequence 80, Appl
c 216	14.4	0.4	20	1	US-10-673-523-66	Sequence 66, Appl
c 217	14.4	0.4	20	1	US-10-182-644A-2	Sequence 2, Appli
c 218	14.4	0.4	20	1	US-10-316-540-87	Sequence 87, Appl
c 219	14.4	0.4	20	1	US-10-316-540-153	Sequence 153, App

ALIGNMENTS

RESULT 1
US-09-908-975-8608
; Sequence 8608, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 8608
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-8608
Query Match 1.8%; Score 60; DB 1; Length 60;

Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1295 GAAGGATTCATGAAGCTGTGGGAAATCATGTCTTCTGCAGCCACACCTAAGCAT 1354
DB 1 GAAGGATTCATGAAGCTGTGGGAAATCATGTCTTCTGCAGCCACACCTAAGCAT 60

RESULT 2

US-10-005-956-665/c
; Sequence 665, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 665
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-005-956-665

Query Match 1.2%; Score 41; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 TTGTGACATGCACCTAAATAATGTCTGATATCATTCCTAG 2193
DB 41 TTGTGACATGCACCTAAATAATGTCTGATATCATTCCTAG 1

RESULT 3

US-10-005-956-697/c
; Sequence 697, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 697
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-005-956-697

Query Match 1.2%; Score 39.4; DB 1; Length 41;
Best Local Similarity 97.6%; Pred. No. 0.038;
Matches 40; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 41 TTGTGACATGCACCTAAATAATGTCTGATATCATTCCTAG 1

RESULT 4

US-10-005-956-1231
; Sequence 1231, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1231
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-005-956-1231

Query Match 0.8%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2125 TTTGAACCAAGAATCTCCTTTAATT 2151
DB 1 TTTGAACCAAGAATCTCCTTTAATT 27

RESULT 5

US-10-005-956-1228
; Sequence 1228, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1228
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-005-956-1228

Query Match 0.8%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 TCGAAAAGTTTGTAAACCCAGATAATC 515
DB 1 TCGAAAAGTTTGTAAACCCAGATAATC 26

RESULT 6

US-10-005-956-1319/c
; Sequence 1319, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company

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; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1319
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: wherein "n" equals a C3 phosphoramidite linker.
US-10-005-956-1319

Query Match      0.8%; Score 26; DB 1; Length 27;
Best Local Similarity 96.3%; Pred. No. 2.9;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2174 GTGCTCATATCATCTCTAGAACTGAA 2200
Db 27 GTGCTCATATNATTCCTAGAACTGAA 1

RESULT 7
US-10-005-956-1227
; Sequence 1227, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1227
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-005-956-1227

Query Match      0.7%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1885 GCTGAAGACCAAGCAAGAAATTC 1908
Db 1 GCTGAAGACCAAGCAAGAAATTC 24

RESULT 8
US-09-866-108-13747/c
; Sequence 13747, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
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; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 13747
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-13747

Query Match      0.6%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 20;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2213 ATCAGGATGTCCTCGAGCGGTATCA 2237
Db 25 ATCAGGCTGTCCGAGCGGATCA 1

RESULT 9
US-10-723-361-13747/c
; Sequence 13747, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
```

; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 13747
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-13747

Query Match 0.6%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 20;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2213 ATCAGGATGTCGCCGAGCGGTATCA 2237
|||||
DB 25 ATCAGGCTGTCCCGAGCGGTATCA 1

RESULT 10

US-09-866-108-13746/c
; Sequence 13746, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 13746
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-13746

Query Match 0.6%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2214 TCAGGATGTCGCCGAGCGGTATCA 2237
|||||
DB 25 TCAGGCTGTCCCGAGCGGTATCA 2

RESULT 11

US-09-866-108-13748/c
; Sequence 13748, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine

; SEQ ID NO 13748
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-13748

Query Match 0.6%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2213 ATCAGGATGTCCTCCGAGCGGTATC 2236
||||| ||||| ||||| ||||| |||||
Db 24 ATCAGGCTGTCCCGAAGCCGGATC 1

RESULT 12

US-10-723-361-13746/c
; Sequence 13746, Application US/10723361
; Publication No. US20040137589A1

GENERAL INFORMATION:

; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN

; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine

; SEQ ID NO 13746
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-723-361-13746

Query Match 0.6%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2214 TCAGGATGTCCTCCGAGCGGTATCA 2237
||||| ||||| ||||| ||||| |||||
Db 25 TCAGGCTGTCCCGAAGCCGGATCA 2

RESULT 13

US-10-723-361-13748/c
; Sequence 13748, Application US/10723361
; Publication No. US20040137589A1

GENERAL INFORMATION:

; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN

; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine

; SEQ ID NO 13748
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-723-361-13748

Query Match 0.6%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2213 ATCAGGATGTCCTCCGAGCGGTATC 2236
||||| ||||| ||||| ||||| |||||
Db 24 ATCAGGCTGTCCCGAAGCCGGATC 1

RESULT 14

US-10-005-956-601/c
; Sequence 601, Application US/10005956
; Publication No. US20030113726A1

GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 601
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-005-956-601


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Query Match      0.6%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2164 ACCTAAAATGTCTGAT 2182
Db 19 ACCTAAAATGTCTGAT 1

RESULT 15
US-10-187-975-224/c
; Sequence 224, Application US/10187975
; Publication No. US20030224982A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Shenoy, Suresh
; APPLICANT: Patturajan, Meera
; APPLICANT: Ellerman, Karen
; APPLICANT: Gorman, Linda
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Spytek, Kimberly
; APPLICANT: Miller, Charles
; APPLICANT: Edinger, Shalomit
; APPLICANT: Hjalt, Tord
; APPLICANT: Gerlach, Valerie
; APPLICANT: Shinkets, Richard
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Anderson, David
; APPLICANT: Guo, Xiaojia
; APPLICANT: Baumgartner, Jason
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glennda
; APPLICANT: Casman, Stacie
; APPLICANT: Voss, Edward
; APPLICANT: Boldog, Ferenc
; APPLICANT: Pena, Carol
; APPLICANT: Chapoval, Andrei
; APPLICANT: Rastelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Vernte, Corine
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING
; FILE REFERENCE: 21402-397A
; CURRENT APPLICATION NUMBER: US/10/187,975
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 60/303,046
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/303,828
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/304,502
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/305,011
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/305,262
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/305,673
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/306,085
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 60/307,536
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/308,228
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/308,877
; PRIOR FILING DATE: 2001-07-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 288
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 224
; LENGTH: 26

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-10-187-975-224

Query Match      0.6%; Score 18.8; DB 1; Length 26;
Best Local Similarity 90.9%; Pred. No. 34;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1305 ATGAAGCTGTGGGAAATCAT 1326
Db 26 ATGAAGCTGTGGGACATCAT 5

RESULT 16
US-10-085-906-3/c
; Sequence 3, Application US/10085906
; Publication No. US20030054371A1
; GENERAL INFORMATION:
; APPLICANT: Ying, Vincent
; APPLICANT: Wu, Paul
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
; FILE REFERENCE: GNN-5343CP2
; CURRENT APPLICATION NUMBER: US/10/085,906
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/126,215
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 09/534,061
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: PCT/US00/07938
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 545
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-906-3

Query Match      0.5%; Score 18.6; DB 1; Length 26;
Best Local Similarity 84.0%; Pred. No. 36;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1389 AAGAAGACAATGAAACAGAAATAAA 1413
Db 25 AAGAAGAAAAGGAAAAGAAAAA 1

RESULT 17
US-09-866-108-13745/c
; Sequence 13745, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
```

; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 13745
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-13745

Query Match 0.5%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2215 CAGGATGTCGCGAGCGCGATCA 2237
||||| ||||||| ||||||| |||||
Db 25 CAGGCTGTCCGAGCGCGATCA 3

RESULT 18
US-09-866-108-13749/c
; Sequence 13749, Application US/09866108
; Patent No. US2002048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEMONICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 13745
; LENGTH: 25
; TYPE: DNA

; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 13749
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-13749

Query Match 0.5%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2213 ATCAGGATGTCGCGAGCGCGAT 2235
||||| ||||||| ||||||| |||||
Db 23 ATCAGGCTGTCCGAGCGCGAT 1

RESULT 19
US-10-723-361-13745/c
; Sequence 13745, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 13745
; LENGTH: 25
; TYPE: DNA

```
; ORGANISM: Homo sapiens
US-10-723-361-13745

Query Match          0.5%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2215 CAGGATGTCGGGAGCGGTATCA 2237
      ||||| ||||| ||||| ||||| |||||
Db 25 CAGGCTGTCCGAGCGCGGTATCA 3

RESULT 20
US-10-723-361-13749/c
; Sequence 13749, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 13749
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-13749

Query Match          0.5%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2213 ATCAGGATGTCGGGAGCGGTAT 2235
      ||||| ||||| ||||| ||||| |||||
Db 23 ATCAGGCTGTCCGAGCGGTAT 1

RESULT 21
US-10-005-956-1232
; Sequence 1232, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS

; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1232
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-005-956-1232

Query Match          0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 884 TGCCTCCCTGCTCATTTG 901
      ||||| ||||| ||||| |||||
Db 1 TGCCTCCCTGCTCATTTG 18

RESULT 22
US-10-098-263B-2714/c
; Sequence 2714, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 2714
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-2714

Query Match          0.5%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 45;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2018 GAAATGTACTGTTCGATCA 2038
      ||||| ||||| ||||| ||||| |||||
Db 25 GAAATGTTTCTGTTCGATCA 5

RESULT 23
US-09-866-108-15237/c
; Sequence 15237, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
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; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 15237
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-15237

Query Match 0.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 49;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 391 GCTCGAGGCTCTTCAGCAAAATGG 414
||| ||||| ||||| ||||| |||||
Db 25 GCTCGGGCTCTTCTTCAAAATGG 2

RESULT 24
US-09-866-108-15238/c
; Sequence 15238, Application US/09866108
; Patent No. US2002048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 15238
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-15238

Query Match 0.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 49;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 391 GCTCGAGGCTCTTCAGCAAAATGG 414
||| ||||| ||||| ||||| |||||
Db 24 GCTCGGGCTCTTCTTCAAAATGG 1

RESULT 25
US-10-098-263B-122061/c
; Sequence 122061, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 122061
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-122061

Query Match 0.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 49;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 531 TACTTGAACACAGGTTTGATGAAA 554
||||| ||||| ||||| ||||| |||||
Db 24 TACTTGAACCTGTTTACTTTAAA 1

RESULT 26
US-10-723-361-15237/c
; Sequence 15237, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 15237
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-15237

Query Match 0.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 49;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 391 GCTGCAGGCTCTTCACAAATGG 414
||| ||||| ||||| |||||
Db 25 GCTCGGGCTCTTCTTCAAAATGG 2

RESULT 27
US-10-723-361-15238/c
; Sequence 15238, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 15238
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-15238

Query Match 0.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 49;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 391 GCTGCAGGCTCTTCACAAATGG 414
||| ||||| ||||| |||||
Db 24 GCTCGGGCTCTTCTTCAAAATGG 1

RESULT 28
US-10-005-956-633/c
; Sequence 633, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 633
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-005-956-633

Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 43;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2164 ACCTAAAAATGTCTGAT 2182
||| ||||| ||||| |||||
Db 19 ACCTAAAAACGTCTGAT 1

RESULT 29
US-09-971-894-1
; Sequence 1, Application US/09971894
; Publication No. US20030044804A1
; GENERAL INFORMATION:
; APPLICANT: Kashi, Yechezkel
; APPLICANT: Gur-Arie, Riva
; APPLICANT: Cohen, Cyril
; APPLICANT: Bitan, Yuval
; APPLICANT: Shelef, Leora
; APPLICANT: Hallerman, Eric
; TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND HYPERPOLYMORPHIC SIMPLE SEQUENCE R
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR PROKARYOTE CLASSIFICAT
; FILE REFERENCE: 01/22569

```
; CURRENT APPLICATION NUMBER: US/09/971,894
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/472,035
; PRIOR FILING DATE: 1999-12-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-971-894-1

Query Match          0.5%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2751 GATTTTGTATTAGAGTATATTA 2772
Db 1 GATTTTGCATATGAGTATATTA 22

RESULT 30
US-09-940-185-2386/c
; Sequence 2386, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2386
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-2386

Query Match          0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 54;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1100 CTACGGACCCAGGAATGTTTC 1121
Db 23 CTGAGGGACCCAGGAGATGTTTC 2

RESULT 31
US-10-162-497-14/c
; Sequence 14, Application US/10162497
; Publication No. US20030158398A1
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/10/162,497
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US/09/657,474
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 09/268,992
; PRIOR FILING DATE: 1999-03-16
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; PRIOR APPLICATION NUMBER: 09/236,134
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/106,056
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/088,312
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/078,044
; PRIOR FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-162-497-14

Query Match          0.5%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3356 CAAAGCAGACACTCAATAAA 3375
Db 22 CACAGCAGACACACAATAAA 3

RESULT 32
US-10-629-313-14/c
; Sequence 14, Application US/10629313
; Publication No. US20040176572A1
; GENERAL INFORMATION:
; APPLICANT: Nelson B. Freimer
; APPLICANT: Victor I. Reus
; APPLICANT: Susan K. Service
; APPLICANT: Lynne Alison McInnes
; APPLICANT: Pedro Leon
; APPLICANT: Lodewijk Sandkuijl
; TITLE OF INVENTION: Method and Compositions for Diagnosing and Treating Chromosome-1
; TITLE OF INVENTION: Related Disorders
; FILE REFERENCE: UCAL-154CIPS
; CURRENT APPLICATION NUMBER: US/10/629,313
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 09/722,544
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/631,275
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 09/268,992
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/236,134
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/078,044
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: 60/088,312
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/106,056
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-629-313-14

Query Match          0.5%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3356 CAAAGCAGACACTCAATAAA 3375
```

Db 22 CACAGCAGACACACAATAAA 3

```

RESULT 33
US-10-092-208-34
; Sequence 34, Application US/10092208
; Publication No. US20030170637A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Hyunsoo
; APPLICANT: Pirrung, Michael C.
; TITLE OF INVENTION: METHOD OF ANALYZING m
; TITLE OF INVENTION: (APEX)
; FILE REFERENCE: 5405-274
; CURRENT APPLICATION NUMBER: US/10/092,208
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleo
US-10-092-208-34

```

Query Match 0.5%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 62;
Matches 17; Conservative 0; Mismatches 1; Indels

QY 1928 GACTGGAGTCCATATGCA 1945
|||
Db 3 GACTGGAGTCCATATCCA 20

```
RESULT 34
US-10-126-355-28/c
; Sequence 28, Application US/10126355
; Publication No. US20030198965A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATORS
; FILE REFERENCE: 11-BETA DEHYDRO-11-OXO-2-NALANOL-3-PHOSPHATE
; CURRENT APPLICATION NUMBER: US/10/126-355-28
; CURRENT FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 1.0
; SEQ ID NO 28
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-126-355-28
```

Query Match 0.5%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 62;
Matches 17; Conservative 0; Mismatches 1; Indels

QY 1738 AAACCTCTACAGAAGCTGG 1755
Db 20 AAACCTCTACAGAAGCTGG 3

RESULT 35
US-10-173-208-43
; Sequence 43, Application US/10173208
; Publication No. US2003023435A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTIGENSE MODULA
; FILE REFERENCE: HTS-0023

```

; CURRENT APPLICATION NUMBER: US/10/173,208
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-173-208-43

```

```
Query Match          0.5%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 62;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 1326 TGTCACTTCTGCAGCCA 1343
|||
Db 1 TGTCACTTCTTCAGCCA 18

```

RESULT 36
US-10-173-208-74/c
; Sequence 74, Application US/10173208
; Publication No. US20030232435A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF AMYLOID BETA PROTEIN PRECURSOR EXPRESSION
; FILE REFERENCE: HTS-0023
; CURRENT APPLICATION NUMBER: US/10/173,208
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 74
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-10-173-208-74

```

```
Query Match          0.5%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 62;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 1326 TGTCACCTTCTGCAGCCA 1343
Db 20 TGTCACCTTCTGCAGCCA 3

RESULT 37
US-10-335-977-9818
; Sequence 9818, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
;

DIAGNOSIS AND THE
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 9818:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...22
SEQUENCE DESCRIPTION: SEQ ID NO: 9818:
US-10-335-977-9818

Query Match 0.5%; Score 16.4; DB 1; Length 22;
Best Local Similarity 94.4%; Pred. No. 66;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 672 TGGCAAGAGCAAAATCAAT 689
Db 1 TGGAAAGAGCAAAATCAIT 18
|||||

RESULT 38

US-10-455-470-10/c
Sequence 10, Application US/10455470
Publication No. US20040170613A1
GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
APPLICANT: Hillan, Kenneth J.
APPLICANT: Le Couter, Jennifer
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR LIVER GROWTH AND LIVER PROTECTION
FILE REFERENCE: P1849PLUS
CURRENT APPLICATION NUMBER: US/10/455,470
CURRENT FILING DATE: 2003-06-05
PRIOR APPLICATION NUMBER: US 60/386,637
PRIOR FILING DATE: 2002-06-05
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 10
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
FEATURE:
NAME/KEY: PCR primer
LOCATION: Full
OTHER INFORMATION: IL-6 forward
US-10-455-470-10

Query Match 0.5%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 68;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1808 GCATTGGAAAATGTTGTAGGA 1828
Db 21 GCATTGGAAAATGGGGTAGGA 1
|||||

RESULT 39

US-09-912-976-82/c

Sequence 82, Application US/09912976
Publication No. US20030212255A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Mezes, Peter
APPLICANT: Burgess, Catherine
APPLICANT: Casman, Stacie
APPLICANT: Grosse, William M
APPLICANT: Alsobrook II, John P
APPLICANT: Lepley, Denise M
APPLICANT: Gerlach, Valerie L
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
APPLICANT: Mishra, Vishnu
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-070
CURRENT APPLICATION NUMBER: US/09/912,976
CURRENT FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/221,336
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/238,333
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/260,675
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: 60/271,025
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 60/278,164
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/280,876
PRIOR FILING DATE: 2001-04-02
NUMBER OF SEQ ID NOS: 99
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 82
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Agl269 PCR
OTHER INFORMATION: Primer Sequences
US-09-912-976-82

Query Match 0.5%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2637 CAGAAAATAATTTGTCACAG 2657
Db 22 CAGAAAATAATTTGTCACAG 2
|||||

RESULT 40

US-10-116-993-24
Sequence 24, Application US/10116993
Publication No. US2003004947A1
GENERAL INFORMATION:
APPLICANT: The Board of Regents of the University of Nebraska
TITLE OF INVENTION: ALCOHOL OXIDASE 1 REGULATORY NUCLEOTIDE SEQUENCES FOR HETEROLOGOUS
TITLE OF INVENTION: EXPRESSION IN YEAST
FILE REFERENCE: UNL 3071.1
CURRENT APPLICATION NUMBER: US/10/116,993
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US 60/281,861
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(22)
OTHER INFORMATION: Primer

US-10-116-993-24

Query Match 0.5%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1054 TGTGGTCTTCCTAATATGAC 1074
| | | | | | | | | | | | | | | | | | | | | |
Db 2 TCTTGGAAATTCCTAATATGAC 22

RESULT 41

US-10-743-163-24
; Sequence 24, Application US/10743163
; Publication No. US20040137591A1
; GENERAL INFORMATION:
; APPLICANT: The Board of Regents of the University of Nebraska
; TITLE OF INVENTION: ALCOHOL OXIDASE 1 REGULATORY NUCLEOTIDE SEQUENCES FOR
; TITLE OF INVENTION: HETEROLOGOUS GENE EXPRESSION IN YEAST
; FILE REFERENCE: UNL 3071.1
; CURRENT APPLICATION NUMBER: US/10/743,163
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(22)
; OTHER INFORMATION: Primer
US-10-743-163-24

Query Match 0.5%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1054 TGTGGTCTTCCTAATATGAC 1074
| | | | | | | | | | | | | | | | | | | | | |
Db 2 TCTTGGAAATTCCTAATATGAC 22

RESULT 42

US-10-449-741B-30/c
; Sequence 30, Application US/10449741B
; Publication No. US20040142387A1
; GENERAL INFORMATION:
; APPLICANT: LERNMARK, Ake
; APPLICANT: LUO, Dong
; APPLICANT: MACMURRAY, Armand
; APPLICANT: ETTINGER, Ruth
; APPLICANT: MORALEJO, Daniel
; APPLICANT: RUTLEDGE, Elizabeth A.
; TITLE OF INVENTION: MUTANTS OF GAD65 AND IANS RELATING TO DIABETES
; FILE REFERENCE: 16336-19
; CURRENT APPLICATION NUMBER: US/10/449,741B
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: US 60/383,913
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-449-741B-30

Query Match 0.5%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 490 TGGAAAAGTTTGTAAACCCAGA 510
| | | | | | | | | | | | | | | | | | | | | |
Db 22 TGGAGAGTTTGTACCCACA 2

RESULT 43

US-10-349-143-4843/c
; Sequence 4843, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4843
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-1814 for SEQ 909,
US-10-349-143-4843

Query Match 0.5%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 TTTCGTCTCTGGATT 2724
| | | | | | | | | | | | | | | | | | | | | |
Db 17 TTTCGTCTCTGGATT 2

RESULT 44

US-10-262-473-17/c
; Sequence 17, Application US/10262473
; Publication No. US20030199442A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John,
; APPLICANT: Burgess, Catherine,
; APPLICANT: Gorman, Linda,
; APPLICANT: Guo, Xiaojia,
; APPLICANT: Lepley, Denise,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rastelli, Luca,
; APPLICANT: Reiger, Daniel,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-462B
; CURRENT APPLICATION NUMBER: US/10/262,473
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/349,575
; PRIOR FILING DATE: 2001-10-29

```
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Curasequest version 0.1
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-10-262-473-17

Query Match          0.5%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3144 TCCAAGTGCTGTGATC 3159
Db 20 TCCAAGTGCTGTGATC 5

RESULT 45
US-09-978-385-11/c
; Sequence 11, Application US/09978385
; Patent No. US20020177211A1
; GENERAL INFORMATION:
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Petrie, Charles
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: ZACE2: A HUMAN METALLOENZYME
; FILE REFERENCE: 99-24C1
; CURRENT APPLICATION NUMBER: US/09/978,385
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/133,952
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/151,181
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 09/563,516
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer.
US-09-978-385-11

Query Match          0.5%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 75;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 876 CAATTGGATGCTCCTCTC 894
Db 20 CCACTGGATGCTCCTCTC 2

RESULT 46
US-10-319-893-79
; Sequence 79, Application US/10319893
; Publication No. US20040115649A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF ABCS5 EXPRESSION
; FILE REFERENCE: RTS-0419
; CURRENT APPLICATION NUMBER: US/10/319,893
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 157
; SEQ ID NO 79
; LENGTH: 20
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-319-893-79

Query Match          0.5%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 75;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 363 AAATTCAGATCTCAGT 381
Db 1 AAATTCAGATCTTACAGT 19

RESULT 47
US-09-216-393-193/c
; Sequence 193, Application US/09216393
; Patent No. US20010014447A1
; GENERAL INFORMATION:
; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND
; FILE REFERENCE: TX-1-C2
; CURRENT APPLICATION NUMBER: US/09/216,393
; CURRENT FILING DATE: 1998-12-18
; EARLIER APPLICATION NUMBER: 08/994,825
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 193
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-216-393-193

Query Match          0.5%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3132 TGCTTTTTCACCTCCAAAGG 3150
Db 21 TGCITTCGCACTTCCAAAGG 3

RESULT 48
US-10-321-856-193/c
; Sequence 193, Application US/10321856
; Publication No. US20030194393A1
; GENERAL INFORMATION:
; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THERE
; FILE REFERENCE: TX-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/321,856
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/216,393
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,825
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 193
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-10-321-856-193

Query Match          0.5%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 80;
```

```
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3132 TGTCTTTTCCACTTCCCAAGG 3150
Db 21 TGTCTTCTGCATCTTCCCAAGG 3

RESULT 49
US-10-321-039-468
; Sequence 468, Application US/10321039
; Publication No. US20040014067A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lukowiak, Andrew
; APPLICANT: Jarvis, Nancy
; APPLICANT: Kurensky, David
; TITLE OF INVENTION: Amplification Methods and Compositions
; FILE REFERENCE: FORS-06960
; CURRENT APPLICATION NUMBER: US/10/321,039
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/998,157
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/329,113
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/360,489
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 759
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 468
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-321-039-468

Query Match 0.5%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1130 GTCTGCATCCACAGCTT 1148
Db 1 GTCTGCCTTCTCACAGCTT 19

RESULT 50
US-08-983-605-250/c
; Sequence 250, Application US/08983605A
; Publication No. US20020066118A1
; GENERAL INFORMATION:
; APPLICANT: Roder, Marion
; TITLE OF INVENTION: Microsatellite Markers for Plants of the Species
; TITLE OF INVENTION: Triticum aestivum and Tribe Triticeae and the Use of
; TITLE OF INVENTION: Said Markers
; FILE REFERENCE: 2936.10400
; CURRENT APPLICATION NUMBER: US/08/983,605A
; CURRENT FILING DATE: 1998-05-01
; EARLIER APPLICATION NUMBER: DE 195 25 284.5
; EARLIER FILING DATE: 1995-06-28
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 250
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-08-983-605-250

Query Match 0.5%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 85;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3369 CAATAATGCTAGATTACACA 3390
|| ||||||||| |||||
```

```
Db 22 CAGAAATGCTAGACTTACGCA 1

RESULT 51
US-09-938-689-47/c
; Sequence 47, Application US/09938689
; Publication No. US20030028911A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Manley
; APPLICANT: Harding, Fiona
; TITLE OF INVENTION: TRANSGENIC MAMMAL CAPABLE OF FACILITATING PRODUCTION OF
; TITLE OF INVENTION: DONOR-SPECIFIC FUNCTIONAL IMMUNITY
; FILE REFERENCE: 9342-028
; CURRENT APPLICATION NUMBER: US/09/938,689
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/651,361
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,688
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-09-938-689-47

Query Match 0.5%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 85;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 391 GCTGCAGGCTCTTCAGCAAAAT 412
|| ||||||||| |||||
Db 22 GCAGCAGGCTCTGCAGCCACAT 1

RESULT 52
US-10-115-482-125/c
; Sequence 125, Application US/10115482
; Publication No. US20030212257A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, et al.
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM
; TITLE OF INVENTION: AND METHODS
; TITLE OF INVENTION: OF USING THE SAME
; FILE REFERENCE: 21404-322D
; CURRENT APPLICATION NUMBER: US/10/115,482
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/281,086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: 60/285,890
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 60/286,068
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/286,292
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/287,213
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 60/288,257
```

; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/291,134
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/282,020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/291,725
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/294,771
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/296,965
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/299,128
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 149
; SEQ ID NO 125
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-10-115-482-125

Query Match 0.5%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 85;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2428 AAGTGGAGAAATCCTTATGCC 2449
||| ||||| ||||| ||||| |||||
Db 22 AAAGGAGAAATCCTTGTGCC 1

RESULT 53
US-10-182-230-12/c
; Sequence 12, Application US/10182230
; Publication No. US20030215817A1
; GENERAL INFORMATION:
; APPLICANT: Leonardi, Amedeo
; APPLICANT: Sartani, Abraham
; APPLICANT: Glass, James R.
; APPLICANT: Sutcliffe, J. Gregor
; APPLICANT: Hasel, Karl W.
; TITLE OF INVENTION: Modulation of Gene Expression in Formation of Fatty Atherosclerosis
; TITLE OF INVENTION: Lesions
; FILE REFERENCE: 216019-143
; CURRENT APPLICATION NUMBER: US/10/182,230
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 60/177,963
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Oryctolagus cuniculus
US-10-182-230-12

Query Match 0.5%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 85;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2094 TTTTGGGGAGGAGATGTGCG 2115
||||| ||||| ||||| ||||| |||||
Db 22 TTTTGGGGAGGAGCTGACCG 1

RESULT 54
US-10-379-008-24
; Sequence 24, Application US/10379008
; Publication No. US20040018511A1
; GENERAL INFORMATION:
; APPLICANT: Cai, Li
; APPLICANT: Taylor, Jerry
; APPLICANT: Smyth, Kerrie-Ann

; APPLICANT: Findeisen, Brian
; APPLICANT: Lehn, Cathi
; APPLICANT: Davis, Scott
; APPLICANT: Davis, Sara
; TITLE OF INVENTION: Quantitative Trait Loci and Somatostatin
; FILE REFERENCE: TAMK:262 12740.0262.NPUS01
; CURRENT APPLICATION NUMBER: US/10/379,008
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,589
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Bovine SST primer
US-10-379-008-24

Query Match 0.5%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 85;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 160 CACCATGTGAGGACAGGCCAAG 181
||||| ||||| ||||| ||||| |||||
Db 1 CCCATGCGAGGAACTGGCCAAG 22

RESULT 55
US-09-780-533A-2672
; Sequence 2672, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2672
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2672

Query Match 0.5%; Score 15.4; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 77;
Matches 10; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1491 TCITTAAGGGGAATT 1507
:||||| ||||| ||||| :||
Db 1 UCUUUAAGGGGAU 17

RESULT 56
US-09-780-533A-2673
; Sequence 2673, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene

FILE REFERENCE: MBH00.878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2673
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-780-533A-2673

Query Match 0.5%; Score 15.4; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 77;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1492 CTTTAAAGGGGAATTC 1508
|:::|||||||:::
DB 1 CUUUAAGGGGAUAUUC 17

RESULT 57
US-09-930-423-294/c
Sequence 294, Application US/09930423
Publication No. US20030092003A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: MBH00.918-A 400/027
CURRENT APPLICATION NUMBER: US/09/930,423
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 4553
SOFTWARE: PatentIn version 3.0
SEQ ID NO 294
LENGTH: 17
TYPE: RNA
ORGANISM: Homo Sapiens
US-09-930-423-294

Query Match 0.5%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 149 GCTGCTCAGTCACCAT 165
|:::|||||||:::
DB 17 GCTGCTCAGGCACCAT 1

RESULT 58
US-09-745-237A-294/c
Sequence 294, Application US/09745237A
Publication No. US20030143708A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: 400/007 (MBH00-918-A)
CURRENT APPLICATION NUMBER: US/09/745,237A
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 4550
SOFTWARE: PatentIn version 3.0
SEQ ID NO 294
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-745-237A-294

Query Match 0.5%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 77;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 149 GCTGCTCAGTCACCAT 165
|:::|||||||:::
DB 17 GCTGCTCAGGCACCAT 1

RESULT 59
US-10-349-143-6432
Sequence 6432, Application US/10349143
Publication No. US2004000584A1
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CPI
CURRENT APPLICATION NUMBER: US/10/349,143
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US/09/422,978
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 6432
LENGTH: 18
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..18
OTHER INFORMATION: upstream amplification primer 99-1143 for SEQ 2498,
US-10-349-143-6432

Query Match 0.5%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 80;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 598 GGAAGCTGGAGATCTG 614
|:::|||||||:::
DB 2 GGAAGCTGGAGTCTG 18

RESULT 60
US-09-752-983-245/c
Sequence 245, Application US/09752983
Patent No. US20010016575A1
GENERAL INFORMATION:
APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
APPLICANT: Graham, Brett P. Monia
TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 271
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marlton
STATE: NJ
COUNTRY: U.S.A.
ZIP: 08053
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PC
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/752,983
FILING DATE: 02-Jan-2001
CLASSIFICATION:

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/280,805
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Licata, Jane Massey
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0346
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-810-1515
; TELEFAX: 609-810-1454
; INFORMATION FOR SEQ ID NO: 245:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; US-09-752-983-245

Query Match 0.5%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 81 GTGATCTTGCTCACAG 97
Db 18 GTGATCTTGCTCATG 2

RESULT 61
US-09-730-617-98
; Sequence 98, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Sudhiradas K
; APPLICANT: Shimkets, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Mezes, Peter S
; TITLE OF INVENTION: No. US20020068279A1el Proteins and Nucleic Acids Encoding the Sam
; FILE REFERENCE: 15966-609
; CURRENT APPLICATION NUMBER: US/09/730,617
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/169,056
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/169,886
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/169,866
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/170,252
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/175,740
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: chemically
; OTHER INFORMATION: synthesized
US-09-730-617-98

Query Match 0.5%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 381 TCAAGCTTCAGCTGCAG 397
Db 1 TGAAGCTTCAGCTGCAG 17
```

```

RESULT 62
US-10-005-344-245/c
; Sequence 245, Application US/10005344
; Publication No. US20030203862A1
; GENERAL INFORMATION:
; APPLICANT: Loren J. Miraglia
; APPLICANT: Pamela Nero
; APPLICANT: Mark J. Graham
; APPLICANT: Brett P. Monia
; APPLICANT: Erich Koller
; APPLICANT: Mingyi Chiang
; APPLICANT: Mano Manoharan
; TITLE OF INVENTION: Antisense Modulation of mdm2 expression.
; FILE REFERENCE: ISPH-0622
; CURRENT APPLICATION NUMBER: US/10/005,344
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 09/048,810
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/280,805
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 379
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 245
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-005-344-245

Query Match 0.5%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 81 GTGATCTTGCTCACAG 97
Db 18 GTGATCTTGCTCATG 2

RESULT 63
US-10-292-849-45
; Sequence 45, Application US/10292849
; Publication No. US20040092463A1
; GENERAL INFORMATION:
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: MODULATION OF PIM-1 EXPRESSION
; FILE REFERENCE: RTS-0170
; CURRENT APPLICATION NUMBER: US/10/292,849
; CURRENT FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 138
; SEQ ID NO 45
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-292-849-45

Query Match 0.5%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 594 CTTGGGAAAGCTGGAGA 610
Db 4 CTCGGGAAGCTGGAGA 20

RESULT 64
US-10-304-111-43/c
; Sequence 43, Application US/10304111
; Publication No. US20040102403A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
```



```
Db      20 ATGTTCTAAAGCACTCTGC 1
;
; APPLICANT: Staehling-Hampton, Karen
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; TITLE OF INVENTION: GENOMIC DELETIONS
; FILE REFERENCE: 240083.515C1
; CURRENT APPLICATION NUMBER: US/10/353,150
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-353-150-60

Query Match      0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 91;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1116 ATGTTCAAGAAAGCAGTCTGC 1135
      ||||| ||||| ||||| |||||
Db      20 ATGTTCTAAAGCACTCTGC 1

RESULT 72
US-10-177-573-20
; Sequence 20, Application US/10177573
; Publication No. US20030236206A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF PPP3R1 EXPRESSION
; FILE REFERENCE: RTS-0364
; CURRENT APPLICATION NUMBER: US/10/177,573
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 104
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-177-573-20

Query Match      0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 91;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      928 GACAAATCTGTACTCTTTGA 947
      ||||| ||||| ||||| |||||
Db      1 GACAAATCAGTTCTCTGTGA 20

RESULT 73
US-10-104-047-3957
; Sequence 3957, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3957
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially
```


; OTHER INFORMATION: synthesized primer sequence
US-10-104-047-3957

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 91;
Matches 17; Conservative 0; Mismatches 3; Indels

Qy 888 TCCCTGCTCATTTGCTTGGT 907
Db 1 TACGTGCTCATTTACTTGGT 20

RESULT 74

```

US-10-349-143-6588/C
; Sequence 6588, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6588
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer 99-12960 for SEQ 2654,
US-10-349-143-6588

```

Query Match	0.43;	Score 15.2;	DB 1;	Length 20;
Best Local Similarity	85.0%;	Pred. No. 91;		
Matches 17;	Conservative	0;	Mismatches 3;	Indels 0;
				Gaps 0;

Qy 1042 GTTCCTTTGTATCTGTTGGTC 1061
|||||
Db 20 GTTCATGATTTGTAGGTC 1

RESULT 75

```

US-10-289-762-1301
; Sequence 1301, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1301
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-1301

```

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 91;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1303 CCATGAAGCTGTTGGGAAA 13222
Db 1 CCACGAATCTCTTGGGAAA 20

RESULT 76

```

US-10-289-762-3147
; Sequence 3147, Application US/10289762
; Publication No. US2004006218A1
; GENERAL INFORMATION:
; APPLICANT: Griflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae
; TITLE OF INVENTION: thereof and uses
; TITLE OF INVENTION: and treatment of
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 3147
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-3147

```

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 91;
Matches 17; Conservative 0; Mismatches 3; Indels

QY 475 CACCATCTACAGTACTGGAA 494
|||||
Db 1 CACCACCTACAGTAATGGCA 20

RESULT 77

```

US-10-211-859-41/c
; Sequence 41, Application US/10211859
; Publication No. US20040022765A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF RAN GTPASE ACTIVATING PROTEIN 1 EXPRESSION
; FILE REFERENCE: HTS-0013
; CURRENT APPLICATION NUMBER: US/10/211,859
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-211-859-41

```

Query Match	0.4%	Score 15.2;	DB 1;	Length 20;
Best Local Similarity	85.0%;	Pred. No. 91;		
Matches 17;	Conservative	0;	Mismatches 3;	Indels 0;
				Gaps 0;

Qy 2593 AAGATGATAAAGATATCATT 2612
||| ||| ||| ||| ||| ||| ||| |||
Db 20 AAGATGCTAAAGATGTGATT 1

RESULT 78

```

US-10-211-859-72
; Sequence 72, Application US/10211859
; Publication No. US20040022765A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODUL
; FILE REFERENCE: HTS-0013

```

```

; CURRENT APPLICATION NUMBER: US/10/211,859
;
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 78
;
; SEQ ID NO 72
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-211-859-72

```

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 91;
Matches 17: Conservative 0: Mismatches 3: Indels

QY 2593 AAGATGATAAAGATATCATT 2612
 |||||
 Db 1 AAGATGCTAAAGATGTGATT 20

```

RESULT 79
US-10-274-085-106
; Sequence 106, Application US/10274085
; Publication No. US20040077570A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Sanjay Bhano
; TITLE OF INVENTION: ANTISENSE MODULATION OF FET
; FILE REFERENCE: ISPH-0714
; CURRENT APPLICATION NUMBER: US/10/274,085
; CURRENT FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 225
; SEQ ID NO 106
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-274-085-106

```

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 91;
Matches 17: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	382	CAAGCTTCAGCTGCAGGCTC	401
Dh	1	CCAGCTCCAGCTGCAGGCTC	20

RESULT 80
US-10-628-109-134
Sequence 134, Application US/10628109
Publication No. US20040101886A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Lin, Ying-Chi
APPLICANT: McWhirter, John
APPLICANT: Matuyama, Toshiaki
TITLE OF INVENTION: NESTED OLIGONUCLEOTIDES CONTAINING A HAIRPIN FOR NUCLEIC ACID
TITLE OF INVENTION: AMPLIFICATION
FILE REFERENCE: 1087-35 DIV
CURRENT APPLICATION NUMBER: US/10/628,109
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US 60/254,669
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 60/323,400
PRIOR FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: US 10/014,012
PRIOR FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 231
SOFTWARE: PatentIn version 3.2
SEQ ID NO 134

```

; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: boundary oligonucleotide
US-10-628-109-134

```

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 91;
Matches 17; Conservative 0; Mismatches 3; Indels

QY 2385 TCTTCACTGGGATCAGAGAT 2404
 ||| ||| ||| ||| ||| ||| ||| |||
 pb 1 TCTGCCCTGGTATCAGAGAT 20

```

RESULT 81
US-10-755-889-695/c
; Sequence 695, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 695
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized Oligonucleotide.
US-10-755-889-695

```

Query Match	0.4%	Score 15.2;	DB 1;	Length 20;
Best Local Similarity	85.0%	Pred. NO. 91;		
Matches 17:	Conservative	0;	Mismatches 3;	Indels 0;
				Gaps 0;

QY 199 TAACACGAAGCCGAAGACC 218
| | | | | | | | | |
Db 20 TTACCAAGCAGCCGAAGACC 1

```

RESULT 82
US-10-731-739-371/c
; Sequence 371, Application US/10731739
; Publication No. US20040176582A1
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/10/731.739
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US/09/544,398B
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ NOS: 641
; SOFTWARE: FASTSEQ for Windows Version 4.0

```

SEQ ID NO 371
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-10-731-739-371

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 91;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2731 CTGTTCTGTTCTTCAATCAG 2750
Db 20 CTGTTCTGTTCTTCAATCAG 1

RESULT 83

US-09-080-140-20/c
Sequence 20, Application US/09080140
Publication No. US20040018553A1
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA

ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,140
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA: 08/856,653
APPLICATION NUMBER: 15-MAY-1997
FILING DATE: 15-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6105.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-080-140-20

Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 93;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 528 TATTACTTGACCCAGGTTTG 547
Db 20 TATGACTTGAGCCAGGTTTG 1

RESULT 84

US-10-399-091-11/c
Sequence 11, Application US/10399091
Publication No. US20040047875A1
GENERAL INFORMATION:
APPLICANT: Thonnard, Joelle
TITLE OF INVENTION: No. US20040047875A1e1 Compounds
FILE REFERENCE: BM45420
CURRENT APPLICATION NUMBER: US/10/399,091
CURRENT FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: PCT/EP01/11561
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: GB0025169.4
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-10-399-091-11

Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 93;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1680 AAGAAGCACTTGTCAAGCA 1699
Db 21 AACAGCACTTGTCAAGAA 2

RESULT 85

US-10-335-977-9991/c
Sequence 9991, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:

APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400

```
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 9991:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 21 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: circular
;   MOLECULE TYPE: DNA (genomic)
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   ORIGINAL SOURCE:
;   ORGANISM: Helicobacter pylori
;   FEATURE:
;     NAME/KEY: misc feature
;     LOCATION: (B) LOCATION 1...21
;     SEQUENCE DESCRIPTION: SEQ ID NO: 9991:
US-10-335-977-9991

Query Match      0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 93;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      813 ATGAACATCTTCATGSCCTAT 832
Db      21 ATGAACATATTTCAAGCGTAT 2

RESULT 86
US-10-349-143-6151
; Sequence 6151, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6151
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21
; OTHER INFORMATION: upstream amplification primer 99-9405 for SEQ 2217,
US-10-349-143-6151

Query Match      0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 93;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      181 GACATTTTGGACAGTTTA 200
Db      1 GACATTTTGAACCACTATA 20

RESULT 87
US-10-349-143-9328/C
; Sequence 9328, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
```

```
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9328
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplification primer 99-25070 for SEQ 1463, in complete
US-10-349-143-9328

Query Match      0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 93;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2699 TCAGTATTTATTTCTGCTC 2718
Db      20 TCACAAATTTATTTCTGCTC 1

RESULT 88
US-10-349-143-10352
; Sequence 10352, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10352
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplification primer 99-11340 for SEQ 2487, in complete
US-10-349-143-10352

Query Match      0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 93;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3144 TCCAAGGTGCTTGATCAACA 3163
Db      1 TCACAGGTGCTTCAACACA 20
```

```
RESULT 89
US-10-349-143-10665
; Sequence 10665, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020C01
; CURRENT FILING DATE: 2003-01-21
; PRIOR FILING DATE: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10665
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplification primer 99-19050 for SEQ 2800, in complement
US-10-349-143-10665
Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 93;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2628 GACTCTGTTTCAGAAAAA 2647
||||| ||||||| |||||
DB 1 GACTCTCATCAGAGAAAA 20

RESULT 90
US-10-608-436-37
; Sequence 37, Application US/10608436
; Publication No. US20040131633A1
; GENERAL INFORMATION:
; APPLICANT: ELLIS, JOHN TIMOTHY
; APPLICANT: ATKINSON, ROBERT
; APPLICANT: RYCE, CHERYL
; APPLICANT: QUINN, HELEN ELIZABETH
; APPLICANT: MILLER, CATHERINE MARGARET
; APPLICANT: MORISON, DAVID ANDREW
; TITLE OF INVENTION: PARASITE ANTIGENS
; FILE REFERENCE: 47-194
; CURRENT APPLICATION NUMBER: US/10/608,436
; CURRENT FILING DATE: 2003-06-30
; PRIOR FILING DATE: AU PP 9928
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: PCT/AU00/00354
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR primer
US-10-608-436-37
Query Match 0.4%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 89
US-09-969-373-1896
; Sequence 1896, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR FILING DATE: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 1896
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION:
US-09-969-373-1896
Query Match 0.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCAACCCAAAGTTCAA 18
||||| ||||||| |||||
DB 1 CCAACCCAAAGTTCAA 15

RESULT 92
US-10-600-816-32/c
; Sequence 32, Application US/10600816
; Publication No. US20040121362A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION AND MODULATION OF A G-PROTEIN COUPLED RECEPTOR
; TITLE OF INVENTION: (GPCR), RA13, ASSOCIATED WITH CHRONIC OBSTRUCTIVE PULMONARY
; FILE REFERENCE: D0251 NP
; CURRENT APPLICATION NUMBER: US/10/600,816
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: U.S. 60/390,850
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: U.S. 60/407,006
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-600-816-32
Query Match 0.4%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 718 AGACTATGAAGTAAA 732
||||| ||||||| |||||
DB 16 AGACTATGAAGTAAA 2

RESULT 93
```

```
US-09-800-629A-116/c
; TITLE OF INVENTION: METHOD OF ANALYZING mRNA SPLICE VARIANTS USING ARRAYED PRIMER EX
; FILE REFERENCE: (APEX)
; CURRENT APPLICATION NUMBER: US/10/092,208
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide 5-V8.
US-10-092-208-16
Query Match 0.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 96; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

Qy 1928 GACTGGAGTCCATAT 1942
|||||
Db 3 GACTGGAGTCCATAT 17

RESULT 96
US-10-679-532-116/c
; Sequence 116, Application US/10679532
; Publication No. US20040121376A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Kazras, James G
; APPLICANT: McKay, Robert
; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
; TITLE OF INVENTION: TRANSDUCTION
; FILE REFERENCE: ISPH-0537
; CURRENT APPLICATION NUMBER: US/10/679,532
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/800,629A
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT/US00/07318
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 09/280,799
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 116
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-10-679-532-116
Query Match 0.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 96; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

Qy 1005 CCTGGGATGCACAGA 1019
|||||
Db 15 CCTGGGATGCACAGA 1

RESULT 94
US-10-012-456A-24
; Sequence 24, Application US/10012456A
; Publication No. US20030087243A1
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins University
; APPLICANT: Imperial Cancer Research Technology Limited
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: IMPW/P23071PC
; CURRENT APPLICATION NUMBER: US/10/012,456A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PCR primer
US-10-012-456A-24
Query Match 0.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 96; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

Qy 2914 AGGACAGTGCCTGGG 2928
|||||
Db 1 AGGACAGTGCCTGGG 15

RESULT 95
US-10-092-208-16
; Sequence 16, Application US/10092208
; Publication No. US20030170637A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Hyunsoo
; APPLICANT: Pirrung, Michael C.
```

```
; TITLE OF INVENTION: METHOD OF ANALYZING mRNA SPLICE VARIANTS USING ARRAYED PRIMER EX
; FILE REFERENCE: (APEX)
; CURRENT APPLICATION NUMBER: US/10/092,208
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide 5-V8.
US-10-092-208-16
Query Match 0.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 96; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

Qy 1928 GACTGGAGTCCATAT 1942
|||||
Db 3 GACTGGAGTCCATAT 17

RESULT 96
US-10-679-532-116/c
; Sequence 116, Application US/10679532
; Publication No. US20040121376A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Kazras, James G
; APPLICANT: McKay, Robert
; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
; TITLE OF INVENTION: TRANSDUCTION
; FILE REFERENCE: ISPH-0537
; CURRENT APPLICATION NUMBER: US/10/679,532
; CURRENT FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: US/09/800,629A
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT/US00/07318
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 09/280,799
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 116
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-10-679-532-116
Query Match 0.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 96; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

Qy 1005 CCTGGGATGCACAGA 1019
|||||
Db 15 CCTGGGATGCACAGA 1

RESULT 97
US-09-067-638B-26
; Sequence 26, Application US/09067638B
; Patent No. US20020028923A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Brenda F. Baker
; APPLICANT: John McNeil
; APPLICANT: Susan M. Freier
; APPLICANT: Henri M. Sasmor
```

APPLICANT: Douglas G. Brooks
APPLICANT: Cara Ohashi
APPLICANT: Jacqueline R. Wyatt
APPLICANT: Alexander Borchers
APPLICANT: Timothy A. Vickers
TITLE OF INVENTION: Identification of Genetic
TITLE OF INVENTION: Targets for Modulation By Oligonucleotides and
TITLE OF INVENTION: Generation of Oligonucleotides for Gene
TITLE OF INVENTION: Modulation
NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOODCOCK WASHBURN KURTZ
ADDRESSEE: MACKIEWICZ & NORRIS LLP
STREET: 1 LIBERTY PLACE 46TH FLOOR
CITY: PHILADELPHIA
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
COMPUTER: IBM
OPERATING SYSTEM: PC-Windows NT
SOFTWARE: WORD PERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,638B
FILING DATE: 28-APR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/081,483
FILING DATE: 13-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: John W. Caldwell
REGISTRATION NUMBER: 28,937
REFERENCE/DOCKET NUMBER: ISIS-2960
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-067-638B-26

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1608 CTCGTTCCTCCATGTTCTTA 1625
Db 1 CTCGTTCCTCCATGTTCTTA 18

RESULT 98
US-09-287-599-6/c
Sequence 6, Application US/09287599
Patent No. US20020151071A1
GENERAL INFORMATION:
APPLICANT: Handelsman, Jo
APPLICANT: Klimowicz, Amy
TITLE OF INVENTION: Enterotoxin-Deficient Bacillus
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/287,599
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960296
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
US-09-287-599-6

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1543 GAAGCGAGAGATAGTTGG 1560
Db 18 GCAGCGAAAGATAGTTGG 1

RESULT 99
US-09-933-638A-10
Sequence 10, Application US/09933638A
Patent No. US20020160952A1
GENERAL INFORMATION:
APPLICANT: Kazantsev, Aleksey G.
APPLICANT: Thompson, Leslie M.
TITLE OF INVENTION: INHIBITION OF PROTEIN-PROTEIN INTERACTION
FILE REFERENCE: 01997-289001
CURRENT APPLICATION NUMBER: US/09/933,638A
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: US 60/226,502
PRIOR FILING DATE: 2000-08-18
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated primer
US-09-933-638A-10

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 135 TTGTTGCTGTAACGTGCTG 152
Db 1 TTGTTGCTGTTCTGCTG 18

RESULT 100
US-09-961-077-545
Sequence 545, Application US/09961077
Publication No. US20030014775A1
GENERAL INFORMATION:
APPLICANT: Zwick, Michael G.
Edington, Brent E.
McSwiggen, James A.

```
Query Match      0.4%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 66.7%; Pred. No. 96;  
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

QY 150 CTGCTCAGTCCACCATTTG 167
 |:|:|:|:|:|:|:|:
Db 1 CUGCUCCGUCCACCAGUG 18

RESULT 101
US-10-194-584-2
; Sequence 2, Application US/10194584
; Publication No. US20030027288A1
; GENERAL INFORMATION:
; APPLICANT: Housman, David E.
; APPLICANT: Preisinger, Elizabeth A.
; APPLICANT: Kazantsev, Aleksey G.
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGENTS WHICH INHIBIT AGGREGATION
; TITLE OF INVENTION: OF POLYPEPTIDES
; FILE REFERENCE: 01997-261002
; CURRENT APPLICATION NUMBER: US/10/194,584

FILE REFERENCE: 01997-261002
TITLE OF INVENTION: OF POLYPEPTIDES
CURRENT APPLICATION NUMBER: US/10/194,584

; PRIOR APPLICATION NUMBER: 09/067,638
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/081,483
; PRIOR FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030113739A1el Sequence
US-10-116-325-26

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1608 CTCGTTCATGTTCTA 1625
|||||
Db 1 CTCGTTCAGGTGCTA 18

RESULT 104

US-10-168-771-45/c
; Sequence 45, Application US/10168771
; Publication No. US20030148974A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; APPLICANT: Richard A. Roth
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; APPLICANT: LELAND STANFORD JUNIOR UNIVERSITY
; TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION
; FILE REFERENCE: RSP-0322
; CURRENT APPLICATION NUMBER: US/10/168,771
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 09/474,922
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 45
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-168-771-45

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2423 GCAAGAGTGGAGAAAT 2440
|||||
Db 18 GCAAGAGAGAGAGAAAT 1

RESULT 105

US-10-388-263-26
; Sequence 26, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowsett, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasmor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR

; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-26

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1608 CTCGTTCATGTTCTA 1625
|||||
Db 1 CTCGTTCAGGTGCTA 18

RESULT 106

US-10-108-260A-5168/c
; Sequence 5168, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5168
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized i

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1292 AATGAAGATTCCATGAA 1309
|||||
Db 18 AATGAAGATGCCAAGAA 1

RESULT 107

US-10-108-260A-5396
; Sequence 5396, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5396
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized p

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3105 AGAATCCAGGAGACAGGT 3122
DB 1 AGRAGCCAGGAGAGGT 18
|||||

RESULT 108

US-09-985-637A-18
; Sequence 18, Application US/09985637A

; Publication No. US20030119000A1

; GENERAL INFORMATION:

; APPLICANT: Polansky, Jon

; TITLE OF INVENTION: METHODS TO SCREEN AND TREAT INDIVIDUALS WITH GLAUCOMA OR THE PRO

; TITLE OF INVENTION: TO DEVELOP GLAUCOMA

; FILE REFERENCE: 13587.296

; CURRENT APPLICATION NUMBER: US/09/985,637A

; CURRENT FILING DATE: 2001-11-05

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 18

; LENGTH: 19

; TYPE: DNA

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Primer Sequence

US-09-985-637A-18

Query Match 0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 124 CCTTCTCAGCCTTGTC 141
DB 1 CCTTCTCAGCCTTGCTAC 18
|||||

RESULT 109

US-10-467-721-43

; Sequence 43, Application US/10467721

; Publication No. US20040058366A1

; GENERAL INFORMATION:

; APPLICANT: JAPAN SCIENCE AND TECHNOLOGY CORPORATION

; TITLE OF INVENTION: Ema12, novel clock genes

; FILE REFERENCE: A011-15PCT

; CURRENT APPLICATION NUMBER: US/10/467,721

; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: JP 2001/35743

; PRIOR FILING DATE: 2001-02-13

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 43

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:cqf862-primer

US-10-467-721-43

Query Match 0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 85 TCTTGCTCACAGGGAC 102
DB 2 TCTTGATCACAGGGAC 19
|||||

RESULT 110

US-10-244-633-22

; Sequence 22, Application US/10244633

; Publication No. US20030068640A1

; GENERAL INFORMATION:

; APPLICANT: Nguyen, Thai D.

; APPLICANT: Polansky, Jon R.

; APPLICANT: Chen, Pu

; APPLICANT: Chen, Hua

; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,

; TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related

; TITLE OF INVENTION: Disorders

; FILE REFERENCE: 07425.0057.US01

; CURRENT APPLICATION NUMBER: US/10/244,633

; CURRENT FILING DATE: 2002-09-17

; PRIOR APPLICATION NUMBER: US/09/306,828

; PRIOR FILING DATE: 1999-05-07

; PRIOR APPLICATION NUMBER: US 09/227,881

; PRIOR FILING DATE: 1999-01-11

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: Microsoft Word 97

; SEQ ID NO 22

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-244-633-22

Query Match 0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 124 CCTTCTCAGCCTTGTC 141
DB 1 CCTTCTCAGCCTTGCTAC 18
|||||

RESULT 111

US-10-251-117-97/c

; Sequence 97, Application US/10251117

; Publication No. US20030170891A1

; GENERAL INFORMATION:

; APPLICANT: McSwigen, James

; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor

; TITLE OF INVENTION: Gene Expression Using Short Interfering RNA

; FILE REFERENCE: 900/042 (MBHB02-468-A)

; CURRENT APPLICATION NUMBER: US/10/251,117

; CURRENT FILING DATE: 2003-02-24

; PRIOR APPLICATION NUMBER: US 60/393,924

; PRIOR FILING DATE: 2002-07-03

; PRIOR APPLICATION NUMBER: US 10/163,552

; PRIOR FILING DATE: 2002-06-06

; PRIOR APPLICATION NUMBER: US 60/358,580

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: US 09/916,466

; PRIOR FILING DATE: 2001-07-25

; PRIOR APPLICATION NUMBER: US 60/296,249

; PRIOR FILING DATE: 2001-06-06

; NUMBER OF SEQ ID NOS: 1213

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 97

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/sina sense

US-10-251-117-97

Query Match 0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1796 CCTGGACCTAGCATTTG 1813
DB 18 CCTGGACCTAGCATTTG 1
|||||

```
RESULT 112
US-10-251-117-346
; Sequence 346, Application US/10251117
; Publication No. US20030170891A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggan, James
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor R
; FILE REFERENCE: 900/042 (WBH02-468-A)
; CURRENT FILING DATE: 2003-02-24
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 09/916,466
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/296,249
; NUMBER OF SEQ ID NOS: 1213
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 346
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siRNA antisense region
US-10-251-117-346
Query Match 0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 1e+02;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1796 CCTCGACCTAGCATTTG 1813
DB 2 CCUGGACCCGACAG 19

RESULT 113
US-10-741-339-18
; Sequence 18, Application US/10741339
; Publication No. US20040132795A1
; GENERAL INFORMATION:
; APPLICANT: Polansky, Jon
; TITLE OF INVENTION: METHODS TO SCREEN AND TREAT INDIVIDUALS WITH GLAUCOMA OR THE PROH
; FILE REFERENCE: 13587.375
; CURRENT APPLICATION NUMBER: US/10/741,339
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 09/985,637
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 19
; TYPE: DNA
; ORGANISM: synthetic
US-10-741-339-18
Query Match 0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 124 CCTTCTCAGCCTTGTC 141
DB 1 CCTTCTCAGCCTTGTC 18

RESULT 114
```

```
US-09-752-983-87/c
; Sequence 87, Application US/09752983
; Patent No. US20010016575A1
; GENERAL INFORMATION:
; APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
; APPLICANT: Graham, Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 271
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PC
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/752,983
; FILING DATE: 02-Jan-2001
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/280,805
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Licata, Jane Massey
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0346
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-810-1515
; TELEFAX: 609-810-1454
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-09-752-983-87
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 799 GATTAACCATATATGA 816
DB 19 GACTAAACGATTATATGA 2

RESULT 115
US-09-752-639-33/c
; Sequence 33, Application US/09752639
; Patent No. US20020091243A1
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, T.
; APPLICANT: Granger, G.A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
; TITLE OF INVENTION: of Use Thereof
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSER: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
```

```
;
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/752,639
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wu, Frank
; REGISTRATION NUMBER: 41,386
; REFERENCE/DOCKET NUMBER: 22000-20577.21
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-752-639-33

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      589 CTGGCGTTGGGAAGCTG 606
      |||||
Db      20 CTGGCGTTGAGACAGCTG 3

RESULT 116
US-09-984-198-33/c
; Sequence 33, Application US/09984198
; Patent No. US20020106679A1
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, T.
; APPLICANT: Granger, G.A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
; TITLE OF INVENTION: of Use Thereof
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/984,198
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US99/10793
; FILING DATE:
; APPLICATION NUMBER: 09/081,385
; FILING DATE:
; APPLICATION NUMBER: 09/081,385
; FILING DATE:
```

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;
; APPLICATION NUMBER: 08/964,747
; FILING DATE: 05-NOV-1997
; APPLICATION NUMBER: 60/030,761
; FILING DATE: 06-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wu, Frank
; REGISTRATION NUMBER: 41,386
; REFERENCE/DOCKET NUMBER: 22000-20577.21
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-984-198-33

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      589 CTGGCGTTGGGAAGCTG 606
      |||||
Db      20 CTGGCGTTGAGACAGCTG 3

RESULT 117
US-09-791-243-15/c
; Sequence 15, Application US/09791243
; Patent No. US20020147164A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Robert Rothlein
; APPLICANT: Takashi Kei Kishimoto
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF CYTOCHESIN-1 EXPRESSION
; FILE REFERENCE: RTS-0095
; CURRENT APPLICATION NUMBER: US/09/791,243
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-791-243-15

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1005 CCTGGGATGCACAGAGAA 1022
      |||||
Db      18 CCTGGGATCCACAGAGCA 1

RESULT 118
US-09-909-280A-4
; Sequence 4, Application US/09909280A
; Patent No. US20020160375A1
; GENERAL INFORMATION:
; APPLICANT: Bumcrott, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; TITLE OF INVENTION: THERETO
; FILE REFERENCE: CIBT-P02-050
; CURRENT APPLICATION NUMBER: US/09/909,280A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/207,857
; PRIOR FILING DATE: 1998-12-08
```

```
; PRIOR APPLICATION NUMBER: US 60/067,940
; PRIOR FILING DATE: 1997-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-909-280A-4

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 203 CACGAAGCCGAGACCTG 220
Db 1 CACAAAGCCGAGACCTG 18

RESULT 119
US-09-824-322B-500/c
; Sequence 500, Application US/09824322B
; Publication No. US20030022848A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-ALPHA
; FILE REFERENCE: ISPH-0501
; CURRENT APPLICATION NUMBER: US/09/824,322B
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 09/313,932
; PRIOR FILING DATE: 1999-05-18
; PRIOR APPLICATION NUMBER: US 09/166,186
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 503
; SEQ ID NO 500
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-824-322B-500

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3353 GCACAAAGCAGACACTCA 3370
Db 18 GCACACAGAGACACTCA 1

RESULT 120
US-09-771-933-114
; Sequence 114, Application US/09771933
; Publication No. US20030023387A1
; GENERAL INFORMATION:
; APPLICANT: Gill-Garrison, Rosalynn D
; APPLICANT: Martin, Christopher J
; APPLICANT: Sanchez-Felix, Manuel V
; TITLE OF INVENTION: Computer-assisted Means for Assessing Lifestyle Risk
; FILE REFERENCE: 620-130
; CURRENT APPLICATION NUMBER: US/09/771,933
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 114
```

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-771-933-114

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1517 CAGTGGATGAAAAAGTGG 1534
Db 2 CAGTGGTTGAAAAAGTAG 19

RESULT 121
US-09-784-674-601/c
; Sequence 601, Application US/09784674
; Publication No. US20030054346A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Karen W.
; APPLICANT: Wolber, Paul K.
; APPLICANT: Delenstarr, Glenda C.
; APPLICANT: Webb, Peter G.
; APPLICANT: Kincaid, Robert H.
; TITLE OF INVENTION: Methods for evaluating oligonucleotide
; NUMBER OF SEQUENCES: 1165
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Records Manager, Legal Department, Hewlett-Packard
; COMPANY: Company M/S 2050
; STREET: 3000 Hanover Street
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,674
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: No. US20030054346A1 available
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/021,701
; FILING DATE: 10-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Choi, Wendy A.
; REGISTRATION NUMBER: 36,697
; REFERENCE/DOCKET NUMBER: 10971464-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-236-2386
; TELEFAX: 650-852-8063
; INFORMATION FOR SEQ ID NO: 601:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 601:
US-09-784-674-601

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1073 ACTCAAGGATTCTGGAA 1090
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Db      20 ACTCAAGACTTCTGGAA 3
|||||  |||||  |||||
RESULT 122
US-09-784-674-602/c
; Sequence 602, Application US/09784674
; Publication No. US20030054346A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Karen W.
; Wolber, Paul K.
; Delenstarr, Glenda C.
; Webb, Peter G.
; Kincaid, Robert H.
; TITLE OF INVENTION: Methods for evaluating oligonucleotide
; probe sequences
; NUMBER OF SEQUENCES: 1165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
; Company M/S 20B0
; STREET: 3000 Hanover Street
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,674
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: No. US20030054346A1 available
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/021,701
; FILING DATE: 10-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Choi, Wendy A.
; REGISTRATION NUMBER: 36,697
; REFERENCE/DOCKET NUMBER: 10971464-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-236-2386
; TELEFAX: 650-852-8063
; INFORMATION FOR SEQ ID NO: 602:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 602:
US-09-784-674-602
Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1073 ACTCAAGACTTCTGGAA 1090
Db      19 ACTCAAGACTTCTGGAA 2
|||||  |||||  |||||
RESULT 123
US-09-784-674-603/c
; Sequence 603, Application US/09784674
; Publication No. US20030054346A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Karen W.
; Wolber, Paul K.
; Delenstarr, Glenda C.
```

```
Webb, Peter G.
Kincaid, Robert H.
; TITLE OF INVENTION: Methods for evaluating oligonucleotide
; probe sequences
; NUMBER OF SEQUENCES: 1165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
; Company M/S 20B0
; STREET: 3000 Hanover Street
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,674
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: No. US20030054346A1 available
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/021,701
; FILING DATE: 10-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Choi, Wendy A.
; REGISTRATION NUMBER: 36,697
; REFERENCE/DOCKET NUMBER: 10971464-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-236-2386
; TELEFAX: 650-852-8063
; INFORMATION FOR SEQ ID NO: 603:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 603:
US-09-784-674-603
Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1073 ACTCAAGACTTCTGGAA 1090
Db      18 ACTCAAGACTTCTGGAA 1
|||||  |||||  |||||
RESULT 124
US-09-865-993-35/c
; Sequence 35, Application US/09865993
; Publication No. US20030060437A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 5 EXPRESSION
; FILE REFERENCE: RTS-0175
; CURRENT APPLICATION NUMBER: US/09/865,993
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-865-993-35
```

```
Query Match          0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1672 CCAGTTTCAAGAAGCACT 1689
Db 19 CCACATTTCAGAAGCAAT 2

RESULT 125
US-09-953-047-59
; Sequence 59, Application US/09953047
; Publication No. US20030087854A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 3 EXPRE
; FILE REFERENCE: RTS-0157
; CURRENT APPLICATION NUMBER: US/09/953,047
; CURRENT FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-953-047-59

Query Match          0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2084 CAGATGATCTCTTTGGG 2101
Db 2 CAGATGTTCTCTTTGGG 19

RESULT 126
US-10-630-401-59
; Sequence 59, Application US/10630401
; Publication No. US20040048824A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 3 EXPRE
; FILE REFERENCE: RTS-0157
; CURRENT APPLICATION NUMBER: US/10/630,401
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/953,047
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-630-401-59

Query Match          0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2084 CAGATGATCTCTTTGGG 2101
Db 2 CAGATGTTCTCTTTGGG 19

RESULT 127
US-10-618-540-1
; Sequence 1, Application US/10618540
; Publication No. US20040052771A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Lim, Sai K.
; TITLE OF INVENTION: Hemangioblast Progenitor Cells
; FILE REFERENCE: 4810-66314
; CURRENT APPLICATION NUMBER: US/10/618,540
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: 10/197,189
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 60/426,789
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-618-540-1

Query Match          0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 614 GAGTCGGCAAGCAGCTG 631
Db 2 GAGATCAGCAGCAGCTG 19

RESULT 128
US-10-095-929-26/c
; Sequence 26, Application US/10095929
; Publication No. US20020197232A1
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. Ralph
; APPLICANT: Cioffli, Joseph
; APPLICANT: Zupancic, Thomas Joel
; APPLICANT: Shafer, Alan Wayne
; TITLE OF INVENTION: METHODS FOR USING THE OBSE
; GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
; DEVELOPMENT
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pennie & Edmonds LLP
; STREET: 1155 Avenue of The Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/095,929
; FILING DATE: 12-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/618,957
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 008907-0033-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

```
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-095-929-26

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 595 TTGGAAAGCTGGAGATC 612
Db 20 TTGAGAAAGCTGGGGAAC 3

RESULT 129
US-10-045-621-17
; Sequence 17, Application US/10045621
; Publication No. US20030082558A1
; GENERAL INFORMATION:
; APPLICANT: The Perkin-Elmer Corporation
; TITLE OF INVENTION: POLYMERASE EXTENSION AT 3' TERMINUS OF PNA-DNA CHIMERA
; FILE REFERENCE: 4468 US
; CURRENT APPLICATION NUMBER: US/10/045,621
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US/09/373,845
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Mouse Murine Xist gene
US-10-045-621-17

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1006 CTGGGATGCACAGAGAT 1023
Db 2 CTGGGATGCACAGAGCAT 19

RESULT 130
US-10-181-846-135/c
; Sequence 135, Application US/10181846
; Publication No. US20030083297A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
; FILE REFERENCE: RTSP-0363
; CURRENT APPLICATION NUMBER: US/10/181,846
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: PCT/US01/01416
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 09/490,692
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 135
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-181-846-135

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 384 AGCTTCAGCTCAGGCTC 401
Db 19 AGCTTCAGCTCCTGGCTC 2

RESULT 131
US-10-035-485A-84/c
; Sequence 84, Application US/10035485A
; Publication No. US20030105044A1
; GENERAL INFORMATION:
; APPLICANT: Brenda P. Baker
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF MATRIX METALLOPROTEINASE 1 EXPRESSION
; FILE REFERENCE: RTS-0139
; CURRENT APPLICATION NUMBER: US/10/035,485A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 84
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-035-485A-84

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2673 AGAGAGCATCTTCATTGA 2690
Db 18 AGAGAGCATCTTCATTGA 1

RESULT 132
US-10-003-919-47
; Sequence 47, Application US/10003919
; Publication No. US20030114401A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHIP-1 EXPRESSION
; FILE REFERENCE: RTS-0256
; CURRENT APPLICATION NUMBER: US/10/003,919
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 47
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-003-919-47

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 953 CCCTTTGGACAGAAACCA 970
Db 2 CCCTTTGGACAGAAACCA 19

RESULT 133
US-10-017-621-60
; Sequence 60, Application US/10017621
; Publication No. US20030138952A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; APPLICANT: Mark P. Roach
; TITLE OF INVENTION: ANTISENSE MODULATION OF PCTAIRE PROTEIN KINASE 1 EXPRESSION
; FILE REFERENCE: RTS-0350
; CURRENT APPLICATION NUMBER: US/10/017,621
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 60
```



```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-017-621-60

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2016 ATGAATGTACCTTCC 2033
Db 1 ATGAAGTGTAGCTTCC 18

RESULT 134
US-10-180-781-69/c
; Sequence 69, Application US/10180781
; Publication No. US20030180880A1
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; Schellenberg, Gerard D.
; Wasco, Wilma
; Levy-Lahad, Ephrat
; Bird, Thomas D.
; Galas, David J.
; TITLE OF INVENTION: CHROMOSOME 1 GENE AND GENE PRODUCTS RELATED TO
; ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Ave, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/180,781
; FILING DATE: 24-Jun-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 920010.571C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4300
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-10-180-781-69

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3203 GAATCCCGAGCATGCC 3220
Db 18 GAGCTCTCAGAGCATGCC 1

RESULT 135
US-10-058-597-13
```

```
; Sequence 13, Application US/10058597
; Publication No. US20030186236A1
; GENERAL INFORMATION:
; APPLICANT: Kapiil, Sanjay
; APPLICANT: Shanmukhappa, Kumar
; TITLE OF INVENTION: IDENTIFICATION AND APPLICATIONS OF PORCINE REPRODUCTIVE AND RESP;
; TITLE OF INVENTION: SYNDROME VIRUS HOST SUSCEPTIBLE FACTOR(S) FOR IMPROVED SWINE BRI
; TITLE OF INVENTION: DEVELOPMENT OF NON-SIMIAN RECOMBINANT CELL LINE FOR PROPAGATION
; TITLE OF INVENTION: A TARGET FOR A NOVEL CLASS OF ANTIVIRAL COMPOUNDS
; FILE REFERENCE: 30921-C1P1
; CURRENT APPLICATION NUMBER: US/10/058,597
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 09/772,044
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Simian Gen. Sp.
US-10-058-597-13

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 386 CTTCAGCTGCAGGCTCTT 403
Db 1 CTCAGCTTCAGGCTCTT 18

RESULT 136
US-10-005-344-87/c
; Sequence 87, Application US/10005344
; Publication No. US20030203862A1
; GENERAL INFORMATION:
; APPLICANT: Loren J. Miraglia
; APPLICANT: Pamela Nero
; APPLICANT: Mark J. Graham
; APPLICANT: Brett P. Monia
; APPLICANT: Erich Koller
; APPLICANT: Mingvi Chiang
; APPLICANT: Mano Manoharan
; TITLE OF INVENTION: Antisense Modulation of mdm2 expression.
; FILE REFERENCE: ISPH-0622
; CURRENT APPLICATION NUMBER: US/10/005,344
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 09/048,810
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/280,805
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 379
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-005-344-87

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 799 GATTAAACCATTTATGA 816
Db 19 GACTAAACGATTATGA 2

RESULT 137
US-10-181-875-46
; Sequence 46, Application US/10181875
```

```
; Publication No. US20030216333A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Robert McKay
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 ALPHA EXPRESSION
; FILE REFERENCE: RTSP-0356
; CURRENT APPLICATION NUMBER: US/10/181,875
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 09/488,856
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 46
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-181-875-46

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2192 AGAAGTGAAGTTGAAAG 2209
      |||||
DB 2 AGCACTGAAGTTGAAGAG 19

RESULT 138
US-10-189-256-70
; Sequence 70, Application US/10189256
; Publication No. US20040005569A1
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF NF-KAPPA-B P50 SUBUNIT EXPRESSION
; FILE REFERENCE: PTS-0050
; CURRENT APPLICATION NUMBER: US/10/189,256
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 143
; SEQ ID NO 70
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-256-70

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3356 CAAAGCAGACACTCAATA 3373
      |||||
DB 2 CAAAGCTGCCACTCAATA 19

RESULT 139
US-10-189-256-133/C
; Sequence 133, Application US/10189256
; Publication No. US20040005569A1
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF NF-KAPPA-B P50 SUBUNIT EXPRESSION
; FILE REFERENCE: PTS-0050
; CURRENT APPLICATION NUMBER: US/10/189,256
; CURRENT FILING DATE: 2002-07-02
```

```
; NUMBER OF SEQ ID NOS: 143
; SEQ ID NO 133
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-189-256-133

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3356 CAAAGCAGACACTCAATA 3373
      |||||
DB 19 CAAAGCTGCCACTCAATA 2

RESULT 140
US-10-289-762-4789/C
; Sequence 4789, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4789
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-4789

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 951 TTCCTTTGGACAGAAC 968
      |||
DB 20 TTCTCTTTGGACAGAGAC 3

RESULT 141
US-10-447-136-193/C
; Sequence 193, Application US/10447136
; Publication No. US20040009948A1
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and
; TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase
; FILE REFERENCE: 032396-023
; CURRENT APPLICATION NUMBER: US/10/447,136
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/249,247
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/023,040
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-08-02
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/039,959
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/904,901
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 193
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-10-447-136-193
```

```
Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 277 TGTCACAAACATGAATAA 294
Db 19 TGTCGGAACCTGAATAA 2

RESULT 142
US-10-150-811-132/c
; Sequence 132, Application US/10150811
; Publication No. US20040010120A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar et al.
; TITLE OF INVENTION: No. US20040010120A1el Polypeptides and Nucleic Acids Encoding Sam
; FILE REFERENCE: 15966-675CIP2CONI
; CURRENT APPLICATION NUMBER: US/10/150,811
; CURRENT FILING DATE: 2002-05-17
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/182,733
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/182,724
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/183,896
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/184,497
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/224,157
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,744
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/197,083
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/233,405
; PRIOR FILING DATE: 2000-09-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 132
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
; US-10-150-811-132

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2991 TCAAGGATGACATGCTTT 3008
Db 18 TCAAGGACGACATGCTGT 1

RESULT 143
US-10-161-493-167
; Sequence 167, Application US/10161493
; Publication No. US20040018555A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Li, Li
; APPLICANT: Zhong, Mei
; APPLICANT: Casman, Stacie J
; APPLICANT: Gerlach, Valerie
; APPLICANT: Shinkets, Richard A
; APPLICANT: Gorman, Linda

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1221 ATCATGAGATGGGGCATA 1238
Db 3 ATCAGGACATGGGGCATA 20

RESULT 144
US-10-210-290-18
; Sequence 18, Application US/10210290
; Publication No. US20040023378A1
; GENERAL INFORMATION:
; APPLICANT: Ming-Yi Chiang
; APPLICANT: Eric G. Marcussen
; APPLICANT: Kenneth W. Dobie
```

```
; TITLE OF INVENTION: ANTISENSE MODULATION OF KIAA1531 PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0367
; CURRENT APPLICATION NUMBER: US/10/210,290
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 134
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-290-18

Query Match          0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 881 GGATGCGCTCCCTGCTCAT 898
Db 2 GGATGCGCGCTGCTCAT 19

RESULT 145
US-10-210-290-94/c
; Sequence 94, Application US/10210290
; Publication No. US20040023378A1
; GENERAL INFORMATION:
; APPLICANT: Ming-Yi Chiang
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF KIAA1531 PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0367
; CURRENT APPLICATION NUMBER: US/10/210,290
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 134
; SEQ ID NO 94
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-290-94

Query Match          0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 881 GGATGCGCTCCCTGCTCAT 898
Db 2 GGATGCGCGCTGCTCAT 19

RESULT 146
US-10-210-290-94/c
; Sequence 94, Application US/10210290
; Publication No. US20040023378A1
; GENERAL INFORMATION:
; APPLICANT: Ming-Yi Chiang
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF KIAA1531 PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0367
; CURRENT APPLICATION NUMBER: US/10/210,290
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 134
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-290-18

Query Match          0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 881 GGATGCGCTCCCTGCTCAT 898
Db 2 GGATGCGCGCTGCTCAT 19

RESULT 147
US-10-210-802-94/c
; Sequence 94, Application US/10210802
; Publication No. US20040087523A1
; GENERAL INFORMATION:
; APPLICANT: Ming-Yi Chiang
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF KIAA1531 PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0367
; CURRENT APPLICATION NUMBER: US/10/210,802
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 134
; SEQ ID NO 94
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-802-94

Query Match          0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 881 GGATGCGCTCCCTGCTCAT 898
Db 2 GGATGCGCGCTGCTCAT 19

RESULT 148
US-10-304-107-60
; Sequence 60, Application US/10304107
; Publication No. US20040101855A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF PPAR BINDING PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0433
; CURRENT APPLICATION NUMBER: US/10/304,107
; CURRENT FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 148
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-304-107-60

Query Match          0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 309 GGTCTGCCTTTTAAAGG 326
Db 2 GTTCTGCCTTTCTAAAGG 19

RESULT 149
US-10-304-107-126/c
; Sequence 126, Application US/10304107
; Publication No. US20040101855A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF PPAR BINDING PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0433
```

```
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 881 GGATGCGCTCCCTGCTCAT 898
Db 2 GGATGCGCGCTGCTCAT 19

RESULT 147
US-10-210-802-94/c
; Sequence 94, Application US/10210802
; Publication No. US20040087523A1
; GENERAL INFORMATION:
; APPLICANT: Ming-Yi Chiang
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF KIAA1531 PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0367
; CURRENT APPLICATION NUMBER: US/10/210,802
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 134
; SEQ ID NO 94
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-802-94

Query Match          0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 881 GGATGCGCTCCCTGCTCAT 898
Db 19 GGATGCGCGCTGCTCAT 2

RESULT 148
US-10-304-107-60
; Sequence 60, Application US/10304107
; Publication No. US20040101855A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF PPAR BINDING PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0433
; CURRENT APPLICATION NUMBER: US/10/304,107
; CURRENT FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 148
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-304-107-60

Query Match          0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 309 GGTCTGCCTTTTAAAGG 326
Db 2 GTTCTGCCTTTCTAAAGG 19

RESULT 149
US-10-304-107-126/c
; Sequence 126, Application US/10304107
; Publication No. US20040101855A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF PPAR BINDING PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0433
```

; CURRENT APPLICATION NUMBER: US/10/304,107
; CURRENT FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 148
; SEQ ID NO 126
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-304-107-126

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 309 GGTCGCTTTTAAAGG 326
Db 19 GTTCTGCTTCTTAAAGG 2

RESULT 150
US-10-317-270-86
; Sequence 86, Application US/10317270
; Publication No. US20040110701A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Tamara Balac Sipes
; TITLE OF INVENTION: MODULATION OF ZINEDIN EXPRESSION
; FILE REFERENCE: RFS-0479
; CURRENT APPLICATION NUMBER: US/10/317,270
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 160
; SEQ ID NO 86
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-317-270-86

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2284 ACAGCCAACTTGGACC 2301
Db 1 ACAGCCAACTTGGGCC 18

RESULT 151
US-10-317-270-157/c
; Sequence 157, Application US/10317270
; Publication No. US20040110701A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Tamara Balac Sipes
; TITLE OF INVENTION: MODULATION OF ZINEDIN EXPRESSION
; FILE REFERENCE: RFS-0479
; CURRENT APPLICATION NUMBER: US/10/317,270
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 160
; SEQ ID NO 157
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-317-270-157

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2284 ACAGCCAACTTGGACC 2301
|||||

Db 20 ACAGCCAACTGGGCC 3

RESULT 152
US-10-745-377-21/c
; Sequence 21, Application US/10745377
; Publication No. US20040137423A1
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Pimstone, Simon
; APPLICANT: Brooks-Wilson, Angela R.
; APPLICANT: Clee, Susanne M.
; TITLE OF INVENTION: Compositions and Methods for Modulating
; FILE REFERENCE: HDL Cholesterol and Triglyceride Levels
; FILE REFERENCE: 760050-109
; CURRENT APPLICATION NUMBER: US/10/745,377
; CURRENT FILING DATE: 2003-12-23
; PRIOR FILING DATE: 2003-12-23
; PRIOR FILING DATE: 2000-09-01
; PRIOR FILING DATE: 1999-03-15
; PRIOR FILING DATE: 1999-06-08
; PRIOR FILING DATE: 1999-06-17
; PRIOR FILING DATE: 1999-09-01
; PRIOR FILING DATE: 2000-03-15
; PRIOR FILING DATE: 2000-03-15
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 256
; SOFTWARE: Word for Windows Version 6.0 (ASCII Text)
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: homo sapien
US-10-745-377-21

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 78 GATGTGATCTTGGCTCAC 95
Db 18 GGTGTGATCTGGGCTCAC 1

RESULT 153
US-10-652-795-500/c
; Sequence 500, Application US/10652795
; Publication No. US20040142346A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR- α
; FILE REFERENCE: ISPH-0501
; CURRENT APPLICATION NUMBER: US/10/652,795
; CURRENT FILING DATE: 2003-08-29
; PRIOR FILING DATE: US/09/824,322B
; PRIOR FILING DATE: 2001-04-02
; PRIOR FILING DATE: 1999-05-18
; PRIOR FILING DATE: 1999-05-18
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 503
; SEQ ID NO 500
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-652-795-500

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3353 GCACAAAGCAGACACTCA 3370
|||||
Db 18 GCACACAGAGACACTCA 1

RESULT 154

US-10-647-918-500/c
; Sequence 500, Application US/10647918
; Publication No. US20040152652A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-ALPHA
; FILE REFERENCE: ISPH-0501
; CURRENT FILING DATE: 2003-08-26
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US/09/824,322B
; PRIOR FILING DATE: 1999-05-18
; PRIOR APPLICATION NUMBER: US 09/313,932
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 503
; SEQ ID NO 500
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-647-918-500

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3353 GCACAAAGCAGACACTCA 3370
|||||
Db 18 GCACACAGAGACACTCA 1

RESULT 155

US-08-983-605-185/c
; Sequence 185, Application US/08983605A
; Publication No. US20020066118A1
; GENERAL INFORMATION:
; APPLICANT: Roder, Marion
; TITLE OF INVENTION: Microsatellite Markers for Plants of the Species
; TITLE OF INVENTION: Triticum aestivum and Tribe Triticeae and the Use of
; FILE REFERENCE: 2936.10400
; CURRENT FILING DATE: 1998-05-01
; PRIOR FILING DATE: 1995-06-28
; EARLIER APPLICATION NUMBER: DE 195 25 284.5
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 185
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-08-983-605-185

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2633 TGTTCAGAAAAAAATTG 2650
|||||
Db 19 TGGTCAGAAAAAAGATTG 2

RESULT 156

US-08-983-605-297/c
; Sequence 297, Application US/08983605A
; Publication No. US20020066118A1
; GENERAL INFORMATION:
; APPLICANT: Roder, Marion
; TITLE OF INVENTION: Microsatellite Markers for Plants of the Species
; TITLE OF INVENTION: Triticum aestivum and Tribe Triticeae and the Use of
; FILE REFERENCE: 2936.10400
; CURRENT FILING DATE: 1998-05-01
; PRIOR FILING DATE: 1995-06-28
; EARLIER APPLICATION NUMBER: DE 195 25 284.5
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 297
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-08-983-605-297

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2633 TGTTCAGAAAAAAATTG 2650
|||||
Db 19 TGGTCAGAAAAAAGATTG 2

RESULT 157

US-09-987-456-95
; Sequence 95, Application US/09987456
; Patent No. US20020123057A1
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice
; APPLICANT: Ernest S. Smith
; TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
; TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
; FILE REFERENCE: 1821.0070004
; CURRENT FILING DATE: 2001-11-14
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/262,067
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/298,087
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/249,268
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-987-456-95

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 878 ATTGGATGCTCCCTGCT 895
|||||
Db 3 ATTGTTGCTCCCTGCT 20

RESULT 158

US-09-818-991-49
; Sequence 49, Application US/09818991
; Publication No. US20030022157A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Smith, Ernest S.
; TITLE OF INVENTION: Methods of Producing a Library and Methods of Selecting Polynucle
; TITLE OF INVENTION: Of Interest
; FILE REFERENCE: 1821.0050004
; CURRENT APPLICATION NUMBER: US/09/818,991
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/192,586
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/203,343
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 60/263,226
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/271,426
; PRIOR FILING DATE: 2001-02-27
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 49
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Gus antisense
US-09-818-991-49

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 878 ATTGGATGCTCCCTGCT 895
|||||
Db 3 ATTGTTGCTCCCTGCT 20

RESULT 159

US-09-845-042-5/c
; Sequence 5, Application US/09845042
; Publication No. US20030092177A1
; GENERAL INFORMATION:
; APPLICANT: BELARDELLI, FILIPPO
; APPLICANT: SANTINI, STEFANO MARIA
; APPLICANT: PARLATO, STEFANIA
; APPLICANT: DI PUCCHIO, TIZIANA
; APPLICANT: LOGOZZI, MARIANTONIA
; APPLICANT: LAPENTA, CATERINA
; APPLICANT: FERRANTINI, MARIA
; APPLICANT: SANTODONATO, LAURA
; APPLICANT: D'AGOSTINO, GIUSEPPINA
; TITLE OF INVENTION: METHOD FOR GENERATING HIGHLY ACTIVE HUMAN DENDRITIC
; TITLE OF INVENTION: CELLS FROM MONOCYTES
; FILE REFERENCE: 618742-8/JP/B-4161
; CURRENT APPLICATION NUMBER: US/09/845,042
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-845-042-5

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 386 CTTACAGCTGCAGGCTCTT 403
|||||
Db 20 CTTACAGCTGCAGGCTCTT 3

RESULT 160

US-09-997-213-10
; Sequence 10, Application US/09997213
; Publication No. US20020164584A1
; GENERAL INFORMATION:
; APPLICANT: PamGene B.V.
; APPLICANT: van Damme, Hendrik Sibolt
; APPLICANT: Kreuwel, Hermanus Johannes Maria
; APPLICANT: Kievits, Tim
; APPLICANT: van Beuningen, Marinus Gerardus Johannus
; APPLICANT: Boender, Pieter Jacob
; TITLE OF INVENTION: DEVICE FOR PERFORMING AN ASSAY, A METHOD OF MANUFACTURING SAID
; TITLE OF INVENTION: DEVICE, AND USE OF A MEMBRANE IN THE MANUFACTURE OF SAID DEVICE
; FILE REFERENCE: 65959/7
; CURRENT APPLICATION NUMBER: US/09/997,213
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 09/843,929
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe G of Table 2
US-09-997-213-10

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 480 TGTACAGTACTGGAAG 497
|||||
Db 2 TGTACAGTACTGGAAG 19

RESULT 161

US-10-061-395-84
; Sequence 84, Application US/10061395
; Publication No. US20020192675A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Smith, Ernest S.
; TITLE OF INVENTION: Methods of Identifying Regulator Molecules
; FILE REFERENCE: 1821.0080003
; CURRENT APPLICATION NUMBER: US/10/061,395
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/271,423
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/265,880
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/265,589
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: Gus antisense specific primer
US-10-061-395-84

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 878 ATTGATGCTCCCTGCT 895
| | | | | | | | | | | | | | | | | | | | | |
Db 3 ATTGTTGCCTCCCTGCT 20

RESULT 162

US-10-052-942-127

Sequence 127, Application US/10052942

Publication No. US20030104402A1

GENERAL INFORMATION:

APPLICANT: Zauderer, Maurice

APPLICANT: Smith, Ernest

APPLICANT: Wei, Chunghwen

TITLE OF INVENTION: Methods of Producing or Identifying Intrabodies in Eukaryotic Cell

FILE REFERENCE: 1821.0090004

CURRENT APPLICATION NUMBER: US/10/052,942

CURRENT FILING DATE: 2002-01-23

PRIOR APPLICATION NUMBER: 60/298,095

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/271,422

PRIOR FILING DATE: 2001-02-27

PRIOR APPLICATION NUMBER: 60/263,200

PRIOR FILING DATE: 2001-01-24

PRIOR APPLICATION NUMBER: 60/263,225

PRIOR FILING DATE: 2001-01-23

NUMBER OF SEQ ID NOS: 154

SOFTWARE: PatentIn version 3.0

SEQ ID NO 127

LENGTH: 21

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: primer

US-10-052-942-127

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 878 ATTGATGCTCCCTGCT 895
| | | | | | | | | | | | | | | | | | | | | |
Db 3 ATTGTTGCCTCCCTGCT 20

RESULT 163

US-10-184-085A-124/c

Sequence 124, Application US/10184085A

Publication No. US20030152950A1

GENERAL INFORMATION:

APPLICANT: Garner, Harold R.

APPLICANT: Minna, John D.

APPLICANT: Luebke, Kevin, J.

APPLICANT: Balog, Robert P.

TITLE OF INVENTION: Identification of Chemically Modified Polymers

FILE REFERENCE: 119929-1035

CURRENT APPLICATION NUMBER: US/10/184,085A

CURRENT FILING DATE: 2002-10-01

PRIOR APPLICATION NUMBER: US 60/301,370

PRIOR FILING DATE: 2001-06-27

NUMBER OF SEQ ID NOS: 1291

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 124

LENGTH: 21

TYPE: DNA

ORGANISM: Homo sapiens

US-10-184-085A-124

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1548 GAGAGATAGTTGGGTGG 1565
| | | | | | | | | | | | | | | | | | | | | |
Db 20 GTGAGTTAGTTGGGTGG 3

RESULT 164

US-10-277-161-49

Sequence 49, Application US/10277161

Publication No. US20030194696A1

GENERAL INFORMATION:

APPLICANT: Zauderer, Maurice

APPLICANT: Smith, Ernest S.

TITLE OF INVENTION: Methods of Producing a Library and Methods of Selecting Polynucle

FILE REFERENCE: 1821.0050006

CURRENT APPLICATION NUMBER: US/10/277,161

CURRENT FILING DATE: 2002-10-22

PRIOR APPLICATION NUMBER: 60/192,586

PRIOR FILING DATE: 2000-03-28

PRIOR APPLICATION NUMBER: 60/203,343

PRIOR FILING DATE: 2000-05-10

PRIOR APPLICATION NUMBER: 60/263,226

PRIOR FILING DATE: 2001-01-23

PRIOR APPLICATION NUMBER: 60/271,426

PRIOR FILING DATE: 2001-02-27

PRIOR APPLICATION NUMBER: 09/818,991

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 76

SOFTWARE: PatentIn version 3.0

SEQ ID NO 49

LENGTH: 21

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Gus antisense

US-10-277-161-49

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 878 ATTGATGCTCCCTGCT 895
| | | | | | | | | | | | | | | | | | | | | |
Db 3 ATTGTTGCCTCCCTGCT 20

RESULT 165

US-10-405-877-112/c

Sequence 112, Application US/10405877

Publication No. US2003023263A1

GENERAL INFORMATION:

APPLICANT: Stahl, Andreas

APPLICANT: Hirsch, David J.

APPLICANT: Lodish, Harvey F.

APPLICANT: Gimeno, Ruth E.

APPLICANT: Tartaglia, Louis A.

TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS

FILE REFERENCE: 0399.1180-030

CURRENT APPLICATION NUMBER: US/10/405,877

CURRENT FILING DATE: 2003-04-01

PRIOR APPLICATION NUMBER: US 09/611,197

PRIOR FILING DATE: 2000-07-02

PRIOR APPLICATION NUMBER: US 09/506,252

PRIOR FILING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: US 09/465,280

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: US 09/405,504


```
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/405,505
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/232,197
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: US 09/232,200
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: US 09/232,201
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: US 09/232,195
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: US 09/232,191
; PRIOR FILING DATE: 1999-01-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 112
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Mus musculus
; OTHER INFORMATION: Targeting Sequence
US-10-403-877-112

Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1559 GGGTGGTGGACCTGTG 1576
DB 18 GGGCGGGGGACCTGTG 1

RESULT 166
US-10-349-143-10297/c
; Sequence 10297, Application US/10349143
; Publication No. US2004000584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Iliya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10297
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplification primer 99-10978 for SEQ 2432, in complement
US-10-349-143-10297

Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1961 GTGAGGATAGCCTAAAT 1978
DB 20 GTAAGGAAAGCCTAAATA 3

RESULT 167
US-10-294-228-56
```

```
; Sequence 56, Application US/10294228
; Publication No. US20040018176A1
; GENERAL INFORMATION:
; APPLICANT: Tolentino, Michael J.
; APPLICANT: Reich, Samuel Jotham
; TITLE OF INVENTION: Compositions and Methods for siRNA
; TITLE OF INVENTION: Inhibition of Angiogenesis
; FILE REFERENCE: 43826-1
; CURRENT APPLICATION NUMBER: US/10/294,228
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US 60/398,417
; PRIOR FILING DATE: 2002-07-24
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Targeting Sequence
US-10-294-228-56
```

```
Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2411 AAGAAAATAAAGCAAGA 2428
DB 2 AAGAAAGATAGACCAAGA 19
```

```
RESULT 168
US-10-294-228-57
; Sequence 57, Application US/10294228
; Publication No. US20040018176A1
; GENERAL INFORMATION:
; APPLICANT: Tolentino, Michael J.
; APPLICANT: Reich, Samuel Jotham
; TITLE OF INVENTION: Compositions and Methods for siRNA
; TITLE OF INVENTION: Inhibition of Angiogenesis
; FILE REFERENCE: 43826-1
; CURRENT APPLICATION NUMBER: US/10/294,228
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US 60/398,417
; PRIOR FILING DATE: 2002-07-24
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Targeting Sequence
US-10-294-228-57
```

```
Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2411 AAGAAAATAAAGCAAGA 2428
DB 1 AAGAAAGATAGACCAAGA 18
```

```
RESULT 169
US-10-287-226-536
; Sequence 536, Application US/10287226
; Publication No. US20040086875A1
; GENERAL INFORMATION:
; APPLICANT: Agee, Michele L.,
; APPLICANT: Alsobrook, John P.,
; APPLICANT: Berghs, Constance,
; APPLICANT: Boldog, Ference,
```



```
; Publication No. US20040110183A1
; GENERAL INFORMATION:
; APPLICANT: Ashby, Matthew
; TITLE OF INVENTION: Methods for the Survey and Genetic Analysis of Populations
; FILE REFERENCE: ASHBY/1 DIV
; CURRENT APPLICATION NUMBER: US/10/607,077A
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 09/829855
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: PCT/US01/11609
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 60/196063
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/196258
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 244
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: ribosomal DNA sequence tag isolated from
; OTHER INFORMATION: microbes in soil sample collected
; OTHER INFORMATION: in Wyoming, USA
US-10-607-077A-76

Query Match          0.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1144 AGCTTGGGACCTGGG 1159
Db 16 AGCTTGGGCTCGGG 1

RESULT 173
US-09-780-533A-2674
; Sequence 2674, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowirra, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH800.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2674
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2674

Query Match          0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1493 TTTAAAGGGGAATTC 1508
Db 1 UUUUAAAGGGGAUAUC 16

RESULT 174
US-09-848-754A-40/c
; Sequence 40, Application US/09848754A
; Publication No. US20030073207A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBH800-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-40

Query Match          0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1503 AAATTCCTCAAGACCA 1518
Db 17 AAATTCCTCAAGACCA 2

RESULT 175
US-09-848-754A-3125/c
; Sequence 3125, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBH800-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3125
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-3125

Query Match          0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1503 AAATTCCTCAAGACCA 1518
Db 16 AAATTCCTCAAGACCA 1

RESULT 176
US-09-930-423-295/c
; Sequence 295, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH800.918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 295
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-295

Query Match          0.4%; Score 14.4; DB 1; Length 17;
```

```
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 149 GCTGCTCAGTCACCA 164
Db 16 GCTGCTCAGGCACCA 1

RESULT 177
US-09-745-237A-295/c
; Sequence 295, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 295
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-295

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 149 GCTGCTCAGTCACCA 164
Db 16 GCTGCTCAGGCACCA 1

RESULT 178
US-10-339-782-462/c
; Sequence 462, Application US/10339782
; Publication No. US20030166026A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Goodman, Laurie J
; APPLICANT: Bowen, Benjamin A
; TITLE OF INVENTION: Identification of Specific Biomarkers for Breast Cancer Cells
; FILE REFERENCE: 37-000100S
; CURRENT APPLICATION NUMBER: US/10/339,782
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 462
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-782-462

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2073 AAGTAAATAATCAGAT 2088
Db 17 AAGTAAATAATCAGAT 2

RESULT 179
US-10-339-793-135/c
; Sequence 135, Application US/10339793
; Publication No. US20030180764A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Shang, Jin
```

```
; APPLICANT: Bowen, Benjamin
; TITLE OF INVENTION: GENES AFFECTED BY CHOLESTEROL TREATMENT AND DURING ADIPOGENESIS
; FILE REFERENCE: 37-000310US
; CURRENT APPLICATION NUMBER: US/10/339,793
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 443
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 135
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-793-135

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 786 ATACCTTTGAAGAGAT 801
Db 17 ATACCTCTGAAGAGAT 2

RESULT 180
US-10-339-793-332/c
; Sequence 332, Application US/10339793
; Publication No. US20030180764A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Shang, Jin
; APPLICANT: Bowen, Benjamin
; TITLE OF INVENTION: GENES AFFECTED BY CHOLESTEROL TREATMENT AND DURING ADIPOGENESIS
; FILE REFERENCE: 37-000310US
; CURRENT APPLICATION NUMBER: US/10/339,793
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 443
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 332
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-793-332

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2073 AAGTAAATAATCAGAT 2088
Db 17 AAGTAAATAATCAGAT 2

RESULT 181
US-10-138-674-4306/c
; Sequence 4306, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4306
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-4306
```

```
Query Match          0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. NO. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 317 TTTTAAAGGAACAGT 332
|||
Db 16 TTTTAAAGTAACAGT 1

RESULT 182
 US-10-287-949A-4306/c
 ; Sequence 4306, Application US/10287949A
 ; Publication No. US20040102389A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to the Treatment of Vascular Endothelial Growth Factor Receptor
 ; FILE REFERENCE: MEHB00-876-N (400/049)
 ; CURRENT APPLICATION NUMBER: US/10/287,949A
 ; CURRENT FILING DATE: 2003-04-11
 ; NUMBER OF SEQ ID NOS: 20822
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4306
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-10-287-949A-4306

```
Query Match          0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 317 TTTTAAAGGAACAGT 332
|||||
Db 16 TTTTAAAGTAACAGT 1

```

RESULT 183
US-09-925-548-17
; Sequence 17, Application US/09925548
; Patent No. US20020107216A1
; GENERAL INFORMATION:
; APPLICANT: Dedhar, Shoukat
; APPLICANT: Hannigan, Greg
; APPLICANT: Yee, Arthur
; TITLE OF INVENTION: INTEGRIN-LINKED KINASE AND ITS USES
; FILE REFERENCE: KINE001C1P4
; CURRENT APPLICATION NUMBER: US/09/925,548
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 09/390,425
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 09/035,706
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: 08/955,841
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 08/752,345
; PRIOR FILING DATE: 1996-11-19
; PRIOR APPLICATION NUMBER: 60/009,074
; PRIOR FILING DATE: 1995-12-21
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-548-17

```

Query Match 0.4%; Score 14.4; DB 1; Length 18;

Best Local Similarity	93.8%;	Pred. No. 1.1e+02;	
Matches	15; Conservative	0; Mismatches	1; Indels
			0; Gaps
			0;

Qy 3152 GCTTGATCAACATCTC 3167
|||
Db 3 GCATGATCAACATCTC 18

```

RESULT 184
US-09-969-373-2519
; Sequence 2519, Application US/09969373
; Patent NO. US2002033852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Haughe, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10152879/A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 2519
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-2519

```

```
Query Match          0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 1281 GAAATGGAGCTAATGA 1296
|||
Db 3 GAAATGGTGCTAATGA 18

```

RESULT 185
US-10-321-589-2/c
; Sequence 2, Application US/10321589
; Publication No. US20030198575A1
; GENERAL INFORMATION:
; APPLICANT: Hitachi, Ltd.
; TITLE OF INVENTION: Methods and the device for micro-particle array fabrication
; FILE REFERENCES: NIO2P0154
; CURRENT APPLICATION NUMBER: US/10/321,589
; CURRENT FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
;   - OTHER INFORMATION: Template DNA originating from synthesized oligonucleotide
US-10-321-589-2

```

```
Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 3109 TCCAGGGAACAGGTAG 3124
|||
Db 16 TCCAGGGAGCAGGTAG 1

RESULT 186
US-10-321-589-4
; Sequence 4, Application US/10321589

```
; Publication No. US20030198575A1
; GENERAL INFORMATION:
; APPLICANT: Hitachi, Ltd.
; TITLE OF INVENTION: Methods and the device for micro-particle array fabrication
; FILE REFERENCE: NT02P0154
; CURRENT APPLICATION NUMBER: US/10/321,589
; CURRENT FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Template DNA originating from synthesized oligonucleotide
US-10-321-589-4

Query Match          0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3109 TCCAGGGACACAGGTAG 3124
Db      ||||| ||||| ||||| |||||
        3 TCCAGGGAGCAGGTAG 18

RESULT 187
US-10-349-143-5818/c
; Sequence 5818, Application US/10349143
; Publication No. US2004000584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5818
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-7107 for SEQ 1884,
US-10-349-143-5818

Query Match          0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1607 TCTCTGTTCCCATGTTT 1622
Db      ||||| ||||| ||||| |||||
        17 TGTCTGTTCCCATGTTT 2

RESULT 188
US-10-128-560-86/c
; Sequence 86, Application US/10128560
; Publication No. US20030134272A1
; GENERAL INFORMATION:
; APPLICANT: Universiteit Gent
; TITLE OF INVENTION: Improved mutation analysis of the NF1 Gene
```

```
; FILE REFERENCE: UG-005-PCT
; CURRENT APPLICATION NUMBER: US/10/128,560
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 99870216.1
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: EP 00870122.9
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: UG 60/211,929
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-128-560-86

Query Match          0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1493 TTAAAGGGGAAATTC 1508
Db      ||||| ||||| ||||| |||||
        18 TTACAGGGGAAATTC 3

RESULT 189
US-10-128-560-186/c
; Sequence 186, Application US/10128560
; Publication No. US20030134272A1
; GENERAL INFORMATION:
; APPLICANT: Universiteit Gent
; TITLE OF INVENTION: Improved mutation analysis of the NF1 Gene
; FILE REFERENCE: UG-005-PCT
; CURRENT APPLICATION NUMBER: US/10/128,560
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 99870216.1
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: EP 00870122.9
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: UG 60/211,929
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 186
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-128-560-186

Query Match          0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1493 TTAAAGGGGAAATTC 1508
Db      ||||| ||||| ||||| |||||
        18 TTACAGGGGAAATTC 3

RESULT 190
US-10-251-117-573/c
; Sequence 573, Application US/10251117
; Publication No. US20030170891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: MCSwigen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor
; FILE REFERENCE: 900/042 (MH02-468-A)
; CURRENT APPLICATION NUMBER: US/10/251,117
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
```

;; PRIOR APPLICATION NUMBER: US 10/163,552
;; PRIOR FILING DATE: 2002-06-06
;; PRIOR APPLICATION NUMBER: US 60/358,580
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: US 09/916,466
;; PRIOR FILING DATE: 2001-07-25
;; PRIOR APPLICATION NUMBER: US 60/296,249
;; PRIOR FILING DATE: 2001-06-06
;; NUMBER OF SEQ ID NOS: 1213
;; SOFTWARE: Patentin version 3.0
;; SEQ ID NO 573
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
US-10-251-117-573

Query Match 0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1503 AAATTCCTCCCAAGACCA 1518
|||||
Db 18 AAATTCCTCCCAAGACCA 3

RESULT 191
US-10-251-117-880
;; Sequence 880, Application US/10251117
;; Publication No. US20030170891A1
;; GENERAL INFORMATION:
;; APPLICANT: Ribozyme Pharmaceuticals, Inc.
;; APPLICANT: McSwiggen, James
;; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor R
;; TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
;; FILE REFERENCE: 900/042 (MHB02-468-A)
;; CURRENT APPLICATION NUMBER: US/10/251,117
;; CURRENT FILING DATE: 2003-02-24
;; PRIOR APPLICATION NUMBER: US 60/393,924
;; PRIOR FILING DATE: 2002-07-03
;; PRIOR APPLICATION NUMBER: US 10/163,552
;; PRIOR FILING DATE: 2002-06-06
;; PRIOR APPLICATION NUMBER: US 60/358,580
;; PRIOR FILING DATE: 2002-02-20
;; PRIOR APPLICATION NUMBER: US 09/916,466
;; PRIOR FILING DATE: 2001-07-25
;; PRIOR APPLICATION NUMBER: US 60/296,249
;; PRIOR FILING DATE: 2001-06-06
;; NUMBER OF SEQ ID NOS: 1213
;; SOFTWARE: Patentin version 3.0
;; SEQ ID NO 880
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-251-117-880

Query Match 0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 81.2%; Pred. No. 1.1e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1503 AAATTCCTCCCAAGACCA 1518
|||||
Db 2 AAATTCCTCCCAAGACCA 17

RESULT 192
US-10-240-689-30
;; Sequence 30, Application US/10240689
;; Publication No. US20030175743A1
;; GENERAL INFORMATION:
;; APPLICANT: Brett P. Monia
;; APPLICANT: Jacqueline Wyatt

;; APPLICANT: NG, Wee Chit
;; TITLE OF INVENTION: Molecular Markers
;; FILE REFERENCE: 6565-65001/RJP
;; CURRENT APPLICATION NUMBER: US/10/240,689
;; CURRENT FILING DATE: 2002-09-30
;; PRIOR APPLICATION NUMBER: SG 200002150-1
;; PRIOR FILING DATE: 2000-04-18
;; NUMBER OF SEQ ID NOS: 41
;; SOFTWARE: Patentin version 3.2
;; SEQ ID NO 30
;; LENGTH: 19
;; TYPE: DNA
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: Primer
US-10-240-689-30

Query Match 0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2455 CGATATTGACCAAGGA 2470
|||||
Db 2 CGATATTGACCAAGGA 17

RESULT 193

US-10-349-143-8906/c
;; Sequence 8906, Application US/10349143
;; Publication No. US2004000584A1
;; GENERAL INFORMATION:
;; APPLICANT: Cohen, Daniel
;; APPLICANT: Blumenfeld, Marta
;; APPLICANT: Chumakov, Ilya
;; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;; FILE REFERENCE: GENSET.020CPI
;; CURRENT APPLICATION NUMBER: US/10/349,143
;; CURRENT FILING DATE: 2003-01-21
;; PRIOR APPLICATION NUMBER: US/09/422,978
;; PRIOR FILING DATE: 1999-10-20
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;; NUMBER OF SEQ ID NOS: 11796
;; SEQ ID NO 8906
;; LENGTH: 19
;; TYPE: DNA
;; ORGANISM: Homo Sapiens
;; FEATURE:
;; NAME/KEY: primer_bind
;; LOCATION: 1..19
;; OTHER INFORMATION: downstream amplification primer 99-1964 for SEQ 1041, in compleme
US-10-349-143-8906

Query Match 0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 429 CAGAGACCAAGACCA 444
|||||
Db 19 CAGAGACCAAGACCA 4

RESULT 194

US-09-754-167-65
;; Sequence 65, Application US/09754167
;; Patent No. US20010019328A1
;; GENERAL INFORMATION:
;; APPLICANT: Brett P. Monia
;; APPLICANT: Jacqueline Wyatt

```
; TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
; FILE REFERENCE: RTS-0140
; CURRENT APPLICATION NUMBER: US/09/754,167
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-754-167-65

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2582 ATAGAAAATATAAGAT 2597
Db 1 ATAGAAAATATAAAT 16
|||||

RESULT 195
US-09-912-724-49/c
; Sequence 49, Application US/09912724
; Publication No. US20030083280A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; TITLE OF INVENTION: ANTISENSE MODULATION OF C-REACTIVE PROTEIN EXPRESSION
; FILE REFERENCE: ISPH-0584
; CURRENT APPLICATION NUMBER: US/09/912,724
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 63
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-912-724-49

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1980 CAGCTCTGGAGATAA 1995
Db 20 CAGATCTGGAGATAA 5
|||||

RESULT 196
US-09-920-033-106/c
; Sequence 106, Application US/09920033
; Publication No. US20030087853A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; TITLE OF INVENTION: ANTISENSE MODULATION OF APOLIPOPROTEIN B EXPRESSION
; FILE REFERENCE: ISPH-0592
; CURRENT APPLICATION NUMBER: US/09/920,033
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 106
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-920-033-106

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
```

```
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1294 TGAAGGATTCATGAA 1309
Db 17 TGAAGGATTCATGAA 2
|||||

RESULT 197
US-10-282-174-132/c
; Sequence 132, Application US/10282174
; Publication No. US2003024380A1
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; FILE REFERENCE: 37481-3308
; CURRENT APPLICATION NUMBER: US/10/282,174
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-282-174-132

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1935 GTCCATATGCAGACCA 1950
Db 16 GTCCATATGCAGATCA 1
|||||

RESULT 198
US-10-238-443-41
; Sequence 41, Application US/10238443
; Publication No. US20030083302A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF RECOL5 EXPRESSION
; FILE REFERENCE: RTS-0203
; CURRENT APPLICATION NUMBER: US/10/238,443
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US/09/798,185
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 92
```



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; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-238-443-41

Query Match          0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 615 AGTCGCGCAAGCAGCT 630
      ||||| ||||| |||||
Db 1 AGTCGCGCAAGCAGCT 16

RESULT 199
US-10-309-362-41
; Sequence 41, Application US/10309362
; Publication No. US20030114412A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; TITLE OF INVENTION: ANTISENSE MODULATION OF REOQL5 EXPRESSION
; FILE REFERENCE: RTS-0203
; CURRENT APPLICATION NUMBER: US/10/309,362
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/798,185
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 92
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-309-362-41

Query Match          0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 615 AGTCGCGCAAGCAGCT 630
      ||||| ||||| |||||
Db 1 AGTCGCGCAAGCAGCT 16

RESULT 200
US-10-012-984-66
; Sequence 66, Application US/10012984
; Publication No. US20030118561A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE 4 EXPRESSION
; FILE REFERENCE: RTS-0334
; CURRENT APPLICATION NUMBER: US/10/012,984
; CURRENT FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 92
; SEQ ID NO 66
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-012-984-66

Query Match          0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1931 TGCAGTCCATATGCAG 1946
      || ||||| ||||| |||||
```

```
Db 2 TGCAGTCCATATGCAG 17

RESULT 201
US-10-388-281-26
; Sequence 26, Application US/10388281
; Publication No. US20030175784A1
; GENERAL INFORMATION:
; APPLICANT: Leary, Jeffrey J.
; APPLICANT: Tal-Singer, Ruth
; TITLE OF INVENTION: Method For Detecting, Analyzing, and
; Mapping RNA Transcripts
; FILE REFERENCE: P50772C1
; CURRENT APPLICATION NUMBER: US/10/388,281
; CURRENT FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: 09/719,714
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/090,464
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: PCT/US99/13813
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-388-281-26

Query Match          0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1477 GTGGAGGTGGATGGTC 1492
      ||||| ||||| |||||
Db 5 GTGGAGGTGGATGGTC 20

RESULT 202
US-10-126-355-109/c
; Sequence 109, Application US/10126355
; Publication No. US20030198965A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF HYDROXYSTERIOD
; FILE REFERENCE: RTS-0428
; CURRENT APPLICATION NUMBER: US/10/126,355
; CURRENT FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-126-355-109

Query Match          0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1214 ACAGTTCATCATGAGA 1229
      ||||| ||||| |||||
Db 17 ACAGTTCATCATGAGA 2

RESULT 203
US-10-147-196-106/c
; Sequence 106, Application US/10147196
; Publication No. US20030215943A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF APOLIPOPROTEIN B EXPRESSION
; FILE REFERENCE: ISFH-0664
; CURRENT APPLICATION NUMBER: US/10/147,196
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 124
; SEQ ID NO 106
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-147-196-106

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1294 TGAAGGATTCATGAA 1309
      ||||| |||||
Db 17 TGAAGGATTCATGAA 2

RESULT 204
US-10-380-931-119
; Sequence 119, Application US/10380931
; Publication No. US20030215944A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
; FILE REFERENCE: RSP-0187
; CURRENT APPLICATION NUMBER: US/10/380,931
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: 09/676,610
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-931-119

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1503 AAATTCCCAAGACCA 1518
      ||||| |||||
Db 1 AAATTCCCAAGACCA 16

RESULT 205
US-10-388-263-642/c
; Sequence 642, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowser, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasnor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
```

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; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; APPLICANT: Isis-4503
; FILE REFERENCE: ISFH-0664
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 642
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-642

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1294 TGAAGGATTCATGAA 1309
      ||||| |||||
Db 17 TGAAGGATTCATGAA 2

RESULT 206
US-10-174-559-73/c
; Sequence 73, Application US/10174559
; Publication No. US20030232773A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF DRK1 EXPRESSION
; FILE REFERENCE: PTS-0006
; CURRENT APPLICATION NUMBER: US/10/174,559
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 112
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-174-559-73

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1797 CCTGGACCTTAGCATT 1812
      ||||| |||||
Db 17 CCTGGACCTTAGCATT 2

RESULT 207
US-10-174-014-24/c
; Sequence 24, Application US/10174014
; Publication No. US20040005292A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMRT EXPRESSION
; FILE REFERENCE: PTS-0012
; CURRENT APPLICATION NUMBER: US/10/174,014
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 24
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
```

US-10-174-014-24

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1027 CAAGGAGCGCAGAG 1042
|||||
Db 19 CAAGGAGCGCAGAG 4

RESULT 208

US-10-174-014-56

; Sequence 56, Application US/10174014
; Publication No. US20040005292A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMRT EXPRESSION
; FILE REFERENCE: PTS-0012
; CURRENT APPLICATION NUMBER: US/10/174,014
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-174-014-56

Query Match

Best Local Similarity 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1027 CAAGGAGCGCAGAG 1042
|||||
Db 2 CAAGGAGCGCAGAG 17

RESULT 209

US-10-349-143-7273

; Sequence 7273, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7273
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1...20
; OTHER INFORMATION: upstream amplification primer 99-3390 for SEQ 3339,
US-10-349-143-7273

Query Match

Best Local Similarity 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3123 AGAGGACATTCCTTTT 3138
|||||
Db 4 AGAGTACATTCCTTTT 19

RESULT 210

US-10-188-883-38

; Sequence 38, Application US/10188883
; Publication No. US20040006005A1
; GENERAL INFORMATION:
; APPLICANT: Bhanot, Sanjay
; TITLE OF INVENTION: USE OF INTEGRIN-LINKED KINASE INHIBITORS FOR TREATING INSULIN RES
; FILE REFERENCE: ISPH-0687
; CURRENT APPLICATION NUMBER: US/10/188,883
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide.
US-10-188-883-38

Query Match

Best Local Similarity 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2884 CTTGTATGGAATACGG 2899
|||||
Db 4 CTTGTATGGAATACGG 19

RESULT 211

US-10-289-762-2103/c

; Sequence 2103, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffois, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2103
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-2103

Query Match

Best Local Similarity 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3254 TGGAGTGAATGGAAT 3269
|||||
Db 20 TGGAGGGAATGGAAT 5

RESULT 212

US-10-131-827-9057/c

; Sequence 9057, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert

```
; APPLICANT: LY, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 9057
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-131-827-9057

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 113 TCTTCTGGCTGCTTC 128
    |||||
Db 18 TCTTCTGGCTGCTTC 3

RESULT 213
US-10-210-429-23
; Sequence 23, Application US/10210429
; Publication No. US20040023379A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HEPATOMA-DERIVED GROWTH FACTOR EXPRESSION
; FILE REFERENCE: PTS-0048
; CURRENT APPLICATION NUMBER: US/10/210,429
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 148
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-429-23

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2187 TTCTAGAACTGAAGT 2202
    |||||
Db 5 TTCTAGAACTGAAT 20

RESULT 214
US-10-363-828-59/c
; Sequence 59, Application US/10363828
; Publication No. US20040076973A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF UBIQUITIN PROTEIN LIGASE EXPRESSION
; FILE REFERENCE: RTPSP-0164
; CURRENT APPLICATION NUMBER: US/10/363,828
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 09/657,481
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 93
```

```
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-363-828-59

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1245 ATGATATGGCATATGC 1260
    |||||
Db 18 ATGATATGGCATCTGC 3

RESULT 215
US-10-302-027-80
; Sequence 80, Application US/10302027
; Publication No. US20040102391A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF GANKYRIN EXPRESSION
; FILE REFERENCE: PTS-0068
; CURRENT APPLICATION NUMBER: US/10/302,027
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 80
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-302-027-80

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2061 AGTACTTTTAAAGT 2076
    |||||
Db 2 AATACTTTTAAAGT 17

RESULT 216
US-10-673-523-66
; Sequence 66, Application US/10673523
; Publication No. US20040110713A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE 4 EXPRESSION
; FILE REFERENCE: RTS-0334
; CURRENT APPLICATION NUMBER: US/10/673,523
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US/10/012,984
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 92
; SEQ ID NO 66
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-673-523-66

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1931 TGGAGTCCATATCCAG 1946
    |||||
```

```
Db      2  TGCAGTCCATATGCAG 17

RESULT 217
US-10-182-644A-2
; Sequence 2, Application US/10182644A
; Publication No. US20040115789A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America
; TITLE OF INVENTION: Hybrid adeno-retroviral vector for the transfection
; TITLE OF INVENTION: of cells.
; FILE REFERENCE: 56873
; CURRENT APPLICATION NUMBER: US/10/182,644A
; CURRENT FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: 60/179,327
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR primer
US-10-182-644A-2

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3178  CAAAACCTAGAGCCAGG 3193
          |||||
Db      2  CAAAACCTAGAGCCTGG 17

RESULT 218
US-10-316-540-87
; Sequence 87, Application US/10316540
; Publication No. US20040126761A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Ravi Jain
; TITLE OF INVENTION: MODULATION OF ALPHA-METHYLACYL-COA RACEMASE EXPRESSION
; FILE REFERENCE: RTS-0471
; CURRENT APPLICATION NUMBER: US/10/316,540
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 87
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-316-540-87

Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1689  TTGTCAAGCAGCTAA 1704
          |||||
Db      5  TTTTCAAGCAGCTAA 20

RESULT 219
US-10-316-540-153/c
; Sequence 153, Application US/10316540
; Publication No. US20040126761A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Ravi Jain
; TITLE OF INVENTION: MODULATION OF ALPHA-METHYLACYL-COA RACEMASE EXPRESSION
; FILE REFERENCE: RTS-0471
```

```
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; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 153
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-316-540-153

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Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1689  TTGTCAAGCAGCTAA 1704
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Db      16  TTTTCAAGCAGCTAA 1

Search completed: September 28, 2004, 08:39:28
Job time : 10 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 28, 2004, 08:40:54 ; Search time 0.001 Seconds
(without alignments)
1573.110 Million cell updates/sec

Title: US-10-798-923A-4
Perfect score: 3405
Sequence: 1 cgcacacccaagtccaag.....acacactcaaaaaaaaaa 3405

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 11 seqs, 231 residues

Total number of hits satisfying chosen parameters: 22

Minimum DB seq length: 8

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 11 summaries

Database : rst4.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	16.8	0.5	23	1	ACCESSION:BG924552
C 2	16.4	0.5	19	1	ACCESSION:AZ775624
C 3	16.2	0.5	23	1	ACCESSION:AZ312575
C 4	15.8	0.5	21	1	ACCESSION:AZ345890
C 5	15.6	0.5	22	1	ACCESSION:AZ387833
C 6	15.4	0.5	22	1	ACCESSION:CF318882
C 7	15.2	0.4	20	1	ACCESSION:AZ609786
C 8	15.2	0.4	20	1	ACCESSION:AZ845673
C 9	15.2	0.4	21	1	ACCESSION:AZ871716
C 10	15	0.4	20	1	ACCESSION:CF319428
C 11	15	0.4	20	1	ACCESSION:AZ772040

ALIGNMENTS

RESULT 1
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LOCUS HNC27-1-H2-R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
DEFINITION 23 bp mRNA linear EST 06-NOV-2001
sequence.
ACCESSION BG924552
VERSION BG924552.1 GI:14319075
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 23)
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
TITLE Identification and initial characterization of 5000 expressed

JOURNAL
MEDLINE
PUBMED
COMMENT
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
Osteoarthr. Cartil. 9 (7), 641-653 (2001)
21482651
11597177
Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@gsk.com
Seq primer: T7.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/notes="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
Directional"

FEATURES

source

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Best Local Similarity 90.0%; Pred. No. 1.8;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3386 ACACACTCAAAAAAAAAA 3405
Db 21 ACACACCCCAAAAAAAAAA 2

RESULT 2

AZ775624

LOCUS

DEFINITION

2M0008E01R Mouse 10kb plasmid UUGCJM library Mus musculus genomic

clone UUGC2M0008E01 R, genomic survey sequence.

ACCESSION AZ775624

VERSION AZ775624.1 GI:12902356

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D. Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0008 row: E column: 01

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

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/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0008E01"

/clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 15.8; DB 1; Length 21;
 Best Local Similarity 89.5%; Pred. No. 3;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2739 TTCTTAATAGATTG 2757
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 Db 19 TTGTGAATAGATTG 1

RESULT 5
 AZ387833 22 bp DNA linear GSS 02-OCT-2000
 LOCUS 1M0147F24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0147F24 R, genomic survey sequence.

ACCESSION AZ387833
 VERSION AZ387833.1 GI:10501541
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

FEATURES
 source
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0147F24"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"

High quality sequence stop: 22.
 Location/Qualifiers

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 15.6; DB 1; Length 22;
 Best Local Similarity 81.8%; Pred. No. 3.1;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2515 CTTTAGAAATCTATGTTT 2536
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 Db 1 CTTTAAATAATATTATTT 22

RESULT 6
 CF318882/c

LOCUS 22 bp mRNA linear EST 15-AUG-2003
 DEFINITION HD--09-C23.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--09-C23, mRNA sequence.

ACCESSION CF318882
 VERSION CF318882.1 GI:33690643
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza. 1 (bases 1 to 22)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..22

/organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="HD--09-C23"
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 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 15.4; DB 1; Length 22;

Query Match	0.4%;	Score 15.2;	DB 1;	Length 20;
Best Local Similarity	85.0%;	Pred. No. 4;		
Matches	17;	Conservative	0;	Mismatches 3; Indels 0; Gaps 0;

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QY      1422 TCACACAGCACTCAGGATT 1441
Db      20 TCACACAGCACTCAGGATT 1

RESULT 9
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LOCUS   AZ871716
DEFINITION 21 bp DNA linear GSS 21-FEB-2001
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          clone UUGC2M0184B14 R, genomic survey sequence.
ACCESSION AZ871716
VERSION   AZ871716.1 GI:13078194
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D. Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Em. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0184 row: B column: 14
          Seq primer: CACACAGGAACAGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 21.
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     /sex="Male"
     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
     /clone_lib="Mouse 10kb plasmid UUGC1M library"
     /notes="vector: PWD42nv; Purified genomic DNA from M.
     musculus C57BL/6J (male) was obtained from the Jackson
     Laboratory Mouse DNA Resource
     (http://www.jax.org/resources/documents/dnares/). The DNA
     was hydrodynamically sheared by repeated passage through a
     0.005 inch orifice at constant velocity. The sheared DNA
     was blunt end-repaired with T4 DNA polymerase and T4
     polynucleotide kinase. Adaptor oligonucleotides were
     ligated to the blunt ends in high molar excess. The
     adaptor DNA was purified and size-selected for a 9.5 to
     10.5 kb range using preparative agarose gel
     electrophoresis. Vector DNA was prepared from a derivative
     of PWD42 [gi14732114|gb|AF129072.1], a copy-number
     inducible derivative of plasmid R1. The vector was ligated
     with adaptors complementary to the insert adaptors and
     purified. The sheared, adaptor mouse DNA was annealed to
     adaptor vector DNA, and transformed into
     chemically-competent E. coli XL10-Gold (Stratagene) cells
     and selected for ampicillin resistance."
Query Match      0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 3.8;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      45 AGCAGGTTTACTCTAGGCA 64
Db      20 AGCAGGTTTATTCAGGCA 1

RESULT 10
CF319428/c
LOCUS   CF319428
DEFINITION 20 bp mRNA linear EST 15-AUG-2003
          HD--09-O20.b1 OshDACL1-overexpressing transgenic rice plasmid cDNA
          library (HD) Oryza sativa cDNA clone HD--09-O20, mRNA sequence.
ACCESSION CF319428
VERSION   CF319428.1 GI:33691189
KEYWORDS  EST.
SOURCE    Oryza sativa
ORGANISM  Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
          Location/Qualifiers
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     /clone="HD--09-O20"
     /tissue_type="callus"
     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
     /lab_host="E.coli DH108"
     /clone_lib="OshDACL1-overexpressing transgenic rice plasmid
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     /notes="vector: pCR4-TOPO; Site 1: EcoRI; Callus was
     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
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     derived from rice Histone Deacetylase overexpression
     line."
Query Match      0.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      20 CTCAAAAAATAAAAAA 6

RESULT 11
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          1M0574G11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
          clone UUGC1M0574G11 R, genomic survey sequence.
ACCESSION AZ772040
VERSION   AZ772040.1 GI:12894936
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D. Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Em. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0184 row: B column: 14
          Seq primer: CACACAGGAACAGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 21.
          Location/Qualifiers
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     /mol_type="genomic DNA"
     /strain="C57BL/6J"
     /db_xref="taxon:10090"
     /clone="UUGC2M0184B14"
     /sex="Male"
     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
     /clone_lib="Mouse 10kb plasmid UUGC1M library"
     /notes="vector: PWD42nv; Purified genomic DNA from M.
     musculus C57BL/6J (male) was obtained from the Jackson
     Laboratory Mouse DNA Resource
     (http://www.jax.org/resources/documents/dnares/). The DNA
     was hydrodynamically sheared by repeated passage through a
     0.005 inch orifice at constant velocity. The sheared DNA
     was blunt end-repaired with T4 DNA polymerase and T4
     polynucleotide kinase. Adaptor oligonucleotides were
     ligated to the blunt ends in high molar excess. The
     adaptor DNA was purified and size-selected for a 9.5 to
     10.5 kb range using preparative agarose gel
     electrophoresis. Vector DNA was prepared from a derivative
     of PWD42 [gi14732114|gb|AF129072.1], a copy-number
     inducible derivative of plasmid R1. The vector was ligated
     with adaptors complementary to the insert adaptors and
     purified. The sheared, adaptor mouse DNA was annealed to
     adaptor vector DNA, and transformed into
     chemically-competent E. coli XL10-Gold (Stratagene) cells
     and selected for ampicillin resistance."
Query Match      0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 3.8;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0574 row: G column: 11
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.

FEATURES

Location/Qualifiers
 1..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U0GCLM0574G11"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid U0GCLM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 15; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.3;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3391 CTCAAAAA 3405
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 Db 16 CTCAAAAA 2

Search completed: September 28, 2004, 08:40:55
 Job time : 1 secs